


```

RN [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL: Q8AYY9; Q8AYY9.
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XX /strain="Hunan"
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XX /product="polyhedrin"
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XX GSVLVINKNSQYKVGISETRFKALKEVREGORNDSDYEYNOISYYPNGDAHKFHSNA
XX KPAIOLIFSPSVWRTIKMAGNSVSPDDYLORSHPMWATGIRKRIKRGDEIYGS
XX HYPELPHEYNISLAVSGVHKNPSSYVWGSANHVMDVFOCDLALRRCNRYMAELELVN
XX HYISPNAPYIDINNHSGVALSNHQ"
XX
SQ Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;
Query Match 0.1%; Score 13; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130468 TGTGTGTGTAGTT 130480
DB 88 TGTGTGTGTAGTT 76

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DR SPTREMBL: Q8AYY9; Q8AYY9.
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XX key Location/Qualifiers
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XX source 1. .747
XX /db_xref="taxon:208509"
XX /mol_type="genomic DNA"
XX /note="substitute-host"
XX /organism="Dendrolimus punctatus cypovirus 1"
XX /strain="Hunan"
XX /specific_host="Spodoptera exigua"
XX 1. .747
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XX /db_xref="SPTREMBL:Q8AYY9"
XX /note="forms crystals/polyhedra"
XX /product="polyhedrin"
XX /protein_id="AA117828.1"
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XX GSVLVINKNSQYKVGISETRFKALKEVREGORNDSDYEYNOISYYPNGDAHKFHSNA
XX KPAIOLIFSPSVWRTIKMAGNSVSPDDYLORSHPMWATGIRKRIKRGDEIYGS
XX HYPELPHEYNISLAVSGVHKNPSSYVWGSANHVMDVFOCDLALRRCNRYMAELELVN
XX HYISPNAPYIDINNHSGVALSNHQ"
XX
SQ Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;
Query Match 0.1%; Score 13; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130468 TGTGTGTGTAGTT 130480
DB 88 TGTGTGTGTAGTT 76

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RESULT 4

MMSPRO2 standard; DNA; VRL; 1122 BP.

AC J02261;

SV J02261.1

XX 07-MAY-1992 (Rel. 31, Created)

DT 17-APR-2002 (Rel. 71, Last updated, Version 6)

XX Moloney murine sarcoma virus polyprotein gene, partial cds.

DE proviral gene; terminal repeat.

KM

KX Moloney murine sarcoma virus

XX Viruses; Retroviridae; Gammaretrovirus.

OC

XX

RN [1]

RP 16-1122

RA MEDLINE: 81013872.

RX PUBMED: 6251454.

RX Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;

RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of

RT replication, analogy to bacterial transposons, and an unexpected gene";

RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).

XX

RN [2]

RP 1-1122

RA MEDLINE: 81013873.

RX PUBMED: 6251455.

RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;

RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the

RT 5' long terminal repeat and adjacent cellular sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).

XX

RN [3]

RP 1-1122

RA MEDLINE: 81052384.


```

RX PUBMED; 6159543.
RA Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
RT allows detection of a new retroviral gene product";
RL Nature 287(5785):801-805(1980).
XX
XX GOA; Q83401.
DR SPTREMBL; Q83401; Q83401.
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FT source 1..1122
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /proviral
FT /organism="Moloney murine sarcoma virus"
FT <1..1122
FT /product="RNA polII transcript mRNA"
FT CDS
FT <1..564
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FT SLEKSLTSLSEVLDNRGLDLFLKEGCLCAALKECCFADHRTGLYRDSMAKLER
FT LNDROKLFSTOGMEFGLNRSFMTLTISTMGPLIVLMLILKEPCILNKLNVDFKVD
FT RISVVALVLTQOFHOLKPIECEP"
FT <1..282
FT /product="p15e protein"
FT mat_peptide 283..561
FT /product="r protein"
FT 144
FT /note="a may be g (11)"
FT 302
FT /note="t may be c (11)"
FT 530
FT /note="t may be a (11)"
FT 952
FT /note="a may be t (11)"
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Query Match 0.1%; Score 13; DB 1; Length 1122;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125082 AGAAGAGGACT 125094
Db 42 AGAAGAGGACT 54

RESULT 5
MMSPROL standard; DNA; VRL; 660 BP.
XX
XX J02260;
XX
XX J02260.1
XX
XX 05-NOV-1994 (Rel. 41, Created)
XX 12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX
XX Moloney murine sarcoma virus long terminal repeat.
XX terminal repeat.
XX
XX Moloney murine sarcoma virus
XX Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.
XX
XX [1]
XX 1-660
XX
XX RP

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RX MEDLINE; 81013873.
RX PUBMED; 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RT 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [2]
XX 441-545
XX MEDLINE; 82060256.
RX PUBMED; 6946480.
RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT "Identification of a RNA polymerase II initiation site in the long terminal
RT repeat of Moloney murine leukemia viral DNA";
RL Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX
XX On Oct 4, 1994 this sequence version replaced gi:332090.
XX + strand shown. LTR in definition stands for 'long terminal
XX repeat'.
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FH source 1..660
FH /db_xref="taxon:11809"
FH /mol_type="genomic DNA"
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FH /proviral
FH /organism="Moloney murine sarcoma virus"
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FH /product="RNA polII transcript mRNA"
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XX
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Query Match 0.1%; Score 12; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132750 TCCCTCTCCCA 132761
Db 34 TCCCTCTCCCA 45

RESULT 6
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XX
XX J02260;
XX
XX J02260.1
XX
XX 05-NOV-1994 (Rel. 41, Created)
XX 12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX
XX Moloney murine sarcoma virus long terminal repeat.
XX terminal repeat.
XX
XX Moloney murine sarcoma virus
XX Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.
XX
XX [1]
XX 1-660
XX MEDLINE; 81013873.
XX PUBMED; 6251455.
XX
XX Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
XX "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
XX 5' long terminal repeat and adjacent cellular sequences";
XX Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [2]
XX 441-545
XX MEDLINE; 82060256.
XX PUBMED; 6946480.
XX
XX RP

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RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT "Identification of a RNA polymerase II initiation site in the long terminal
RL repeat of Moloney murine leukemia viral DNA";
RR Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX
CC On Oct 4, 1994 this sequence version replaced gi:332090.
CC + strand shown. 'LTR' in definition stands for 'long terminal
CC repeat'.
XX
XX Key Location/Qualifiers
FH
FH source 1. .660
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FT /mol_type="genomic DNA"
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FT /proviral
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FT mRNA 486. .>660
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Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 119809 GCGCTACTTAA 119820
DB 159 GCGCTACTTAA 148

RESULT 7
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XX
XX J02261;
XX
XX J02261.1
XX
XX 07-MAY-1992 (Rel. 31, Created)
XX 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
XX Moloney murine sarcoma virus polyprotein gene, partial cds.
XX proviral gene; terminal repeat.
XX
XX Moloney murine sarcoma virus
XX Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
XX
XX [1]
XX 16-1122
XX MEDLINE; 81013872.
XX PUBMED; 6251454.
XX
XX Surcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
RT replications, analogy to bacterial transposons, and an unexpected gene";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX [2]
XX 1-1122
XX MEDLINE; 81013873.
XX PUBMED; 6251455.
XX
XX Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RT 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [3]
XX 1-1122
XX MEDLINE; 81052384.
XX PUBMED; 6159543.
XX
XX Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence

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RT allows detection of a new retroviral gene product";
RL Nature 287(5785):801-805(1980).
XX
XX GOA; 083401.
XX SPTREMBL; 083401; 083401.
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XX Key Location/Qualifiers
FH
FH source 1. .1122
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FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
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FT CDS <1. .564
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FT /db_xref="SPTREMBL:083401"
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FT SNEKSLTSLSEVVLNRRGLDLFLKEGGICAAIKKECCFYADHTGLYRDSMAKTRER
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FT /product="r protein"
FT 144
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FT 302
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FT 530
FT /note="t may be a ([1])"
FT 952
FT /note="a may be t ([1])"
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Query Match 0.1%; Score 12; DB 1; Length 1122;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 119809 GCGCTACTTAA 119820
DB 653 GCGCTACTTAA 642

RESULT 8
ADREAR3RE
ID ADREAR3RE standard; DNA; VRL; 1980 BP.
XX
XX M94458;
XX
XX M94458.1
XX
XX 11-DEC-1992 (Rel. 34, Created)
XX 04-MAR-2000 (Rel. 63, Last updated, Version 5)
XX
XX Mastadenovirus serotype 11 early 3 region.
XX early 3 region.
XX
XX Human adenovirus type 11
XX Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
XX Human adenovirus B.
XX
XX [1]
XX 1-1980
XX MEDLINE; 93033102.
XX PUBMED; 1413499.

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RA Mei Y.-F., Madell G.;
RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
of genome type Ad1p and Ad11a.";
RL Virology 191(1):125-133(1992).
XX
DR GOA: P15140.
DR SWISS-PROT: P15140; E3GL_ADE35.
DR SWISS-PROT: P35768; E320_ADE1P.
DR SWISS-PROT: P35770; E321_ADE1P.
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Query Match 0.1%; Score 12; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 4.9; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 0;
QY 131630 ACNAAACCATGT 131641
DB 1331 ACNAAACCATGT 1342
RESULT 9
AF541985 standard; DNA; VRL; 747 BP.
XX AF541985;
XX AF541985.1
SV
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.
XX
XX
OS Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX
RN [1]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT
RL Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
DR SPTREMBL: Q8AYY9; Q8AYY9.
XX
FH Key Location/Qualifiers
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FT /strain="Hunan"
FT /codon_start=1
FT CDS

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FT /product="polyhedrin"
FT /protein_id="A01782.1"
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KPRALQIIFSPVNWRTIMAKGNSVSPDDYLOSHPMETAGIKYRKIRGGEIYGS
HFEELPHEVNSISLAVSGVHKNPSSYVNSAHNMVDVFOCDLALRFCHRYMAEELVN
HYISPRAYVLDINNSYGVALSNNQ"
XX
SQ Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;
Query Match 0.1%; Score 11; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Gaps 0;
Matches 11; Conservative 0; Indels 0;
QY 122009 TTCTGCACCG 122019
DB 628 TTCTGCACCG 638
RESULT 10
AF541986 standard; DNA; VRL; 747 BP.
XX AF541986;
XX AF541986.1
SV
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polyhedrin gene, complete cds.
XX
XX
OS Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX
RN [1]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT
RL Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
DR SPTREMBL: Q8AYY9; Q8AYY9.
XX
FH Key Location/Qualifiers
FT source 1. .747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /note="substitute-host"
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FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
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FT /db_xref="SPTREMBL:Q8AYY9"
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FT /product="polyhedrin"
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FT      HTSPNAVPEYLDINNHSYVALSNHQ"
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      Best Local Similarity 100.0%; Pred. No. 15;
      Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      122009 TTCTGCACACG 122019
      |||||||
Db      628 TTCTGCACACG 638

RESULT 11
ADREAR3RE/C
ID      ADREAR3RE      standard; DNA; VRL; 1980 BP.
XX
AC      M94458;
XX
SV      M94458.1
XX
DT      11-DEC-1992 (Rel. 34, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 5)
XX
DE      Mastadenovirus serotype 11 early 3 region.
XX
FH      early 3 region.
XX
OS      Human adenovirus type 11
OC      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
XX      Human adenovirus B.
XX      [1]
XX      1-1980
XX      MEDLINE: 93033102.
XX      PUBMED: 1413499.
XX      RA      Mel Y.-F., Wadell G.;
XX      RT      "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
XX      of genome type Ad1p and Ad11a.";
XX      Virology 191(1):125-133(1992).
XX
DR      GOA: P15140.
DR      SWISS-PROT: P15140; E3GL_ADEJ35.
DR      SWISS-PROT: P35768; E320_ADE1P.
DR      SWISS-PROT: P35770; E321_ADE1P.
XX
FH      Key      Location/Qualifiers
FH
FT      source      1. 1980
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Slobitski"
XX
SQ      Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;
      Query Match      0.1%; Score 11; DB 1; Length 1980;
      Best Local Similarity 100.0%; Pred. No. 7.6;
      Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      123558 GGGTGTGGTGG 123568
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Db      1004 GGGTGTGGTGG 994

RESULT 12
ADRE3GENE
ID      ADRE3GENE      standard; DNA; VRL; 2480 BP.
XX
AC      L08231;
XX
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SV      L08231.1
XX
XX      08-JUL-1993 (Rel. 36, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 3)
XX
DE      Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
XX
XX      fiber protein.
XX
OS      Human adenovirus type 11
OC      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
XX      Human adenovirus B.
XX      [1]
XX      1-2480
XX      MEDLINE: 93276532.
XX      PUBMED: 8503168.
XX      RA      Mel Y.-F., Wadell G.;
XX      RT      "Hemagglutination properties and nucleotide sequence analysis of the fiber
XX      gene of adenovirus genome types 11p and 11a";
XX      Virology 194(2):453-462(1993).
XX
DR      GOA: P35774.
DR      SWISS-PROT: P35774; F1BP_ADE1P.
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FH      Key      Location/Qualifiers
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FT      /db_xref="SWISS-PROT:P35774"
FT      /gene="E3"
FT      /protein_id="AAA42490.1"
FT      /translation="MTKRVRLSDSFNFVPEYDESTSQHPFINPGFISPNGFTOSPNGV
FT      LTKCLIPLTGGLGSLQKYGGLVDVTNGFLKENTSATPIYKGTGSLGPLGAGIG
FT      TNEKRLCKIKGGGILTFENSNICIDDDNITLMTGVNPEANCOIMNSSESDCKLITLIV
FT      KTGALVAPYVIVGVSNNRNMTTHRRINTAFELFEDSTGNLTRLSSLEKTPLNHSQ
FT      NMATGATLNKGFEMPTTAYPFNDNSREKENYIYGTCVYASDRAPIDISVNLNRA
FT      INDETSYCIKRTMSWNTGDAPEVQTSATLVTSPEFFYIREDDD"
XX
SQ      Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;
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      Best Local Similarity 100.0%; Pred. No. 6.2;
      Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      124149 TTTAAAGCGCT 124159
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Db      2297 TTTAAAGCGCT 2307

RESULT 13
MMJAI
ID      MMJAI      standard; RNA; VRL; 126 BP.
XX
AC      J02243;
XX
SV      J02243.1
XX
XX      01-OCT-1996 (Rel. 49, Created)
DT      11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX
DE      Macaca mulatta and arcotoides type C retrovirus, 5' end.
XX
XX      Macaca mulatta and arcotoides type C retrovirus;
XX      Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses;
OC
```

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OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX
XX [1]
RN 1-126
RP MEDLINE; 80222887.
RX PUBMED; 6248246.
RA Lovinger G.G., Schochetman G.;
RT "5' terminal nucleotide sequences of type C retroviruses: features common
RT to noncoding sequences of eucaryotic messenger RNAs.";
RL Cell 20(2):441-449(1980).
XX
XX See also <baev5>, <mmcl> & <rd114>.
XX
XX Key Location/Qualifiers
FH
FH source 1. 126
FT /db_xref="taxon:11844"
FT /note="Isolated from spleen cells"
FT /organism="Macaca mulatta and arcotoides type C retrovirus"
XX
SQ Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;
Query Match 0.1%; Score 10; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125409 CCCCAGAGAA 125418
Db 24 CCCCAGAGAA 33
RESULT 14
MMJAI/C standard; RNA; VRL; 126 BP.
XX
XX J02243;
AC
XX
XX J02243.1
SV
XX
XX 01-OCT-1996 (Rel. 49, Created)
DT 11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX
XX Macaca mulatta and arcotoides type C retrovirus, 5' end.
DE
XX
XX
XX
XX Macaca mulatta and arcotoides type C retrovirus
OS Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses;
OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX
XX [1]
RN 1-126
RP MEDLINE; 80222887.
RX PUBMED; 6248246.
RA Lovinger G.G., Schochetman G.;
RT "5' terminal nucleotide sequences of type C retroviruses: features common
RT to noncoding sequences of eucaryotic messenger RNAs.";
RL Cell 20(2):441-449(1980).
XX
XX See also <baev5>, <mmcl> & <rd114>.
XX
XX Key Location/Qualifiers
FH
FH source 1. 126
FT /db_xref="taxon:11844"
FT /note="Isolated from spleen cells"
FT /organism="Macaca mulatta and arcotoides type C retrovirus"
XX
SQ Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;
Query Match 0.1%; Score 10; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 127392 AGCTCCAGCT 127401
Db 99 AGCTCCAGCT 90

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Search completed: September 30, 2003, 03:39:07
Job time : 11 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 03:36:56 ; Search time 18 Seconds
(without alignments)
34.943 Million cell updates/sec

Title: us-09-831-000-1
Perfect score: 40001
Sequence: 1 aaacacatcacgacccgcgc.....caacgacacgcgcgcctt 40001

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7 seqs, 7862 residues

Word size: 0

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: em_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15	0.0	2480 1	ADRE3GENE L08231 Mastadenov
2	14	0.0	1980 1	ADREAR3RE M94458 Mastadenov
3	13	0.0	747 1	AF541985 AF541985 Dendrolim
4	13	0.0	747 1	AF541986 AF541986 Dendrolim
5	13	0.0	1980 1	ADREAR3RE M94458 Mastadenov
6	13	0.0	2480 1	ADRE3GENE L08231 Mastadenov
7	12	0.0	126 1	MMJAI J02243 Macaca mula
8	12	0.0	1122 1	MMSPRO2 J02261 Moloney mur
9	11	0.0	660 1	MMSPRO1 J02260 Moloney mur
10	11	0.0	747 1	AF541985 AF541985 Dendrolim
11	11	0.0	747 1	AF541986 AF541986 Dendrolim
12	11	0.0	1122 1	MMSPRO2 J02261 Moloney mur
13	11	0.0	126 1	MMJAI J02243 Macaca mula
14	10	0.0	126 1	MMJAI J02243 Macaca mula

ALIGNMENTS

RESULT 1
ADRE3GENE/C
ID ADRE3GENE standard; DNA; VRL; 2480 BP.
XX
AC L08231;
XX
SV L08231.1
XX
XX
DT 08-JUL-1993 (Rel. 36, Created)
DT 04-MAR-2000 (Rel. 63, Last updated, Version 3)
XX
DE Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
XX
KW fiber protein.

XX Human adenovirus type 11
OS Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC Human adenovirus B.

XX [1]
RX 1-2480
RX MEDLINE: 93276532.
RX PUBMED: 8503168.
RA Mei Y.-F., Wadell G.;
RT "Hemagglutination properties and nucleotide sequence analysis of the fiber
RT gene of adenovirus genome types 11p and 11a";
RL Virology 194(2):453-462(1993).

DR GOA: P35774.
DR SWISS-PROT: P35774; FIBP_ADE1P.

XX Key Location/Qualifiers

FT source

1. 2480

FT /db_xref="taxon:10541"

FT /mol_type="genomic DNA"

FT /organism="Human adenovirus type 11"

FT /strain="Slobitski"

FT 1094..2071

FT /codon_start=1

FT /db_xref="GOA:P35774"

FT /db_xref="SWISS-PROT:P35774"

FT /gene="E3"

FT /protein_id="AAA42490.1"

FT /translation="MTKRVRLSDSPNPVYPEDESTSQHPFNPGRFISPNPGRNGV
FT LTKCLPTITGGSLQKLVGGGLTVDIDPGLKENSATTPVKRGSHGLPLGAGIG
FT TNNKRCITRIGGSLPNSNNICDDNINFLMGVNPPEANCOIMNSSESVDCLITIV
FT KTGALVATARYIVGVSNRMETLTHNINFTAFDFDSGNLTRLRSLKTPPLNHSQO
FT NMATGATNNAKGFPSPTTAVPNDNSREKENYIVGYTASDRTAFPIDISVWLNRA
FT INDTSYCIRITWSMTGDAPEVOTSATTLVTSPTFEYIREDQ"

XX SQ Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;

Query Match 0.0%; Score 15; DB 1; Length 2480;

Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64041 GTGCTGTGTCGCAC 64055

DB 1355 GTGCTGTGTCGCAC 1341

RESULT 2

ADREAR3RE/C
ID ADREAR3RE standard; DNA; VRL; 1980 BP.

XX M94458;

XX SV M94458.1

DT 11-DEC-1992 (Rel. 34, Created)

DT 04-MAR-2000 (Rel. 63, Last updated, Version 5)

XX Mastadenovirus serotype 11 early 3 region.

XX early 3 region.

OS Human adenovirus type 11

OC Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;

OC Human adenovirus B.

XX [1]

RX MEDLINE: 93033102.

RX PUBMED: 1413499.

RA Mei Y.-F., Wadell G.;

RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison

```
RT of genome type, Ad1p and Ad1a."
RL Virology 191(1):125-133(1992).
XX
DR GOA: P15140.
DR SWISS-PROT: P15140; E3GL_ADE35.
DR SWISS-PROT: P35768; E320_ADE1P.
DR SWISS-PROT: P35770; E321_ADE1P.
XX
FH Key Location/Qualifiers
FH
FT source 1. 1980
FT /db_xref="taxon:10541"
FT /mol_type="genomic DNA"
FT /organism="Human adenovirus type 11"
FT /strain="Siobitski"
XX
SQ Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;
Query Match 0.0%; Score 14; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
CY 78171 GCCACCGCTGCAAC 78184
DB 1054 GCCACCGCTGCAAC 1041
RESULT 3
AF541985/C
ID AF541985 standard; DNA; VRL; 747 BP.
XX
AC AF541985;
XX
SV AF541985.1
XX
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.
XX
XX KW
XX
OS Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
RN 1-747
RN RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX
XX [2]
XX RP 1-747
XX RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX
XX SPTREMBL; Q8AYY9; Q8AYY9.
DR
XX
FH Key Location/Qualifiers
FH
FT source 1. 747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT 1. 747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="Forms crystals/polyhedra"
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FT /product="polyhedrin"
FT /protein_id="AAN17827.1"
FT /translation="MADVAGTSNRDFRGEORLFPNSEQYNNNSLNGEVSVMVAYYS
FT GSVLVINKNSQYKVGISETFKALKEVREGQNDSDYEVEVQSGIYYPGCGAHKFSNA
FT KPAIQTIFSPSVVVRTIKMAKNSVSPDDYLGSRHPWEATGIRKRIKRDGETVGS
FT HYFELPHEINISLAVSGVHKNSPVNGSAHNMVDFQSCDLLALRCNRYMALELVN
FT HYSFNAPVYIDINNHSTGYALSNHQ"
XX
SQ Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;
Query Match 0.0%; Score 13; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
CY 64059 TCGAAGTAATGAC 64071
DB 500 TCGAAGTAATGAC 488
RESULT 4
AF541986/C
ID AF541986 standard; DNA; VRL; 747 BP.
XX
AC AF541986;
XX
SV AF541986.1
XX
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polyhedrin gene, complete cds.
XX
XX KW
XX
OS Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
RN 1-747
RN RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX
XX [2]
XX RP 1-747
XX RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX
XX SPTREMBL; Q8AYY9; Q8AYY9.
DR
XX
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FT /mol_type="genomic DNA"
FT /note="Substitute-host"
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FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
FT 1. 747
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FT /product="polyhedrin"
FT /protein_id="AAN17828.1"
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FT GSVLVINKNSQYKVGISETFKALKEVREGQNDSDYEVEVQSGIYYPGCGAHKFSNA
FT KPAIQTIFSPSVVVRTIKMAKNSVSPDDYLGSRHPWEATGIRKRIKRDGETVGS
FT HYFELPHEINISLAVSGVHKNSPVNGSAHNMVDFQSCDLLALRCNRYMALELVN
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FT      HYSPNAYPYLDINNHSGVALSNHQ"
XX      Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;
SQ
Query Match      0.0%; Score 13; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      64059 TCGAGTATGAC 64071
DB      500 TCGAGTATGAC 488

RESULT 5
ADREAR3RE standard; DNA; VRL; 1980 BP.
XX      M94458;
XX      M94458.1
SV
XX      11-DEC-1992 (Rel. 34, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 5)
XX
XX      Mastadenovirus serotype 11 early 3 region.
DE
XX      early 3 region.
KM
XX
OS      Human adenovirus type 11
OC      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC      Human adenovirus B.
XX
XX      [1]
RN      MEDLINE: 93033102.
RX      PUBMED: 1413499.
RA      Mei Y.-F., Wadell G.;
RT      "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
of genome type Ad1p and Ad11a.";
RL      Virology 191(1):125-133(1992).
XX
XX      GOA: P15140.
DR      SWISS-PROT: P15140; E3GL_ADE35.
DR      SWISS-PROT: P35768; E320_ADE1P.
DR      SWISS-PROT: P35770; E321_ADE1P.
XX
XX      Key      Location/Qualifiers
FH
FH      source      1. 1980
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Slobitski"
XX
SQ      Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;
Query Match      0.0%; Score 13; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      40452 AAAGTTACAGCG 40464
DB      843 AAAGTTACAGCG 855

RESULT 6
ADRE3GENE standard; DNA; VRL; 2480 BP.
XX      L08231;
XX      L08231.1
SV
XX
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```
DT      08-JUL-1993 (Rel. 36, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 3)
XX
XX      Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
DE
XX      fiber protein.
XX
XX      Human adenovirus type 11
OS      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC      Human adenovirus B.
XX
XX      [1]
RN      1-2480
RP      MEDLINE: 93276532.
RX      PUBMED: 8503168.
RA      Mei Y.-F., Wadell G.;
RT      "Hemagglutination properties and nucleotide sequence analysis of the fiber
gene of adenovirus genome types 11p and 11a";
RL      Virology 194(2):453-462(1993).
XX
XX      GOA: P35774.
DR      SWISS-PROT: P35774; FIBP_ADE1P.
XX
XX      Key      Location/Qualifiers
FH
FH      source      1. 2480
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Slobitski"
FT      1094..2071
FT      /codon_start=1
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FT      /db_xref="SWISS-PROT:P35774"
FT      /gene="E3"
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FT      /translation="MTKRVRLSDSEPNVYPYDESTSQHPFINPFIISPNGTOSPNGV
LTKCLPTLTGGSLQKLVGGGLVDDTNGFLKENISATTPLVKTHGSHIGLPLAGLG
TNNKRCITLGGGLTFPNSNNICIDNDINILMTGVNPTFANCOIMNSSESNDCKLITLV
KRGALVTAIVYIVIGVSNRNMLTTHRNINFTALFPDSTGNLTRSSIKTPLNHKSQ
NMAVTATNAKGPMSSTVAIPENDNSREKENIYGYCYTASDRTAFPIDISVMLNRA
INDETSYCIRITWSMNTGDAPEVOTSATTLVSPFFYIRED"
XX
XX      Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;
Query Match      0.0%; Score 13; DB 1; Length 2480;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      53920 ACGCGGCCCAA 53932
DB      592 ACGCGGCCCAA 604

RESULT 7
MMJ1/C
XX      MMJ1 standard; RNA; VRL; 126 BP.
XX      J02243;
XX      J02243.1
SV
XX      01-OCT-1996 (Rel. 49, Created)
DT      11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX
XX      Macaca mulatta and arctoides type C retrovirus, 5' end.
DE
XX      Macaca mulatta and arctoides type C retrovirus, 5' end.
XX
XX      Macaca mulatta and arctoides type C retrovirus
OS      Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses;
OC      1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX
```

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RN [1]
RP 1-126
RX MEDLINE; 80222887.
RX PUBMED; 6248246.
RA Loyinger G.G., Schochetman G.;
RT "5' terminal nucleotide sequences of type C retroviruses: features common
RL Cell 20(2):441-449(1980).
XX
CC See also <baev5>, <mmcl> & <rd114>.
XX
FH Key Location/Qualifiers
FH
FT source 1. 126
FT /db_xref="taxon:11844"
FT /note="Isolated from spleen cells"
FT /organism="Macaca mulatta and arcoides type C retrovirus"
XX
SQ Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;

Query Match 0.0%; Score 12; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72481 CTCGCGTGTCT 72492
Db 44 CTCGCGTGTCT 33

RESULT 8
MMSPRO2
ID MMSPRO2 standard; DNA; VRL; 1122 BP.
XX
AC J02261;
XX
SV J02261.1
XX
DT 07-MAY-1992 (Rel. 31, Created)
DT 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
DE Moloney murine sarcoma virus polyprotein gene, partial cds.
XX
KW proviral gene; terminal repeat.
XX
OS Moloney murine sarcoma virus
OC Viruses; Retroviridae; Gammaretrovirus.
XX
XX [1]
RN 16-1122
RP MEDLINE; 81013872.
RX PUBMED; 6251454.
RA Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
RL replications, analogy to bacterial transposons, and an unexpected gene";
Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX [2]
RN 1-1122
RP MEDLINE; 81013873.
RX PUBMED; 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RL 5' long terminal repeat and adjacent cellular sequences";
Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [3]
RN 1-1122
RP MEDLINE; 81052384.
RX PUBMED; 6159543.
RA Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
RL Nature 287(5785):801-805(1980).

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XX GOA: Q83401.
DR SPTREMBL; Q83401; Q83401.
XX
FH Key Location/Qualifiers
FH
FT source 1. 1122
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /proviral
FT /organism="Moloney murine sarcoma virus"
XX
CC <1. 1122
XX /product="RNA polII transcript mRNA"
XX <1. 564
XX /codon_start=1
XX /db_xref="GOA:Q83401"
XX /db_xref="SPTREMBL:Q83401"
XX /product="polyprotein"
XX /protein_id="AA51623.1"
XX /translation="LIGLTMGIGIAAGIGTGTALMAFQFQQLQAAYDDLRREKSI
XX SNIKSLTSEVVLQNRGIDLFLKEGGICALKKECCFYADHTGLVDSMAKLER
XX LNRQKLFESTGCGFEGFLFNRSPPFTLLISTIMGPLIVLLMILFLGCIILRLVQFVKD
XX RISVQALVLTQGFHQLKPIECEP"
XX <1. 282
XX /product="p15e protein"
XX 283. 561
XX /product="r protein"
XX 144
XX /note="a may be g ([1])"
XX 302
XX /note="t may be c ([1])"
XX 530
XX /note="t may be a ([1])"
XX 952
XX /note="a may be t ([1])"
XX
SQ Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;

Query Match 0.0%; Score 12; DB 1; Length 1122;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45978 AAATPAAAGATT 45989
Db 568 AAATPAAAGATT 579

RESULT 9
MMSPRO1
ID MMSPRO1 standard; DNA; VRL; 660 BP.
XX
AC J02260;
XX
SV J02260.1
XX
DT 05-NOV-1994 (Rel. 41, Created)
DT 12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX
DE Moloney murine sarcoma virus long terminal repeat.
XX
KW terminal repeat.
XX
OS Moloney murine sarcoma virus
OC Viruses; Retroviridae; Gammaretrovirus.
XX
XX [1]
RN 1-660
RP MEDLINE; 81013873.
RX PUBMED; 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RL 5' long terminal repeat and adjacent cellular sequences";

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CC	On Oct 4 1994 this sequence version replaced g1.332090.
CC	+ strand shown. 'LTR' in definition stands for 'long terminal
CC	repeat'.
XX	
FH	Key
FH	Location/Qualifiers
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FT	1..660
FT	/db_xref="taxon:11809"
FT	/mol_type="genomic DNA"
FT	/note="from Balb/c mouse"
FT	/proviral
FT	/organism="Moloney murine sarcoma virus"
FT	486..>660
FT	/product="RNA polII transcript mRNA"
XX	
XX	Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;
QY	Query Match
QY	Best local similarity 100.0%; Score 11; DB 1; Length 660;
QY	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	43290 AGTTCTACAA 43300
QY	
QY	85 AGTTCTACAA 75
Db	
RESULT 11	
AF541985	standard; DNA; VRL; 747 BP.
ID	AF541985
AC	AF541985;
XX	
SV	AF541985.1
XX	
DT	26-SEP-2002 (Rel. 73, Created)
DT	26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX	
DE	Dendrolimus punctatus cyповirus 1 strain Hunan polyhedrin gene, complete
DE	cds.
XX	
KX	
XX	
OS	Dendrolimus punctatus cyповirus 1
OC	Viruses; dsRNA viruses; Reoviridae; Cyповirus; Cyповirus 1.
XX	
XX	[1]
RN	1-747
RP	Hong J., Zhao S., Peng H., Duan J.;
RT	"Comparison of C-polyhedrin genes from 5 type 1 cyповiruses";
RA	unpublished.
RL	
XX	
XX	[2]
RN	1-747
RP	Hong J., Zhao S., Peng H., Duan J.;
RT	;
RA	Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL	Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL	430071, P.R. China
XX	
DR	SPTREMBL; Q8AYY9; Q8AYY9.
XX	
FH	Key
FH	Location/Qualifiers
FT	source
FT	1..747
FT	/db_xref="taxon:208509"
FT	/mol_type="genomic DNA"
FT	/organism="Dendrolimus punctatus cyповirus 1"
FT	/strain="Hunan"
FT	1..747
FT	/codon_start=1
FT	/db_xref="SPTREMBL:Q8AYY9"
FT	/note="forms crystals/polyhedra"
FT	/product="polyhedrin"
FT	
FT	CDS

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FT      /protein_id="AANI7827.1"
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FT      KPRALIOIFSPSVWRTIKMAKNSVSPDDYLQSRHPEWATGIKYRIKRDGETVGS
FT      HYFELPHEYNISLAVSGVHKNPSSYVNGSHANNMDVFGSCDLALRCNRYMALEELVN
FT      HTISPNAVPIYIDINNSHYGVALSNHQ"
FT
XX      Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;
SQ
Query Match      0.0%; Score 11; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45987 ATTCAAACGCC 45997
        |||
        302 ATTCAAACGCC 312

RESULT 12
AF541986 standard; DNA; VRL; 747 BP.
XX      AF541986;
AC      AF541986.1
SV      AF541986.1
XX      26-SEP-2002 (Rel. 73, Created)
DT      26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX      Dendrolimus punctatus cyovirus 1 strain Hunan from Spodoptera exigua
DE      polyhedrin gene, complete cds.
XX
XX      Dendrolimus punctatus cyovirus 1
OS      Dendrolimus punctatus cyovirus 1
OC      Viruses; dsRNA viruses; Reoviridae; Cyovirus; Cyovirus 1.
XX
XX      [1]
RN      1-747
RP      Hong J., Zhao S., Peng H., Duan J.;
RA      "Comparison of C-polyhedrin genes from 5 type 1 cyoviruses";
RT      unpublished.
RL
XX      [2]
RN      1-747
RP      Hong J., Zhao S., Peng H., Duan J.;
RA      Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RT      ;
RL      Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
        430071, P.R. China
XX
XX      SPTREMBL; Q8AYY9; Q8AYY9.
DR
XX      SPTREMBL; Q8AYY9; Q8AYY9.
FH
FH      Key      Location/Qualifiers
FH
FH      source      1. 747
FT      /db_xref="taxon:208509"
FT      /mol_type="genomic DNA"
FT      /note="Substitute-host"
FT      /organism="Dendrolimus punctatus cyovirus 1"
FT      /strain="Human"
FT      /specific_host="Spodoptera exigua"
FT      1. 747
FT      /codon_start=1
FT      /db_xref="SPTREMBL:Q8AYY9"
FT      /note="forms crystals/polyhedra"
FT      /product="polyhedrin"
FT      /protein_id="AANI7828.1"
FT      /translation="MADVAGTSNRDPRGREGQRLFNSDQYNNSLNGEVSVMYAYYS
FT      GSVLVINKNSQYKVISSEFKALKEIREGQNDSDYEYEVQSIYYPNGDAHKFHSNA
FT      KPRALIOIFSPSVWRTIKMAKNSVSPDDYLQSRHPEWATGIKYRIKRDGETVGS
FT      HYFELPHEYNISLAVSGVHKNPSSYVNGSHANNMDVFGSCDLALRCNRYMALEELVN
FT      HTISPNAVPIYIDINNSHYGVALSNHQ"
FT      CDS
FT      HTPSPNAVPIYIDINNSHYGVALSNHQ

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XX      Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;
SQ
Query Match      0.0%; Score 11; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45987 ATTCAAACGCC 45997
        |||
        302 ATTCAAACGCC 312

RESULT 13
MMSPRO2/c
ID      MMSPRO2 standard; DNA; VRL; 1122 BP.
XX      J02261;
AC      J02261.1
SV      J02261.1
XX      07-MAY-1992 (Rel. 31, Created)
DT      17-APR-2002 (Rel. 71, Last updated, Version 6)
XX      Moloney murine sarcoma virus polyprotein gene, partial cds.
DE      proviral gene; terminal repeat.
XX
XX      Moloney murine sarcoma virus
OS      Viruses; Retroviridae; Retroviridae; Gammaretrovirus.
XX
XX      [1]
RN      16-1122
RP      MEDLINE; 81013872.
RX      MEDLINE; 81013872.
RX      PUBMED; 6251454.
RA      Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RT      "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of
        the 5' long terminal repeat and adjacent cellular sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX      [2]
RN      1-1122
RP      MEDLINE; 81013873.
RX      MEDLINE; 81013873.
RX      PUBMED; 6251455.
RA      Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT      "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
        5' long terminal repeat and adjacent cellular sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX      [3]
RN      1-1122
RP      MEDLINE; 81052384.
RX      MEDLINE; 81052384.
RX      PUBMED; 6159543.
RA      Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT      "Chemical synthesis of a polypeptide predicted from nucleotide sequence
        allows detection of a new retroviral gene product";
RL      Nature 287(5785):801-805(1980).
XX
XX      GOA: Q83401.
DR      SPTREMBL; Q83401; Q83401.
FH
FH      Key      Location/Qualifiers
FH
FH      source      1. 1122
FT      /db_xref="taxon:11809"
FT      /mol_type="genomic DNA"
FT      /note="from Balb/mo mouse"
FT      /proviral
FT      /organism="Moloney murine sarcoma virus"
FT      <1. 1122
FT      /product="RNA polII transcript mRNA"
FT      <1. 564
FT      /codon_start=1
FT      /db_xref="GOA:Q83401"

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FT	/db_xref="SPTREMBL:O83401"
FT	/product="polyprotein"
FT	/protein_id="AA51623.1"
FT	/translation="LUGGLMGIIANGTGTATTALMATQDFQQLAAVODDLREYKEIT
FT	SIENKSLISEVVLQNRRLDLFLKEGGLCAALKECCFYADHTGLVROSMALRR
FT	LNRQRLPESTQWFGELGRNSRWFPTLLISTIMGPLIVLMLFGPCILNVLVQFVD
FT	RISVALVLTQGFHQLKPIEECP"
FT	<1.282
FT	/product="p15e protein"
FT	283.561
FT	/product="r protein"
FT	144
FT	/note="a may be g ([1])"
FT	302
FT	/note="t may be c ([1])"
FT	530
FT	/note="t may be a ([1])"
FT	952
FT	/note="a may be t ([1])"
XX	
Q0	Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;

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Oy      44535  AAGACCACCA  44544
        |||||
Db      32    AAGACCACCA  41

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Search completed: September 30, 2003, 03:37:45
Job time : 28 secs

	Query Match	0.0%;	Score 11;	DB 1;	Length 1122;
	Best Local Similarity	100.0%;	Pred. No. 13;		
	Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	57720 ACCATCTGTTTC	57730			
Db	798 ACCATCTGTTTC	788			

Search completed: September 30, 2003, 03:37:45
job time : 28 secs

RESULT 14	
MMJ1	
ID MMJ1	standard; RNA; VRL; 126 BP.

AC	J02243;
XX	
SV	J02243.1

DT	01-OCT-1996 (Rel. 49, Created)
DT	11-FEB-1999 (Rel. 58, Last updated, Version 2)
DT	...

DE Macaca mulatta and arctoides type C retrovirus, 5' end.

05 *Macaca mulatta* and *arctoides* type C retrovirus
0C Viruses; Retroel viruses; Retroviridae; Mammalian type C retroviruses.
0C 1-Mammalian type C virus group; *Macaca mulatta* type C retrovirus.

RN [1]
 RP 1-126
 RX MEDLINE; 80222887.
 RX PUBMED; 6248246.
 RA Lovinger G.G., Schochetman G.;
 RV 5' terminal nucleotide sequences of type C retroviruses: features common
 RT to noncoding sequences of eucaryotic messenger RNAs.";
 Cell 20(2):441-449(1980).

CC	See also <baev5>, <mmc1> & <rl11>.
XX	
FH	
FH	Key
FT	Location/Qualifiers
FT	1. .126
FT	/db_xref="taxon:11844"
FT	/note="isolated from spleen cells"
FT	/organism="Macaca mulatta and arcoides type C retrovirus"
XX	
50	Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;

Query Match	0.0%;	Score 10;	DB 1;	Length 126;
Best Local Similarity	100.0%;	Pred. No. 71;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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RN [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT ;
RL Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RU Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
DR SPTREMBL: Q8AYY9; Q8AYY9.
XX
FH Key Location/Qualifiers
FT source 1..747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT 1..747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="forms crystals/polymedra"
FT /product="Polymedrin"
FT /protein_id="AA17827.1"
FT /translation="MADVACTSNDFRGROQLFNSROYNNNSLNGEVSVMVYAYYSD
FT GSVLVYKNSQYKVGISETRKALKEIREGQRNDSDYEYNQSIYFNGDARFHSNA
FT KPRAIQIIFSPSVNVRTIKAKGNSVSPDDYLQSRHPWEATGIKYRKIRDEIGVYS
FT HYELPHEVNSISLAVSGVHKNPSSVNGSAHNVMDFQSCDIALRRCNRYMALELIVN
FT HTSPNAYPYLDINNHSGVALSNHQ"
XX
SO Sequence 747 BP: 226 A; 188 C; 169 G; 164 T; 0 other;

Query Match 0.0%; Score 14; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97258 ACAACAGCTTAAC 97271
DB 83 ACAACAGCTTAAC 96

RESULT 3
AF541986 standard; DNA; VRL: 747 BP.
AC AF541986;
XX
SV AF541986.1
XX
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polymedrin gene, complete cds.
XX
KW
XX
OS Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
RN [1]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polymedrin genes from 5 type 1 cypoviruses";
RL unpublished.
XX
RN [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT ;
RL Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
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DR SPTREMBL: Q8AYY9; Q8AYY9.
XX
FH Key Location/Qualifiers
FT source 1..747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /note="substitute-host"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
FT 1..747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="forms crystals/polymedra"
FT /product="Polymedrin"
FT /protein_id="AA17828.1"
FT /translation="MADVACTSNDFRGROQLFNSROYNNNSLNGEVSVMVYAYYSD
FT GSVLVYKNSQYKVGISETRKALKEIREGQRNDSDYEYNQSIYFNGDARFHSNA
FT KPRAIQIIFSPSVNVRTIKAKGNSVSPDDYLQSRHPWEATGIKYRKIRDEIGVYS
FT HYELPHEVNSISLAVSGVHKNPSSVNGSAHNVMDFQSCDIALRRCNRYMALELIVN
FT HTSPNAYPYLDINNHSGVALSNHQ"
XX
SO Sequence 747 BP: 230 A; 191 C; 166 G; 160 T; 0 other;

Query Match 0.0%; Score 14; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97258 ACAACAGCTTAAC 97271
DB 83 ACAACAGCTTAAC 96

RESULT 4
MMSPRO2/C
ID MMSPRO2 standard; DNA; VRL: 1122 BP.
AC J02261;
XX
SV J02261.1
XX
DT 07-MAY-1992 (Rel. 31, Created)
DT 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
DE Moloney murine sarcoma virus polyprotein gene, partial cds.
XX
KW proviral gene; terminal repeat.
XX
OS Moloney murine sarcoma virus
OC Viruses; Retroviridae; Gammaretrovirus.
XX
RN [1]
RP 16-1122
RX MEDLINE; 81013872.
RX PUBMED; 6251454.
RA Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
RT replications, analogy to bacterial transposons, and an unexpected gene";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
RN [2]
RP 1-1122
RX MEDLINE; 81013873.
RX PUBMED; 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RT 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
RN [3]
RP 1-1122
RX MEDLINE; 81052384.
RX
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RX PubMed: 6159543.
RA Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
RL Nucleotide detection of a new retroviral gene product";
XX Matur 287(5785):801-805(1980).
DR GOA: Q83401.
DR SPTREMBL: Q83401; Q83401.
XX
XX
FH Key Location/Qualifiers
FH source
FT 1..1122
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /proviral
FT /organism="Moloney murine sarcoma virus"
FT <1..1122
FT /product="RNA polII transcript mRNA"
FT <1..564
FT CDS
FT /codon_start=1
FT /db_xref="GOA:Q83401"
FT /db_xref="SPTREMBL:Q83401"
FT /product="polyprotein"
FT /protein_id="AA51623.1"
FT /translation="ILGLTMCIGTAAIGTGTALMATQFOQLQAAYDDDLREVEKSI
FT SNLEKSTLSSEVVLNRRGLDLFLKEGGLCAALKECCFYADHNGLVDSMAKLRER
FT LNRQKLFESTGCPGEGFLPSPMPFTLLISTINGPLVLMLILFGCINRLVQPFVKD
FT RISVVALVLTQCFHQKPTCECP"
FT <1..282
FT mat_peptide
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FT 283..561
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FT /product="r protein"
FT 144
FT unsure
FT /note="a may be g (11)"
FT 302
FT /note="t may be c (11)"
FT 530
FT unsure
FT /note="t may be a (11)"
FT 952
FT unsure
FT /note="a may be t (11)"
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SQ Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;
Query Match 0.0%; Score 14; DB 1; Length 1122;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 83765 TCCCTGTTCCTATT 83778
DB 52 TCCCTGTTCCTATT 39

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RESULT 5
ADREAR3RE/c
ID ADREAR3RE standard; DNA; VRL; 1980 BP.

XX M94458;

XX M94458.1

XX 11-DEC-1992 (Rel. 34, Created)

DT 04-MAR-2000 (Rel. 63, Last updated, Version 5)

XX Mastadenovirus serotype 11 early 3 region.

XX early 3 region.

XX Human adenovirus type 11

OC Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;

XX Human adenovirus B.

[1]

```

RP 1-1980
RX MEDLINE: 93033102.
RX PubMed: 1413499.
RA Mel Y.-F., Madell G.;
RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
RL of genome type Ad1p and Ad1a.";
XX Virology 191(1):125-133(1992).
DR GOA: P15140.
DR SWISS-PROT: P15140; E3GL_ADE35.
DR SWISS-PROT: P35768; E3Z0_ADE1P.
DR SWISS-PROT: P35770; E3Z1_ADE1P.
XX
XX
FH Key Location/Qualifiers
FH source
FT 1..1980
FT /db_xref="taxon:10541"
FT /mol_type="genomic DNA"
FT /organism="Human adenovirus type 11"
FT /strain="Slobitski1"
XX
SQ Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;
Query Match 0.0%; Score 14; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 94028 TAAAGAGAAATTAA 94041
DB 1167 TAAAGAGAAATTAA 1154

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RESULT 6

ID ADREAR3RE standard; DNA; VRL; 1980 BP.

XX M94458;

XX M94458.1

XX 11-DEC-1992 (Rel. 34, Created)

DT 04-MAR-2000 (Rel. 63, Last updated, Version 5)

XX Mastadenovirus serotype 11 early 3 region.

XX early 3 region.

XX Human adenovirus type 11

OC Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;

XX Human adenovirus B.

XX [1]

XX MEDLINE: 93033102.

XX PubMed: 1413499.

XX Mel Y.-F., Madell G.;

RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison

of genome type Ad1p and Ad1a.";

XX Virology 191(1):125-133(1992).

XX GOA: P15140.

XX SWISS-PROT: P15140; E3GL_ADE35.

XX SWISS-PROT: P35768; E3Z0_ADE1P.

XX SWISS-PROT: P35770; E3Z1_ADE1P.

XX Key Location/Qualifiers

XX source 1..1980

XX /db_xref="taxon:10541"

XX /mol_type="genomic DNA"

XX /organism="Human adenovirus type 11"

XX /strain="Slobitski1"

SO Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;

Query Match 0.0%; Score 13; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83126 ACAGTACTCAATA 83138
|||||
DB 880 ACAGTACTCAATA 892

RESULT 7

ADRE3GENE/c
ID ADRE3GENE standard; DNA; VRL; 2480 BP.

XX AC L08231;
XX SV L08231.1

DT 08-JUL-1993 (Rel. 36, Created)
DT 04-MAR-2000 (Rel. 63, Last updated, Version 3)

XX Mastadenovirus 11 E3 region encoding fiber gene, complete cds.

XX fiber protein.

XX Human adenovirus type 11

OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC Human adenovirus B.

XX [1]

RP 1-2480
RX MEDLINE; 93276532.

XX PUBMED; 8503168.

RA Mel Y.-F., Wade J. G.;

RT "Hemagglutination properties and nucleotide sequence analysis of the fiber
gene of adenovirus genome types 11p and 11a";

RL Virology 194(2):453-462(1993).

XX GOA; P35774.

DR SWISS-PROT; P35774; FIBP_ADE1P.

XX key Location/Qualifiers

FT source 1. 2480

FT /db_xref="taxon:10541"

FT /mol_type="genomic DNA"

FT /organism="Human adenovirus type 11"

FT /strain="Slobitski"

FT CDS 1094..2071

FT /codon_start=1

FT /db_xref="GOA:P35774"

FT /db_xref="SWISS-PROT:P35774"

FT /gene="E3"

FT /protein_id="AAA2490.1"

FT /translation="MTRKRVRSDFNVPYEPEDSTQHPINPGFISPNCFQSPNGV
LTKCLPLPTTGGSLQDKVGGGLVDFTNGELKENISATPLVKTGHSIGLPGAGLG
TNEKRLKIKLGOGILTFPNSNICIDNINITLMTGVNPTPEANQIMNSSESDCKLITLV
KTGALVAFVYVIGVSNPNMILTHRNINFTFAELFDSGTGLTLRLSLKPLNHHKSGO
NMGATITNMGKGFMPSTTAYVPENDSRKEKVIYGTCCYATASDRTAPPIDISVMLNRRRA
INDETSICIRITWMTGDAPEVQTSATITLVTSPTTYIREDP"

FT XX Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;

SO Query Match 0.0%; Score 13; DB 1; Length 2480;

Best Local Similarity 100.0%; Pred. No. 5;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102705 GTTTCTTTCAAA 102717
|||||
DB 1336 GTTTCTTTCAAA 1324

RESULT 8

MMJAI/c
ID MMJAI standard; RNA; VRL; 126 BP.

XX AC J02243;

XX SV J02243.1

DT 01-OCT-1996 (Rel. 49, Created)

DT 11-FEB-1999 (Rel. 58, Last updated, Version 2)

XX Macaca mulatta and arcoides type C retrovirus, 5' end.

XX Macaca mulatta and arcoides type C retrovirus

OS Macaca mulatta and arcoides type C retrovirus

OC Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses;

OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.

XX [1]

RP 1-126

RX MEDLINE; 80222887.

RX PUBMED; 6248246.

RA Lovinger G.G., Schochetman G.;

RT "5' terminal nucleotide sequences of type C retroviruses: features common
to noncoding sequences of eucaryotic messenger RNAs.";

RL Cell 20(2):441-449(1980).

XX See also <baev5> <mmcl> & <rd114>.

XX key Location/Qualifiers

FT source 1. 126

FT /db_xref="taxon:11844"

FT /note="Isolated from spleen cells"

FT /organism="Macaca mulatta and arcoides type C retrovirus"

XX Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;

QY 110203 ATAAAGATCCTT 110214
|||||
DB 78 ATAAAGATCCTT 67

XX Query Match 0.0%; Score 12; DB 1; Length 126;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110203 ATAAAGATCCTT 110214

XX [1]

XX ID MMSPRO1 standard; DNA; VRL; 660 BP.

XX AC J02260;

XX SV J02260.1

DT 05-NOV-1994 (Rel. 41, Created)

DT 12-MAR-2002 (Rel. 71, Last updated, Version 3)

XX Mooney murine sarcoma virus long terminal repeat.

XX terminal repeat.

XX Mooney murine sarcoma virus

OS Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.

OC Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses;

OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.

XX [1]

RP 1-660

RX MEDLINE; 81013873.

RX PUBMED; 6251455.

RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;

RT "Structure of Mooney murine leukemia viral DNA: nucleotide sequence of the
5' long terminal repeat and adjacent cellular sequences";

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RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [2]
RN 441-545
RX MEDLINE: 82060256.
RX PUBMED: 6946480.
RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT "Identification of a RNA polymerase II initiation site in the long terminal
RT repeat of Moloney murine leukemia viral DNA";
RL Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX
XX On Oct 4, 1994 this sequence version replaced g1:332090.
CC + strand shown. 'LTR' in definition stands for 'long terminal
CC repeat'.
XX
FH Key Location/Qualifiers
FH
FT source 1..660
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT
FT
FT
FT mRNA
FT /organism="Moloney murine sarcoma virus"
FT /product="RNA polII transcript mRNA"
SQ
Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;
Query Match 0.0%; Score 12; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 88221 TATGATCTCCTT 88232
DB 5 TATGATCTCCTT 16
RESULT 10
MMSPRO1/c
ID MMSPRO1 standard; DNA; VRL; 660 BP.
XX
XX J02260;
XX
XX J02260.1
XX
XX 05-NOV-1994 (Rel. 41, Created)
DT 12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX
XX Moloney murine sarcoma virus long terminal repeat.
XX terminal repeat.
XX
XX Moloney murine sarcoma virus
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
XX
XX [1]
RN 1-660
RP MEDLINE: 81013873.
RX PUBMED: 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RT 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX
XX [2]
RN 441-545
RP MEDLINE: 82060256.
RX PUBMED: 6946480.
RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT "Identification of a RNA polymerase II initiation site in the long terminal
RT repeat of Moloney murine leukemia viral DNA";
RL Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX

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CC On Oct 4, 1994 this sequence version replaced g1:332090.
CC + strand shown. 'LTR' in definition stands for 'long terminal
CC repeat'.
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FT /product="RNA polII transcript mRNA"
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 304 ACCATCTGTTCT 293
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XX J02261;
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XX J02261.1
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XX 07-MAY-1992 (Rel. 31, Created)
DT 17-APR-2002 (Rel. 71, Last updated, Version 6)
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XX Moloney murine sarcoma virus polyprotein gene, partial cds.
XX
XX proviral gene; terminal repeat.
XX
XX Moloney murine sarcoma virus
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
XX
XX [1]
RN 16-1122
RP MEDLINE: 81013872.
RX PUBMED: 6251454.
RA Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
RT replications, analogy to bacterial transposons, and an unexpected gene";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX [2]
RN 1-1122
RP MEDLINE: 81013873.
RX PUBMED: 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RT 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [3]
RN 1-1122
RP MEDLINE: 81052384.
RX PUBMED: 6159543.
RA Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
RT Nature 287(5785):801-805(1980).
XX
XX GOA: Q83401.
DR SPTREMBL: Q83401; Q83401.

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FT	unsure	530
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Db	621 CTGTAGCTTTGG	632
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XX	J02243.1	
SV		
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DT	11-FEB-1999 (Rel. 58, last updated, Version 2)	
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DE	Macaca mulatta and arctoides type C retrovirus, 5' end.	
XX		
KW		
XX		
OS	Macaca mulatta and arctoides type C retrovirus	
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OC	1-Mammalian type C virus group; Macaca mulatta type C retrovirus.	
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RP	1-126	
RX	MEDLINE; 80222887.	
RX	PUBMED; 6248246.	
RA	Lovinger G.G.; Schochetman G.;	
RT	"5' terminal nucleotide sequences of type C retroviruses: features common	
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XX	Cell 20(2):441-449(1980).	

CC	See also <baev5>, <mmcl> & <rdll4>.
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AC AF541985;	
SV AF541985.1	
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DT 26-SEP-2002 (Rel. 73, Created)	
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)	
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DE Dendrolimus punctatus cyprovirus 1 strain Human polyhedrin gene, complete cds.	
DE	
XX	
KW .	
OS Dendrolimus punctatus cyprovirus 1	
OC Viruses; dsRNA viruses; Reoviridae; Cyprovirus; Cyprovirus 1.	
XX	
[1]	
RN 1-747	
RA Hong J., Zhao S., Peng H., Duan J.;	
RT "Comparison of C-polyhedrin genes from 5 type 1 cyproviruses";	
RL Unpublished.	
XX	
[2]	
RN 1-747	
RP Hong J., Zhao S., Peng H., Duan J.;	
RA Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.	
RT Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei	
RL 430071, P.R. China	
XX	
SPPREMBL; Q8AYY9; Q8AYY9.	
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FT HYEPLEPHENSTSLAASGVCHKNPSSVNGSAHVMDVPQSCDLALRFCINRYWAEELEVNV	
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QY 85686 CCATCTTGATG 85696

DB 373 CCATCTTGATG 363

RESULT 14

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XX AF541986;

XX AF541986.1

XX 26-SEP-2002 (Rel. 73, Created)

DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)

DE Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua

DE polyhedrin gene, complete cds.

OS Dendrolimus punctatus cypovirus 1

OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.

XX [1]

RP 1-747

RA Hong J., Zhao S., Peng H., Duan J.;

XX [2]

RP 1-747

RA Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.

RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei

XX SPTREMBL: Q8AYY9; Q8AYY9.

Key Location/Qualifiers

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/strain="Hunan"

/specific_host="Spodoptera exigua"

1. 747

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SO Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85686 CCATCTTGATG 85696

DB 373 CCATCTTGATG 363

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Job time : 28 secs

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Om nucleic - nucleic search, using sw model

Run on: September 26, 2003, 17:57:32 ; Search time 16 Seconds
(without alignments)
39.310 Million cell updates/sec

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Perfect score: 40000
Sequence: 1 gatcgggaacgcgaggg.....accttatgataactcgttt 40000
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 14

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

Database : em_v1: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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c 1	16	0.0	1980	1	ADREAR3E	M94458 Mastadenov
c 2	15	0.0	2480	1	ADRE3GNE	L08231 Mastadenov
c 3	13	0.0	1980	1	ADREAR3E	M94458 Mastadenov
c 4	12	0.0	760	1	MMSPRO1	J02260 Moloney mu
c 5	12	0.0	747	1	AF541985	J02260 Moloney mu
c 6	12	0.0	747	1	AF541985	J02260 Moloney mu
c 7	12	0.0	747	1	AF541985	J02260 Moloney mu
c 8	12	0.0	747	1	AF541986	J02260 Moloney mu
c 9	12	0.0	747	1	AF541986	J02260 Moloney mu
c 10	12	0.0	1122	1	MMSPRO2	J02261 Moloney mu
c 11	12	0.0	1122	1	MMSPRO2	J02261 Moloney mu
c 12	11	0.0	2480	1	ADRE3GNE	L08231 Mastadenov
c 13	11	0.0	660	1	MMSPRO1	J02260 Moloney mu
c 14	10	0.0	126	1	MMUJ1	J02243 Macaca mul

ALIGNMENTS

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AC	M94458;
XX	
SV	M94458.1
XX	
DT	11-DEC-1992 (Rel. 34, Created)
DT	04-MAR-2000 (Rel. 63, Last updated, Version 5)
XX	
DE	Mastadenovirus serotype 11 early 3 region.
XX	
KW	early 3 region.

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xx Human adenovirus type 11
OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC Human adenovirus B.
XX
RN [1]
RP 1-1980
RX MEDLINE: 93033102.
RX PUBMED: 1413499.
RA Mel Y.-F., Madell G.;
RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
of genome type Ad1p and Ad1a.";
RL Virology 191(1):125-133(1992).
XX
DR GOA: P15140.
DR SWISS-PROT: P15140; E3GL_ADE35.
DR SWISS-PROT: P35768; E320_ADE1P.
DR SWISS-PROT: P35770; E321_ADE1P.
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Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27171 ATGTGTGATPACGT 27186
Db 311 ATGTGTGATPACGT 296
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XX
AC L08231;
SV L08231.1
XX
DT 08-JUL-1993 (Rel. 36, Created)
DT 04-MAR-2000 (Rel. 63, Last updated, Version 3)
XX
DE Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
XX fiber protein.
KW
XX Human adenovirus type 11
OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC Human adenovirus B.
XX
RN [1]
RP 1-2480
RX MEDLINE: 93276532.
RX PUBMED: 8503168.
RA Mel Y.-F., Madell G.;
RT "Hemagglutination properties and nucleotide sequence analysis of the fiber
gene of adenovirus genome types 11p and 11a";
RL Virology 194(2):453-462(1993).
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DR GOA: P35774.
DR SWISS-PROT: P35774; FIBP_ADE1P.
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FT      KTGALVAVFVIVIGVSNFNNLTNRNINFTAELEFDSGTMLTRLSLKTPLNHSQ
FT      NMAFGALITNAGFMPSTTAYPFNDNSREKENYIGCYVYASDRFAFIDISVMLNRA
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DB      1240 ATGTTTACCCTACT 1254

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XX      SV      M94458.1
XX      DT      11-DEC-1992 (Rel. 34, Created)
XX      DT      04-MAR-2000 (Rel. 63, Last updated, Version 5)
XX      DE      Mastadenovirus serotype 11 early 3 region.
XX      KW      early 3 region.
XX      OS      Human adenovirus type 11
XX      OC      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
XX      CC      Human adenovirus B.
XX      [1]
XX      RP      1-1980
XX      RX      MEDLINE; 93033102.
XX      RX      PUBMED; 1413499.
XX      RA      Mel Y.-F., Wadell G.;
RT      "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
RT      of genome type Ad1p and Ad11a.";
RL      Virology 191(1):125-133(1992).
XX      DR      GOA: P15140.
XX      DR      SWISS-PROT: P15140; E3GL_ADE35.
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XX      SV      J02260.1
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XX      DT      12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX      DE      Moloney murine sarcoma virus long terminal repeat.
XX      KW      terminal repeat.
XX      OS      Moloney murine sarcoma virus
XX      OC      Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
XX      [1]
XX      RP      1-660
XX      RX      MEDLINE; 81013873.
XX      RX      PUBMED; 6251455.
XX      RA      Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
XX      RT      "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
XX      RT      5' long terminal repeat and adjacent cellular sequences";
XX      RL      Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX      [2]
XX      RP      441-545
XX      RX      MEDLINE; 82060256.
XX      RX      PUBMED; 6946480.
XX      RA      Fuhrman S.A., Van Beveren C., Verma I.M.;
XX      RT      "Identification of a RNA polymerase II initiation site in the long terminal
XX      RT      repeat of Moloney murine leukemia viral DNA";
XX      RL      Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX      CC      On Oct 4, 1994 this sequence version replaced gi:332090.
XX      CC      + strand shown. 'LTR' in definition stands for 'long terminal
XX      CC      repeat'.
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DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
XX Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.
XX
XX
XX Dendrolimus punctatus cypovirus 1
OS Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
XX 430071, P.R. China
XX
XX SPTREMBL: Q8AY9; Q8AY9.
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XX AF541985;
AC
XX AF541985.1
SV
XX
XX 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
XX Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.

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XX
XX
XX Dendrolimus punctatus cypovirus 1
OS Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
XX 430071, P.R. China
XX
XX SPTREMBL: Q8AY9; Q8AY9.
DR
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XX Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35841 GTTTAAGCTGTT 35852
Db 96 GTTTAAGCTGTT 85
RESULT 7
AF541986 standard; DNA; VRL; 747 BP.
ID AF541986
XX AF541986;
AC
XX AF541986.1
SV
XX
XX 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
XX Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polyhedrin gene, complete cds.
XX
XX
XX Dendrolimus punctatus cypovirus 1
OS Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RP 1-747

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RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
XX 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RP 1-747
RL Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL; Q8AY9; Q8AY9.
DR
XX
XX Key Location/Qualifiers
FH
FH source
FT 1. 747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
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FT /specific_host="Spodoptera exigua"
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FT /db_xref="SPTREMBL:Q8AY9"
FT /note="Forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AAN17828.1"
FT /translation="MADYAGTSNRDFRGREORLPNSQYNNNSLNGEVSVMVAYYSD
FT GSVLVINKSQYKVGISETFKALKEVREGQNDSDYDEVNQSIYYPNGGAHKFHSNA
FT KPRAIQITFSPSVAVRTITKAKGNSVSPDYILORSHPWEATGIKRKIKRDEIGVIS
FT HFPELPHENISILAVSGVHKNPSSYNGSAHNMVDYFQCDLALRFCNRYMAELELVN
FT HYISPNAYPYIDINNHSGYVALSNHQ"
FT
FT CDS
FT 1. 747
SQ Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;

Query Match 0.0%; Score 12; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5686 CCGGATTAAGT 5697
DB 437 CCGGATTAAGT 448

RESULT 8
AF541986/C
ID AF541986 standard; DNA; VRL; 747 BP.
XX
XX AF541986;
AC
XX
XX AF541986.1
SV
XX
XX 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
DE Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polyhedrin gene, complete cds.
XX
XX
XX Dendrolimus punctatus cypovirus 1
OS Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
OC
XX
XX [1]
XX 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
XX 1-747

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RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL; Q8AY9; Q8AY9.
DR
XX
XX Key Location/Qualifiers
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FH source
FT 1. 747
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FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
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FT KPRAIQITFSPSVAVRTITKAKGNSVSPDYILORSHPWEATGIKRKIKRDEIGVIS
FT HFPELPHENISILAVSGVHKNPSSYNGSAHNMVDYFQCDLALRFCNRYMAELELVN
FT HYISPNAYPYIDINNHSGYVALSNHQ"
FT
FT CDS
FT 1. 747
SQ Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27303 ACTGCGAGCGAA 27314
DB 536 ACTGCGAGCGAA 525

RESULT 9
MMSPRO2
ID MMSPRO2 standard; DNA; VRL; 1122 BP.
XX
XX J02261;
AC
XX
XX J02261.1
SV
XX
XX 07-MAY-1992 (Rel. 31, Created)
DT 17-APR-2002 (Rel. 71, Last updated, Version 6)
DE Moloney murine sarcoma virus polyprotein gene, partial cds.
DE proviral gene; terminal repeat.
XX
XX
XX Moloney murine sarcoma virus
OS Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OC
XX
XX [1]
XX 16-1122
XX MEDLINE; 81013872.
XX PUBMED; 6251454.
XX Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RA "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
RT replication, analogy to bacterial transposons, and an unexpected gene";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX [2]
XX 1-1122
RA Moloney J.G., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the

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RT 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
RN [3]
RP 1-1122
RX MEDLINE: 81052384.
RX PUBMED: 6159543.
RA Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.:
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
RL allows detection of a new retroviral gene product";
XX Nature 287(5785):801-805(1980).
DR
DR GOA: Q83401.
DR SPTREMBL: Q83401. Q83401.
XX
XX Key Location/Qualifiers
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FH source 1. 1122
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FT /proviral
FT /organism="Moloney murine sarcoma virus"
FT mRNA <1. 1122
FT /product="RNA polII transcript mRNA"
FT <1. 564
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FT /db_xref="SPTREMBL:Q83401"
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FT /protein_id="AA51623.1"
FT /translation="LVLGLTWGIGIAIGTGTTLMTATQGFQQLDAAYVDDIREVKSIT
FT SNEKSLTISEVVLONRRGLDLFLKEGGLCAALKKECCFYADHTGLVDSMAKLREER
FT LNRORLFEISTQCFEGFLFNRSRFFTLITSTIMGPIVLMLTLFGPILNRLVQFKD
FT RISVVALVYVQGFQHLKIECP"
FT <1. 282
FT mat_peptide
FT /product="p15e protein"
FT 283. 561
FT mat_peptide
FT /product="r protein"
FT 144
FT /note="a may be g ([1])"
FT 302
FT /note="t may be c ([1])"
FT 530
FT /note="t may be a ([1])"
FT 952
FT /note="a may be t ([1])"
FT unsure
XX
XX Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;
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Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28892 CAGGGCCAGAA 28903
IIIIIIIIIIII
DB 779 CAGGGCCAGAA 790
RESULT 10
MSPRO2/C
ID MSPRO2 standard; DNA; VRL; 1122 BP.
XX
XX J02261;
XX
XX J02261.1
XX
XX 07-MAY-1992 (Rel. 31, Created)
DT 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
XX Moloney murine sarcoma virus polyprotein gene, partial cds.
DE
XX proviral gene; terminal repeat.
XX

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Query Match	Best Local Similarity	0.0% ; Score 12; DB 1; Length 1122;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
XX	MOJONEY murine sarcoma virus	
OC	Vituses; Retroid vituses; Retroviridae; Gammaretrovirus.	
XX		
RN	[1]	
RP	16-1122	
XX	MEDLINE: 81013872.	
RX	PUBMED: 6251454.	
RA	Succiliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;	
RT	"Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of	
RL	replications, analogy to bacterial transposons, and an unexpected gene";	
XX	Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).	
RN	[2]	
RP	1-1122	
RX	MEDLINE: 81013873.	
RX	PUBMED: 6251455.	
RA	Van Beveren C., Goddard J.G., Berns A., Verma I.M.;	
RT	"Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the	
RL	5' long terminal repeat and adjacent cellular sequences";	
XX	Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).	
RN	[3]	
RP	1-1122	
RX	MEDLINE: 81052384.	
RX	PUBMED: 6159543.	
RA	Succiliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;	
RT	"Chemical synthesis of a polypeptide predicted from nucleotide sequence	
RL	allows detection of a new retroviral gene product";	
XX	Nature 287(5785):801-805(1980).	
DR	G0A: Q83401.	
XX	SPTREMBL: Q83401; Q83401.	
FH	Key	Location/Qualifiers
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FT		/note="from Balb/mo mouse"
FT		/proviral
FT		/organism="Moloney murine sarcoma virus"
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FT	CDS	<1. .564
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FT		/db_xref="SPTREMBL:Q83401"
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FT		LNDRQRKFESTQCGFGLFNRSFMTTLISTIMGPLIVILMLILRPGCILNLNVQPVKDK
FT		RISVQAQLVTFQDFHQKPECEP"
FT	mat_peptide	<1. .282
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FT	mat_peptide	283. .561
FT		/product="r protein"
FT		144
FT	unsure	/note="a may be g (11)"
FT		302
FT	unsure	/note="t may be c (11)"
FT		530
FT	unsure	/note="t may be a (11)"
FT		952
FT	unsure	/note="a may be t (11)"
XX		
SQ	Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;	

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OY      1890 TTCTATTCTCAG 1901
        |||||||
DB      693 TTCTATTCTCAG 682

RESULT 11
ADRE3GENE/c
ID      ADRE3GENE standard; DNA; VRL; 2480 BP.
XX
XX      L08231;
AC
XX      L08231.1
SV
XX      08-JUL-1993 (Rel. 36, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 3)
XX
XX      Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
DE
XX      fiber protein.
KM
XX      Human adenovirus type 11
OS      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC      Human adenovirus B.
XX
XX      [1]
RN      1-2480
RP      MEDLINE; 93276532.
RX      PUBMED; 8503168.
RA      Mei Y.-F., Madell G.;
RT      "Hemagglutination properties and nucleotide sequence analysis of the fiber
RL      gene of adenovirus genome types 11p and 11a";
XX      Virology 194(2):453-462(1993).
XX
DR      GOA; P35774.
DR      SWISS-PROT; P35774; FIBP_ADELP.
XX
XX      Key      Location/Qualifiers
FH
FH      source      1. 2480
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Siobitski"
FT      1094..2071
FT      CDS
FT      /codon_start=1
FT      /db_xref="GOA:P35774"
FT      /db_xref="SWISS-PROT:P35774"
FT      /gene="E3"
FT      /protein_id="AAA2490.1"
FT      /translation="MTKRVRLSDSFNPVPEYEDSTSOHPINFGEFISPNGFQSPNGV
FT      LTLCLPLPTTGGSLQKVGGLVDDTNGFLKENSATPLVKTGSHSGLPLGAGIG
FT      TNEKRLIKLGGGLTFSNNICIDNINITLTVGVPENQAINSSSNDCKLILTV
FT      KTGLATVAFYVIGVSNNNMGLTNRNINFAELFPGDSTGLRLSLKTPLNHKSQ
FT      NMATGATINAGCEPSTTAYPNDNSREKREYVIGTCYGTASDRTAPPIDISVNLNRA
FT      INDETSICRITWMSMTGDAPEVOTSATTLVTSPTFRYIREDD"
XX
XX      SQ      Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 6.2;
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OY      5623 GTCTTCAGCAGG 5634
        |||||||
DB      855 GTCTTCAGCAGG 844

RESULT 12
MMSPRO1/c
ID      MMSPRO1 standard; DNA; VRL; 660 BP.
XX
XX      J02260;
AC
XX

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SV      J02260.1
XX
XX      05-NOV-1994 (Rel. 41, Created)
DT      12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX
XX      Moloney murine sarcoma virus long terminal repeat.
DE
XX      terminal repeat.
KM
XX      Moloney murine sarcoma virus
OS      Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OC
XX      [1]
RN      1-660
RP      MEDLINE; 81013873.
RX      PUBMED; 6251455.
RA      Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT      "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RL      5' long terminal repeat and adjacent cellular sequences";
XX      Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX      [2]
RN      441-545
RP      MEDLINE; 82060256.
RX      PUBMED; 6946480.
RA      Fuhrman S.A., Van Beveren C., Verma I.M.;
RT      "Identification of a RNA polymerase II initiation site in the long terminal
RL      repeat of Moloney murine leukemia viral DNA";
XX      Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX
XX      CC      On Oct 4, 1994 this sequence version replaced gi:332090.
XX      + strand shown. 'LTR' in definition stands for 'long terminal
XX      repeat'.
XX
XX      FH      Key      Location/Qualifiers
FH
FH      source      1. 660
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FT      /proviral
FT      /organism="Moloney murine sarcoma virus"
FT      /product="RNA polII transcript mRNA"
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XX      mRNA
XX
XX      SQ      Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1891 TCTATTCTCAG 1901
        |||||||
DB      198 TCTATTCTCAG 188

RESULT 13
MMJAL
ID      MMJAL standard; RNA; VRL; 126 BP.
XX
XX      J02243;
AC
XX      J02243.1
SV
XX      J02243.1
DT      01-OCT-1996 (Rel. 49, Created)
DT      11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX
XX      Macaca mulatta and arctoides type C retrovirus, 5' end.
DE
XX      Macaca mulatta and arctoides type C retrovirus, 5' end.
XX
XX      OC      Macaca mulatta and arctoides type C retrovirus
XX      Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses;

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OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.

XX [1]

RN 1-126

RP MEDLINE: 80222887.

RX PUBMED: 6248246.

RA Lovinger G.G., Schochetman G.;

RT "5' terminal nucleotide sequences of type C retroviruses: features common

RL to noncoding sequences of eucaryotic messenger RNAs.";

XX Cell 20(2):441-449(1980).

CC See also <bav5>, <mmcl> & <rd114>.

XX

FH Key Location/Qualifiers

FT source

FT 1. 126

FT /db_xref="taxon:11844"

FT /note="Isolated from spleen cells"

XX /organism="Macaca mulatta and arcotoides type C retrovirus"

SQ .Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 41;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2916 CCCGACGCT 2925

DB 9 CCCGACGCT 18

RESULT 14

MMJAL/C standard; RNA; VRL; 126 BP.

XX J02243;

XX J02243.1

XX J02243.1

XX J02243.1

XX J02243.1

DT 01-OCT-1996 (Rel. 49, Created)

DT 11-FEB-1999 (Rel. 58, Last updated, Version 2)

DE Macaca mulatta and arcotoides type C retrovirus, 5' end.

XX

XX

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XX

OY 1738 ACTCTGTGTG 1747

DB 45 ACTCTGTGTG 36

Search completed: September 27, 2003, 01:19:19
Job time : 24 secs

Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;

Query Match 0.0%; Score 10; DB 1; Length 126;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 11:18:03 ; Search time 1070 Seconds
(without alignments)
12628.907 Million cell updates/sec

Title: us-09-831-000-1
Perfect score: 40000
Sequence: 1 gacgcggaacgcgagaggg.....acctatgataactcgttt 40000

Scoring table: OLIGO_NMC
Gapop 60.0 , Gapext 60.0

Searched: 189188 seqs, 168911627 residues

Word size : 0

Total number of hits satisfying chosen parameters: 378376

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : gb_v1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	40000	100.0	133719 1	AF083501 Macaca mu
2	10772	26.9	130733 1	AF210726 Macaca mu
3	7957	19.9	10595 1	AF029302 Rhesus ma
4	3804	9.5	3804 1	AF087411 Rhesus ma
5	475	1.2	475 1	AF159033 Macaque g
6	331	0.8	395 1	AF159041 Macaque g
7	106	0.3	320 1	AF159040 Macaque g
8	80	0.2	2708 1	AF159031 Macaque g
9	71	0.2	475 1	AF159031 Macaque g
10	56	0.1	475 1	AF159032 Macaque g
11	50	0.1	475 1	AF159032 Macaque g
12	48	0.1	336 1	AF159036 Macaque g
13	48	0.1	336 1	AF159037 Macaque g
14	47	0.1	336 1	AF159035 Macaque g
15	46	0.1	3144 1	SH1DNAPOLA
16	41	0.1	336 1	AF159038 Macaque g
17	38	0.1	475 1	AF282937 Macaque g
18	38	0.1	475 1	AF282938 Macaque g
19	38	0.1	475 1	AF282939 Macaque g
20	38	0.1	475 1	AF282940 Macaque g
21	33	0.1	130733 1	AF210726 Macaca mu
22	33	0.1	133719 1	AF083501 Macaca mu
23	32	0.1	454 1	CRH251574
24	24	0.1	395 1	AF237372 Caprine h
25	23	0.1	395 1	AF159039 Macaque g
26	29	0.1	469 1	AF031811 Bovine he
27	29	0.1	3638 1	AF005477 Kaposi's
28	29	0.1	108873 1	AF318573 Bovine he
29	29	0.1	133661 1	U93872 Kaposi's sa
30	29	0.1	137508 1	U75698 Kaposi's sa
31	27	0.1	480 1	AF031808 Bovine ly
32	27	0.1	1295 1	AF327830 Bovine ly
33	26	0.1	475 1	AF005478 Retroperi

34	26	0.1	3554 1	AF204166 Retroperi
35	23	0.1	475 1	AF250880 Pan trogl
36	23	0.1	1297 1	AF327831 Ovine her
37	23	0.1	1339 1	AF275657 Badger he
38	23	0.1	6165 1	AF376034 Badger he
39	23	0.1	184427 1	EHV020824 Equine herp
40	22	0.1	171096 1	AV037858 Cercopit
41	21	0.1	949 1	AF292063 Unidentif
42	21	0.1	3623 1	AF283477 Caprine h
43	21	0.1	12708 1	AF033822 Walleye d
44	21	0.1	12708 1	TYCGAG
45	21	0.1	130608 1	AF005370 Alcelaphi

ALIGNMENTS

RESULT 1	AF083501	133719 bp	DNA	Linear	VRL 26-JUN-2000
LOCUS	AF083501				
DEFINITION	Macaca mulatta rhadinovirus 17577, complete genome.				
ACCESSION	AF083501				
VERSION	AF083501.3	GI:8714565			
KEYWORDS					
SOURCE					
ORGANISM	Macaca mulatta rhadinovirus 17577				
	Macaca mulatta rhadinovirus 17577				
	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;				
	Gammaherpesvirinae; Rhadinovirus.				
REFERENCE					
AUTHORS	1 (bases 1 to 133719)				
TITLE	Searles, R.P., Bergquam, E.P., Axthelm, M.K. and Wong, S.W.				
	Sequence and genomic analysis of a Rhesus macaque rhadinovirus with				
	similarity to Kaposi's sarcoma-associated herpesvirus/human				
	herpesvirus 8				
JOURNAL	J. Virol. 73 (4), 3040-3053 (1999)				
MEDLINE	99174001				
PUBMED	10074154				
REFERENCE	2 (bases 1 to 133719)				
AUTHORS	Searles, R.P., Bergquam, E.P., Axthelm, M.K. and Wong, S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-AUG-1998) Division of Pathobiology and Immunology,				
	Oregon Health Sciences University/ Oregon Regional Primate Research				
	Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	3 (bases 1 to 133719)				
AUTHORS	Searles, R.P., Bergquam, E.P., Axthelm, M.K. and Wong, S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-JUL-1999) Division of Pathobiology and Immunology,				
	Oregon Health Sciences University/ Oregon Regional Primate Research				
	Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
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AUTHORS	Searles, R.P., Bergquam, E.P., Axthelm, M.K. and Wong, S.W.				
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REMARK	Sequence update by submitter				
COMMENT	On Jun 26, 2000 this sequence version replaced gi:5508840.				
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CDS

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OY	4861	ACAAGCGGAGAAAGTGTCTTAAATAGGAAACAATTAATTAATGAATGAAGAT	4920
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QY	5701	CATTATTCAGAGTTGCCAATAAAGGTGGTTAAAAATATCTATTTGGTGTTCAATGTGTTT	5760
Db	5701	CATTATTCAGAGTTGCCAATAAAGGTGGTTAAAAATATCTATTTGGTGTTCAATGTGTTT	5760
QY	5761	ATGTGTGACCCGTTATAGTTATCGCGCCACCTTGTCGTACATTATATAGCAGATCACT	5820
Db	5761	ATGTGTGACCCGTTATAGTTATCGCGCCACCTTGTCGTACATTATATAGCAGATCACT	5820
QY	5821	TTCCACGTTATACCTTTACAGTACTATATACGCTTAACGTCAACGTGGCGTGCAT	5880
Db	5821	TTCCACGTTATACCTTTACAGTACTATATACGCTTAACGTCAACGTGGCGTGCAT	5880
QY	5881	TGTGGCCGGGCTGAAATATACAAAGGGGTACATATATCCATCCAGCGGCACACATTAG	5940
Db	5881	TGTGGCCGGGCTGAAATATACAAAGGGGTACATATATCCATCCAGCGGCACACATTAG	5940
QY	5941	ACACGTTTATAAACTATATCGAGTGGCCACAAATCACTGTGCTAGGCACACTGATA	6000
Db	5941	ACACGTTTATAAACTATATCGAGTGGCCACAAATCACTGTGCTAGGCACACTGATA	6000
QY	6001	GAAAAACATTTTAAAGCTTTGTTTAGCCACCTTGAAATACATATATGCTTCCAAAGCA	6060
Db	6001	GAAAAACATTTTAAAGCTTTGTTTAGCCACCTTGAAATACATATATGCTTCCAAAGCA	6060
QY	6061	ACGCGGCAACCCCTGGAGAATATATCGAGGGGTCTCGGCCGATATGTCGCGGGAT	6120
Db	6061	ACGCGGCAACCCCTGGAGAATATATCGAGGGGTCTCGGCCGATATGTCGCGGGAT	6120
QY	6121	ACGTGTACGCTATTTCGAACAAGACTTTCCCTTTGGCGAAGCGCTGCATACTCGCAACA	6180
Db	6121	ACGTGTACGCTATTTCGAACAAGACTTTCCCTTTGGCGAAGCGCTGCATACTCGCAACA	6180
QY	6181	GACCATCTGATCTGCGGCTTTTCTCGCTACCAATCTTTAGGACTTACAGTTAGACAGC	6240
Db	6181	GACCATCTGATCTGCGGCTTTTCTCGCTACCAATCTTTAGGACTTACAGTTAGACAGC	6240
QY	6241	AATTCOCCTCACCGTAAAGCCGATACAAAAAGTTGACACCAACGACGCTGCCGCTTA	6300
Db	6241	AATTCOCCTCACCGTAAAGCCGATACAAAAAGTTGACACCAACGACGCTGCCGCTTA	6300
QY	6301	AGGTGACGTGCTTTACAGAGAGGTATATGTGTTTCACAATGCAAGTTTATTCAGGCCGG	6360
Db	6301	AGGTGACGTGCTTTACAGAGAGGTATATGTGTTTCACAATGCAAGTTTATTCAGGCCGG	6360
QY	6361	TGTTTGACGCTACCGGCTTTAACGAACTATGCGAGGAAGCCAGGCGCTCTTTGGGTACA	6420
Db	6361	TGTTTGACGCTACCGGCTTTAACGAACTATGCGAGGAAGCCAGGCGCTCTTTGGGTACA	6420
QY	6421	CGAGATTATTAAGAACCGGGGTCCACTCCACACATATGGAACCCCTCTGGAATGTCCGAGT	6480
Db	6421	CGAGATTATTAAGAACCGGGGTCCACTCCACACATATGGAACCCCTCTGGAATGTCCGAGT	6480
QY	6481	TACCGGACAGAGATGAGATGTTTCTTGCGCTTGTGTTTACGGAAGGGTTTAAGGAAAAGAC	6540

Db	6481	TAACGGACAAGGTGAGATGTTCTTGGGCTGTTTACGGAAAGGTTTAAGAAAGAC	6540
QY	6541	TGTGAGGGGCTGTCTCCTTCCCGGGTTCAGACCCAGCAGGTGACATTCGCCGAC	6600
Db	6541	TGTGAGGGGCTGTCTCCTTCCCGGGTTCAGACCCAGCAGGTGACATTCGCCGAC	6600
QY	6601	GCCAGCGTTTAAAGTGCCGTTGTACGACGAAGACCTGTTTGCACCTCAACGGTATAGAA	6660
Db	6601	GCCAGCGTTTAAAGTGCCGTTGTACGACGAAGACCTGTTTGCACCTCAACGGTATAGAA	6660
QY	6661	TGCGAAGGTTTACCTAAGACGTTAAGCGGTACCTCTACGACTTCCCTTTACAGCA	6720
Db	6661	TGCGAAGGTTTACCTAAGACGTTAAGCGGTACCTCTACGACTTCCCTTTACAGCA	6720
QY	6721	TGCGCCAGGCGCTGAGACTCAAGAGCGTGACGGGTCAATCCAGCCACAGAAAACAT	6780
Db	6721	TGCGCCAGGCGCTGAGACTCAAGAGCGTGACGGGTCAATCCAGCCACAGAAAACAT	6780
QY	6781	TCATGCAAGACATTACAAATTTGCCAAGATAGTGCAGGCAAAACAGTTTTCACGACGC	6840
Db	6781	TCATGCAAGACATTACAAATTTGCCAAGATAGTGCAGGCAAAACAGTTTTCACGACGC	6840
QY	6841	TGCCGAAAACGACAGCGGGTGTCCACATATTTGTGACAGCGTTCGCGCAGACTCG	6900
Db	6841	TGCCGAAAACGACAGCGGGTGTCCACATATTTGTGACAGCGTTCGCGCAGACTCG	6900
QY	6901	CCCTTAGTACGGCTGTATGTTTCTCAGAGTGTCCCGAGACGCGTSCGATGCTGAAC	6960
Db	6901	CCCTTAGTACGGCTGTATGTTTCTCAGAGTGTCCCGAGACGCGTSCGATGCTGAAC	6960
QY	6961	ACGATAGCTGCGCCATATTGATGTTGTGACTCACACGAGGCTAAGGTTTAAACGCGTTAG	7020
Db	6961	ACGATAGCTGCGCCATATTGATGTTGTGACTCACACGAGGCTAAGGTTTAAACGCGTTAG	7020
QY	7021	ACGCGTGTGCGGCCAAGCGCGCTTCACTGCGCGGCTCAACTGTCGCTGCCAATTGCG	7080
Db	7021	ACGCGTGTGCGGCCAAGCGCGCTTCACTGCGCGGCTCAACTGTCGCTGCCAATTGCG	7080
QY	7081	TGCTGTACTTAACCTAAAGTGCAGAAAGCAGCCGACGAGGAGCAAAAGGAGACGTAACG	7140
Db	7081	TGCTGTACTTAACCTAAAGTGCAGAAAGCAGCCGACGAGGAGCAAAAGGAGACGTAACG	7140
QY	7141	TGTACAACCTCTTTTCTCCACAACGAGCTGGGGTTTTTAAATGAGGCCACGATCAAG	7200
Db	7141	TGTACAACCTCTTTTCTCCACAACGAGCTGGGGTTTTTAAATGAGGCCACGATCAAG	7200
QY	7201	AAAAGGCAAGGACGCTTAAAGGCGTACCTCAAAACGCGCTCGATGGTTCTTGCTTCA	7260
Db	7201	AAAAGGCAAGGACGCTTAAAGGCGTACCTCAAAACGCGCTCGATGGTTCTTGCTTCA	7260
QY	7261	GCGCGTATACCTTGCGCTTACGCGCGCTTCTTCCGCCATCTGCTGGGAGGATATGTT	7320
Db	7261	GCGCGTATACCTTGCGCTTACGCGCGCTTCTTCCGCCATCTGCTGGGAGGATATGTT	7320
QY	7321	ATTACATGCACTTTCGCAACACCAAAAAGCTTCACGAACGAGCGTTTAAACATGCTCC	7380
Db	7321	ATTACATGCACTTTCGCAACACCAAAAAGCTTCACGAACGAGCGTTTAAACATGCTCC	7380
QY	7381	ATTATGTGGCAACCGCCGCCCACTCAGAGATGTGCAGCTATGTACAGGCAACAGCCGG	7440
Db	7381	ATTATGTGGCAACCGCCGCCCACTCAGAGATGTGCAGCTATGTACAGGCAACAGCCGG	7440
QY	7441	CAAGCTGCTCAACACGCTGTTCTATAGACTGAAGATAGTTTCCCGCCGTAACACACCC	7500
Db	7441	CAAGCTGCTCAACACGCTGTTCTATAGACTGAAGATAGTTTCCCGCCGTAACACACCC	7500
QY	7501	CTCAGCGCAGGAGCCCTTACGCTGTGACGGAACAGCCGGGACCTTTAAACGACTGGAGA	7560
Db	7501	CTCAGCGCAGGAGCCCTTACGCTGTGACGGAACAGCCGGGACCTTTAAACGACTGGAGA	7560
QY	7561	TTCTGGGCAACTTCGCGAGCTTTAGAACCGGAGAGAGAGGAAACCCGGCCGACGAGC	7620
Db	7561	TTCTGGGCAACTTCGCGAGCTTTAGAACCGGAGAGAGAGGAAACCCGGCCGACGAGC	7620
Db	7621	ACCCAAAGTACAGTACTGGCAGCTATGTACAGCCGTGACAGAAAAGCTATCCGAGATTG	7680
QY	7621	ACCCAAAGTACAGTACTGGCAGCTATGTACAGCCGTGACAGAAAAGCTATCCGAGATTG	7680
Db	7681	GAATCAGGAGAACACAGATTAATCACGTGACCTCATCCAAATCCAAAGTTTCTCA	7740
QY	7681	GAATCAGGAGAACACAGATTAATCACGTGACCTCATCCAAATCCAAAGTTTCTCA	7740
Db	7741	GGGTGTCAAGGGTATCGACTCAATTTGTGAGGAGGAGGTGATGAAGTTCTGTAATTCGA	7800
QY	7741	GGGTGTCAAGGGTATCGACTCAATTTGTGAGGAGGAGGTGATGAAGTTCTGTAATTCGA	7800
Db	7801	TGATTTAAATTAACCTTTATTTCCGAGACAGTCGTAATTCGATCATCATCTCCAGT	7860
QY	7801	TGATTTAAATTAACCTTTATTTCCGAGACAGTCGTAATTCGATCATCATCTCCAGT	7860
Db	7861	TCGTCTGCAAGCTGTATTTGGCAGGCGCGTGCAGGCTGTTCTGTAATCTGTACCAAT	7920
QY	7861	TCGTCTGCAAGCTGTATTTGGCAGGCGCGTGCAGGCTGTTCTGTAATCTGTACCAAT	7920
Db	7921	CCCTGTGTGATTCATTCAGATTCGTGCTGCGCTGACTGATGATTCAGCAACAAAGTA	7980
QY	7921	CCCTGTGTGATTCATTCAGATTCGTGCTGCGCTGACTGATGATTCAGCAACAAAGTA	7980
Db	7981	ATCCGGCGATGGGCAATCCCTCCCTCCAGTGGCTTAAAGATGATTTTCAGAGCTTGGA	8040
QY	7981	ATCCGGCGATGGGCAATCCCTCCCTCCAGTGGCTTAAAGATGATTTTCAGAGCTTGGA	8040
Db	8041	CGAATTTTAAAGCGCGGTGTCTGACACCGCGGGTCTCAACGGGGTGCAGATGAAATTCG	8100
QY	8041	CGAATTTTAAAGCGCGGTGTCTGACACCGCGGGTCTCAACGGGGTGCAGATGAAATTCG	8100
Db	8101	TACACGGGACATGTTTCTGCACTTCTTGACACCGAGCGGGGTCCAAACGGCTTAATGG	8160
QY	8101	TACACGGGACATGTTTCTGCACTTCTTGACACCGAGCGGGGTCCAAACGGCTTAATGG	8160
Db	8161	CCCCCTTTAAATGCAAGTTTAAATAGCCCGAGCCATGATGTTGCTCCGAATCAATTA	8220
QY	8161	CCCCCTTTAAATGCAAGTTTAAATAGCCCGAGCCATGATGTTGCTCCGAATCAATTA	8220
Db	8221	AAATTAATAATTAATTAATTTTTCACACCGCGGGATCCGAGCGGTGCAGTGGGGT	8280
QY	8221	AAATTAATAATTAATTAATTTTTCACACCGCGGGATCCGAGCGGTGCAGTGGGGT	8280
Db	8281	TGCTCAAAACCGAGGGAACCAAGGACCTTACGTGTGGCGGAGCGTACATGAATGTTTC	8340
QY	8281	TGCTCAAAACCGAGGGAACCAAGGACCTTACGTGTGGCGGAGCGTACATGAATGTTTC	8340
Db	8341	TCACCTGCTGCATGCGCGCTGTTCCCGAGACCCAAGACGCGCGCTGTACCTGTGGC	8400
QY	8341	TCACCTGCTGCATGCGCGCTGTTCCCGAGACCCAAGACGCGCGCTGTACCTGTGGC	8400
Db	8401	ACAAATCTCCAGACCAAAACCAAAACCCAGTTCTGAAAAGAGTCCCGGACACGAGCTGG	8460
QY	8401	ACAAATCTCCAGACCAAAACCAAAACCCAGTTCTGAAAAGAGTCCCGGACACGAGCTGG	8460
Db	8461	CGGAGCTGTGTGTAAGCTTAAAGAACACAGCTGCGCTTGAGGAGAAAGAAAGAGCTGGG	8520
QY	8461	CGGAGCTGTGTGTAAGCTTAAAGAACACAGCTGCGCTTGAGGAGAAAGAAAGAGCTGGG	8520
Db	8521	ACGTGTTTCCGGATTCATCTATGTCGTACGGAGAGATCAAACTGAAGCGGGCCATTTCTAA	8580
QY	8521	ACGTGTTTCCGGATTCATCTATGTCGTACGGAGAGATCAAACTGAAGCGGGCCATTTCTAA	8580
Db	8581	GGGCAATGTGGCAGATTCAAGTTCTACGCCACGAGCTGCACTGCTCACGCCGGGTCTAC	8640
QY	8581	GGGCAATGTGGCAGATTCAAGTTCTACGCCACGAGCTGCACTGCTCACGCCGGGTCTAC	8640
Db	8641	AGAGATGATGTCGAGGAATACCCCAAGCTGTGGGCTTCGCGGCAATTCGCAACACCGG	8700
QY	8641	AGAGATGATGTCGAGGAATACCCCAAGCTGTGGGCTTCGCGGCAATTCGCAACACCGG	8700

Qy	8701	TGCGTTACCTGGCGAATAATACGGCGCGCACCGCCCTACCGCTCAGACGACGCGCGCTC	8760
Db	8701		
Qy	8761	AGCGCGTGGCGGCACAGGGCGCCCTGGCTCCCGTGAATACCGTTCCATGGTACTCAACA	8820
Db	8761		
Qy	8821	AATAACAGGGGGTCAACGGGAACAACGTTTTCACCTGGCGGAACCTGGGGTACTTCG	8880
Db	8821		
Qy	8881	CGGGGCGCGGCTGGAGCAGCACTGTGGCGGAAACCTCCCTTTAAGAAACGGGCG	8940
Db	8881		
Qy	8941	TCAGCGCATGCTAAGAAGAAGACACGTATGATGACCCCATTTATCGACCGCTAATAA	9000
Db	8941		
Qy	9001	AGCGAGCGGGGGAACACAATCAGCAGCTTCGAGGGGGAAGCGTTAAAAAGGCGTGC	9060
Db	9001		
Qy	9061	AGCGCGTGTAGAGATAGAGACAACTTAACCTATTGAAGTCGTAATCTTGGAGCTTA	9120
Db	9061		
Qy	9121	TACGACACCTGGGGAAAGGGCTGCCAGACTTAAGCTCCGAGGAGCTGCAATATTACCTCG	9180
Db	9121		
Qy	9181	GTACACTTGTATGTTGACGAGAGAGTTTTATTATTTAGTTGATTAATATAGCACAGTCAAG	9240
Db	9181		
Qy	9241	GCGTGCCTGAGATATCAGAGAGCGGGTGCCTTAATAGAGATCCGACGAGCAGACAG	9300
Db	9241		
Qy	9301	ATCTTCAAGTTCTAGACAGGACGAGATATGCCACCGCTTCTGTACAGCCCCCGAGAAC	9360
Db	9301		
Qy	9361	AGCTACGAGCCCTAGCGCGCGCCCTACTGGCGGGGAAGACGAAAAATTAAACCGCG	9420
Db	9361		
Qy	9421	TGCTGAGCGATCTAGACCTTTAGAAAAACCGTGGCAGCGGCGCAACATGGCCAGGAAAC	9480
Db	9421		
Qy	9481	TCGCGAGCATTAATACGGCGACCTGTGGCGCTCGCCGCTGCACTTGAGTCTGTGTTATCTTTG	9540
Db	9481		
Qy	9541	CGGACCGGGAAGATGAGGAGTCCCGCATTTCTAAAAAACAACACATAGAGAAC	9600
Db	9541		
Qy	9601	TGAACCGGACCTTTCGCGCTGCTACGCGAAGAAACCTCGGTAAGACCTCCAGCTGT	9660
Db	9601		
Qy	9661	CGCTCGAAGTGAAGACACTTGGCCAAAAAATCGAGGACAACTCGGAGACTGGAGCGCA	9720
Db	9661		
Qy	9721	GTCGCGCGAGAGATATTTCAGAGCGAGAGATTTTGAACAATACACTAGAGCCCAAT	9780
Db	9721		
Qy	9781	GTCACATACACTACGAGTACTTCTTCAAGTTTACGGGGCGGGTTAATAGATTAACA	9840
Db	9781		
Qy	9841	TGTGCTAATTAACGATGTAGAACTGCTGTGTAAAGACTAAGGAGTGTGTTTATTGCA	9900
Db	9841		
Qy	9901	TCGGTGCAAAAGAGCTGTCCGGATTGAACCGGGTTCTGACCTTTCTGTCAACACTGC	9960
Db	9901		
Qy	9961	GGGGTATCTCCCGATCCGACACCACTATATGTCAGTCACTGCTTGGCTACAGT	10020
Db	9961		
Qy	10021	GCTGAGGGAATCGAACTGCTGTAACCAATCAGGGGTCAGTTTACTGCGGTGTTGGCAG	10080
Db	10021		
Qy	10081	ACCGACACTGCGATCACCCTCTGTAAAGGTTAGGGGGAAGCCAAATACAGGCTGTTTG	10140
Db	10081		
Qy	10141	AGACAGAACTGAGCGACCTGGTCTTAAAGTAAACAAACGTTGCGAGCGCCACGACGACG	10200
Db	10141		
Qy	10201	GCGTCCGGTCTCTGACGATCAGTTAAAGGAGTGTGCTGGCGGCATACAAAGATCACA	10260
Db	10201		
Qy	10261	ATAATTTCAACGGGGTCCCGCTCAATCATGAACTATGCAATCTTAATTTATTGAAACG	10320
Db	10261		
Qy	10321	CCGGGCAAAACGGGCTCCAGACCGGAGCCGAAAAAGAGTCTCAAAATGGCCAGACTGC	10380
Db	10321		
Qy	10381	TAAACACGAGGGCGGATATGACAGAGCACCGTGGCTTAATTAACCCAACTAAGCGCGA	10440
Db	10381		
Qy	10441	CTCACCTCTACGACTGTTTCGAGCGGATCCCATAGAAATCCCTGTGTGGCGGCTTTT	10500
Db	10441		
Qy	10501	TTAACCTATAGAGACACCATTAACGCACTGAGCCGGGATTTGCTCCGTGACCTTTTC	10560
Db	10501		
Qy	10561	AACAGCAAACTATACCAAGCTTATGCGAAAAACAAACGAGCTGTTCACCAAGCTCAATA	10620
Db	10561		
Qy	10621	GCATCTCTGCGTCAAGGGGAGGCGGGAATCGCAAAAACCGGCCACCCCTCGGAGGACAGGA	10680
Db	10621		
Qy	10681	CCACACAGTGGCGGCAACCGCGCAAGGACGTCATCAAAAGACGACATATCGCAAAAG	10740
Db	10681		
Qy	10741	AACAGTACATGAAAAAGGTGGCCAGGAGCGCTTTTAAAAAACTAACAGAGTGTCTGCAGA	10800
Db	10741		
Qy	10801	CGCAGACCGGGGTGTGGCAAAAGCACTTGTGATGGCGGTAATGGGGGGGGTGGCTTAACG	10860
Db	10801		
Qy	10861	GCGAGCGGTCCGAGCTGTGAACCATTTTCTCTCAGCGGGCGCTTGTGCGGCTTCCCT	10920
Db	10861		

Dp	10861	GGCGGGGCTCGAGGCTGAGTGAACCATTTTCTCTCAGGGGGCTTCGTGGCTTCCT	10920
Qy	10921	GGGAGGGCGCTCGCTCGGTGGATTCACATTTTATTCGAAAACTCGAAATCATTTAAAACT	10980
Dp	10921	GGGAGGGCGCTCGCTCGGTGGATTCACATTTTATTCGAAAACTCGAAATCATTTAAAACT	10980
Qy	10981	CACATATTTCCAGCGCTCAGTGGCGAACGCTAGAGTATATCACGCTGCAGTTTACG	11040
Dp	10981	CACATATTTCCAGCGCTCAGTGGCGAACGCTAGAGTATATCACGCTGCAGTTTACG	11040
Qy	11041	GGCTGATAACGGGCCCCCTGACGGCGCAGAGGATCTCTTCCGGCCCCCGGCAACGTG	11100
Dp	11041	GGCTGATAACGGGCCCCCTGACGGCGCAGAGGATCTCTTCCGGCCCCCGGCAACGTG	11100
Qy	11101	CGCTGGCCCGAGTGTTCGAGAGCGGGCGGAATGCTTCGCGATCAAGATGCTGTGTGAG	11160
Dp	11101	CGCTGGCCCGAGTGTTCGAGAGCGGGCGGAATGCTTCGCGATCAAGATGCTGTGTGAG	11160
Qy	11161	AGATGATATGGCCCCAGATTTCAACGGAAGACTGATAGACAGACATTTTAATCGTTTTT	11220
Dp	11161	AGATGATATGGCCCCAGATTTCAACGGAAGACTGATAGACAGACATTTTAATCGTTTTT	11220
Qy	11221	ACCAACTTCCCGAAGGTGATATCAACGGCGTACAAAATGCCGCTGCTCTTATACGAG	11280
Dp	11221	ACCAACTTCCCGAAGGTGATATCAACGGCGTACAAAATGCCGCTGCTCTTATACGAG	11280
Qy	11281	AGCTGCTCCTCTGGGTGGCGCTTATATATGCGACGTGGGAAAAAGAGCGCTCGGATATTTT	11340
Dp	11281	AGCTGCTCCTCTGGGTGGCGCTTATATATGCGACGTGGGAAAAAGAGCGCTCGGATATTTT	11340
Qy	11341	CCCTAGCGCGCGAAGAACTCTCCATCTCCACCTAGACGTAAAGGCTGACGTCCGGCC	11400
Dp	11341	CCCTAGCGCGCGAAGAACTCTCCATCTCCACCTAGACGTAAAGGCTGACGTCCGGCC	11400
Qy	11401	TGTATCTAAGTACGAGCAAGAGAGCGCCCTGCTTATTTCTCAAAATACCGGCTGGA	11460
Dp	11401	TGTATCTAAGTACGAGCAAGAGAGCGCCCTGCTTATTTCTCAAAATACCGGCTGGA	11460
Qy	11461	TATTTAAAGACGTAGAGCTCTCTGTACATACCTGTGACGTGCCAGGCCATGATG	11520
Dp	11461	TATTTAAAGACGTAGAGCTCTCTGTACATACCTGTGACGTGCCAGGCCATGATG	11520
Qy	11521	ATAACTAACCGAAACGGCTGCTCTCGGGGCGTGGGTGTATATATCGCATGCGGACG	11580
Dp	11521	ATAACTAACCGAAACGGCTGCTCTCGGGGCGTGGGTGTATATATCGCATGCGGACG	11580
Qy	11581	GGGTTTGGCGAAAACGTACACACCCCCCAAGGGGCGACACACCGCGAAGCGCAACGGCG	11640
Dp	11581	GGGTTTGGCGAAAACGTACACACCCCCCAAGGGGCGACACACCGCGAAGCGCAACGGCG	11640
Qy	11641	GGCGCCGTCGAGCGCCACACCTCCCGAGAACCCACTAGAGGCCGAGGCGTTTAAAGTTTGC	11700
Dp	11641	GGCGCCGTCGAGCGCCACACCTCCCGAGAACCCACTAGAGGCCGAGGCGTTTAAAGTTTGC	11700
Qy	11701	GTTGTGAGCGCTCTGGGCGACCGGCGGAATCTTCAGGTTTAACTGTGAAAAAAAGTGTGCG	11760
Dp	11701	GTTGTGAGCGCTCTGGGCGACCGGCGGAATCTTCAGGTTTAACTGTGAAAAAAAGTGTGCG	11760
Qy	11761	GGCACCGAGACAAGACGCAACCAAGAAGGATCTATGTGTTTAAAAAAATATTTGTC	11820
Dp	11761	GGCACCGAGACAAGACGCAACCAAGAAGGATCTATGTGTTTAAAAAAATATTTGTC	11820
Qy	11821	CCGCAACATCTTTTAAAGGTGAGAGGTATCCGGAAGGTGGCAACCTCGGTGACCGTATGCA	11880
Dp	11821	CCGCAACATCTTTTAAAGGTGAGAGGTATCCGGAAGGTGGCAACCTCGGTGACCGTATGCA	11880
Qy	11881	GGGTGGAACCAAGACCGCGTGAACGGGCAAGCAAGAGGTATCCGACACGGTGGCGAGTAC	11940
Dp	11881	GGGTGGAACCAAGACCGCGTGAACGGGCAAGCAAGAGGTATCCGACACGGTGGCGAGTAC	11940
Qy	11941	GAGATTAACCAACATGACACAGACCTACAGTGTTCAGCTCCATGCGCGCTAAACGTCAAC	12000
Dp	11941	GAGATTAACCAACATGACACAGACCTACAGTGTTCAGCTCCATGCGCGCTAAACGTCAAC	12000

Db	11941	AAGATCAACCAACNATGGAACAGCAACCTACACAGTGTTCACGCTCCATGCGGGTAACGCTCAAC	12000
QY	12001	GGCATAGTAACACCTTACAGGAGACGAGCTTCACATAACAGACCGTGTTCGCAACCG	12060
Db	12001	GGCATAGTAACACCTTACACGAGACGAGACTTCACATAACCGAGACCGTGTTCGCAACCG	12060
QY	12061	GTCGAGGGGCTCACGGGATACATCAGGATACACTTCAGTCAGCGGGGCTGTACACGCA	12120
Db	12061	GTCGAGGGGCTCACGGGATACATCAGGATACACTTCAGTCAGCGGGGCTGTACACGCA	12120
QY	12121	CCGGGATGGTTCGCGGGAATTTACAGGGTCCAGAACCAAGTCAACTGGGAGATCGTGGAC	12180
Db	12121	CCGGGATGGTTCGCGGGAATTTACAGGGTTCAGAACCAAGTCAACTGGGAGATCGTGGAC	12180
QY	12181	ATGATCGCGCTTCGCGCGGAACCGTACTCGTATTTTGTCCACGCCCTTGGAGACGGTA	12240
Db	12181	ATGATCGCGCTTCGCGCGGAACCGTACTCGTATTTTGTCCACGCCCTTGGAGACGGTA	12240
QY	12241	GAGGTGTCCCGCTTCTGGCCAAACGACTCAACGTGCTCGGTGCGGGGGAATAACCGGAAC	12300
Db	12241	GAGGTGTCCCGCTTCTGGCCAAACGACTCAACGTGCTCGGTGCGGGGGAATAACCGGAAC	12300
QY	12301	GGCCTCGGCGCGCGCTGCTCACAAATATACACATCGTCGACTTCGCGACCCGCGACGCC	12360
Db	12301	GGCCTCGGCGCGCGCTGCTCACAAATATACACATCGTCGACTTCGCGACCCGCGACGCC	12360
QY	12361	ACCAACCGAAGCGGGGTCTTCGCCGACTCGGAGAGATACACCGTATCGTGAAGGCGGAG	12420
Db	12361	ACCAACCGAAGCGGGGTCTTCGCCGACTCGGAGAGATACACCGTATCGTGAAGGCGGAG	12420
QY	12421	GACCCCAAGTGGGGGTCTGGCGGTGAGCGCTGTGGAAACCTTCCAGGGGCGATACAG	12480
Db	12421	GACCCCAAGTGGGGGTCTGGCGGTGAGCGCTGTGGAAACCTTCCAGGGGCGATACAG	12480
QY	12481	ACGAGCGCAGAGGCGCAGCTTACACTTCGTGGGCCAAACGAGTGAAGGCGCACCTTACGTC	12540
Db	12481	ACGAGCGCAGAGGCGCAGCTTACACTTCGTGGGCCAAACGAGTGAAGGCGCACCTTACGTC	12540
QY	12541	CCGCTCTCCAGGTAACCTTACACGGGACGTAACCCCTGCTCATATGATGTTATTCAG	12600
Db	12541	CCGCTCTCCAGGTAACCTTACACGGGACGTAACCCCTGCTCATATGATGTTATTCAG	12600
QY	12601	AAAACCTTCAACGCGCACCATTAAGAAGGTGTCCGATACCCACGGAACAAAGGATCGGAG	12660
Db	12601	AAAACCTTCAACGCGCACCATTAAGAAGGTGTCCGATACCCACGGAACAAAGGATCGGAG	12660
QY	12661	CAGTACTACGAACCGAGGGGGGTCTGTTTCTCCGTGGGCGAGCGTTAAACCCCTTAAGC	12720
Db	12661	CAGTACTACGAACCGAGGGGGGTCTGTTTCTCCGTGGGCGAGCGTTAAACCCCTTAAGC	12720
QY	12721	CTAGCTGACGAGATCGCGGAATTTAAACGGGACCAACGCCAGCACCCTCCACACACCTCA	12780
Db	12721	CTAGCTGACGAGATCGCGGAATTTAAACGGGACCAACGCCAGCACCCTCCACACACCTCA	12780
QY	12781	ACCGGCAACCGCGTTCGAAAGAGGTGCGTACGAACGAGCGAGCGAAGCGAGACTTAACG	12840
Db	12781	ACCGGCAACCGCGTTCGAAAGAGGTGCGTACGAACGAGCGAGCGAAGCGAGACTTAACG	12840
QY	12841	GGCGCCCGAGTGCAGTTGCGCTTACGACAAAGCTCCGCGGAGCATCAAAAGTCTGTGAG	12900
Db	12841	GGCGCCCGAGTGCAGTTGCGCTTACGACAAAGCTCCGCGGAGCATCAAAAGTCTGTGAG	12900
QY	12901	GAGCTCTTCAGAGGGGTGGTGGCCGGAACAGGATGAAGGACACCTACATGTGGTACGAATG	12960
Db	12901	GAGCTCTTCAGAGGGGTGGTGGCCGGAACAGGATGAAGGACACCTACATGTGGTACGAATG	12960
QY	12961	AGCAAGATTTAAACCCACAGCGTAATGACGGCGATATACGGGCGCGCGTGTGCGCAAG	13020
Db	12961	AGCAAGATTTAAACCCACAGCGTAATGACGGCGATATACGGGCGCGCGTGTGCGCAAG	13020
QY	13021	TTTCGTGGGCGACGCCATCTCCGTGACGAGACTGCGGGGGGGTGGACAAAGCGTCCGTACG	13080
Db	13021	TTTCGTGGGCGACGCCATCTCCGTGACGAGACTGCGGGGGGGTGGACAAAGCGTCCGTACG	13080

OY	13081	ATCCACAAGAGCCTCCGCACTCCACCCCGGGGATCTGCTACTCGCGCCCCCGGCTACG	13140
Db	13081	ATCCACAAGAGCCTCCGCACTCCACCCCGGGGATCTGCTACTCGCGCCCCCGGCTACG	13140
OY	13141	TTCAAGTTCCTCACAAGCAGCACCGGTTCAAGGGGCGACTGGGAGCCCAAGAAAGATC	13200
Db	13141	TTCAAGTTCCTCACAAGCAGCACCGGTTCAAGGGGCGACTGGGAGCCCAAGAAAGATC	13200
OY	13201	ATACTGACGACACACAGGTGGAGCGTGCAAAAGAGAGCTGCGAACCTACTTCATAGCG	13260
Db	13201	ATACTGACGACACACAGGTGGAGCGTGCAAAAGAGAGCTGCGAACCTACTTCATAGCG	13260
OY	13261	AGCAACGTAACTACTACTACAAACACTACGCTTCCTGTAAAAAAATTAACACTCCGAG	13320
Db	13261	AGCAACGTAACTACTACTACAAACACTACGCTTCCTGTAAAAAAATTAACACTCCGAG	13320
OY	13321	ATATCCACCCTCGTACGTTCACTCCGCCCTGAACCTTCGTTTATAGAAACATAGATTTC	13380
Db	13321	ATATCCACCCTCGTACGTTCACTCCGCCCTGAACCTTCGTTTATAGAAACATAGATTTC	13380
OY	13381	AGGTCATCAGACTGTACAGCCCGCGGAAAAAGCTGTCCGGAGCGTTTCGATATA	13440
Db	13381	AGGTCATCAGACTGTACAGCCCGCGGAAAAAGCTGTCCGGAGCGTTTCGATATA	13440
OY	13441	GAAACCATGTTTCAAGGAATATCAACTACTACAGCAACGCTGGCGGAGACTCCGGAGAGAC	13500
Db	13441	GAAACCATGTTTCAAGGAATATCAACTACTACAGCAACGCTGGCGGAGACTCCGGAGAGAC	13500
OY	13501	CTGGACAACAGATCGACTGAACCGCGACCGCGCTGGCCGCACTGTCGAGATAGTC	13560
Db	13501	CTGGACAACAGATCGACTGAACCGCGACCGCGCTGGCCGCACTGTCGAGATAGTC	13560
OY	13561	GCGGACCTGGGGGATGTGGCGCGCAAGCGATTAAGTGCGCACTAGCGGATACCCCTG	13620
Db	13561	GCGGACCTGGGGGATGTGGCGCGCAAGCGATTAAGTGCGCACTAGCGGATACCCCTG	13620
OY	13621	TTGCGATCAATGTGAGCGGGTTCACTTAACCTTTATAAAGAGTCGTTGGGGGCACTC	13680
Db	13621	TTGCGATCAATGTGAGCGGGTTCACTTAACCTTTATAAAGAGTCGTTGGGGGCACTC	13680
OY	13681	ATGATCCGTGTATTTGTGGCGGTCGTCGATCGTGTTCGGCTAAACCGGCGCACCAAC	13740
Db	13681	ATGATCCGTGTATTTGTGGCGGTCGTCGATCGTGTTCGGCTAAACCGGCGCACCAAC	13740
OY	13741	GCCATCGGCCAGGCCCCCATCAAGATGATCTACCCGCACTAGACAAATAGCAGCCCTCT	13800
Db	13741	GCCATCGGCCAGGCCCCCATCAAGATGATCTACCCGCACTAGACAAATAGCAGCCCTCT	13800
OY	13801	GCGGTTAAAGTGCACAGGAGCAGATTAAAAACATTTCTCGCGGATGACACAGCTACAG	13860
Db	13801	GCGGTTAAAGTGCACAGGAGCAGATTAAAAACATTTCTCGCGGATGACACAGCTACAG	13860
OY	13861	CAGGAAGAGCGTAGGCGGTGTACAGCAACGAGAGTCAAGCGCCCTGTTTCCGGCGC	13920
Db	13861	CAGGAAGAGCGTAGGCGGTGTACAGCAACGAGAGTCAAGCGCCCTGTTTCCGGCGC	13920
OY	13921	GCGTACAGCGGACTTAAAGCTGCGCTTTAGGGGATATAAACCCGTTGGAAAAAGAGGCT	13980
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OY	13981	CAGAAGTATGAATAGCAATATACACACACACAGCCTGTACTTGGCGCGCCAGAG	14040
Db	13981	CAGAAGTATGAATAGCAATATACACACACACAGCCTGTACTTGGCGCGCCAGAG	14040
OY	14041	CCGCGCGGCATTCGATTCGCGCACCCCGCGGCTCCCGACACCCCTTCAGCGCCCGGG	14100
Db	14041	CCGCGCGGCATTCGATTCGCGCACCCCGCGGCTCCCGACACCCCTTCAGCGCCCGGG	14100
OY	14101	CGTCCGCGGTCTGTATCAATCATAGATTTCCTTTAACCCGCTACCTGGGCGCTCGCGACCA	14160
Db	14101	CGTCCGCGGTCTGTATCAATCATAGATTTCCTTTAACCCGCTACCTGGGCGCTCGCGACCA	14160

QY	14161	CGCCCCCACTCACACAGAGGACCGATGCTCCGCCCTCGCGGCGCGGAGCGTTTCAG	14220
Db	14161	CGCCCCCACTCACACAGAGGACCGCATGCTCCGCCCTCGCGGCGCGGAGCGTTTCAG	14220
QY	14221	CGCGACACAGAGTTTGGAGGCTATCCCGCGCTCTCCCGAAGCCACAGGGGCAAGCGGG	14280
Db	14221	CGCGACACAGAGTTTGGAGGCTCATCCCGCGCTCTCCCGAAGCCACAGGGGCAAGCGGG	14280
QY	14281	ATGATCCCGGTCCAGATCCCGTTCCCGCAACGTAATTCCAGAAACGTTCTCGCGAGAC	14340
Db	14281	ATGATCCCGGTCCAGATCCCGTTCCCGCAACGTAATTCCAGAAACGTTCTCGCGAGAC	14340
QY	14341	GTGCTGCTCGCCAACGAACGGTTCATGTGGACGGCGCGGACCGCAAGCCGTCGCCCG	14400
Db	14341	GTGCTGCTCGCCAACGAACGGTTCATGTGGACGGCGCGGACCGCAAGCCGTCGCCCG	14400
QY	14401	GACCCCCAAGACCAATCCATCATCGTTTACAGCGGTACGACGTCGTTGAAAACAACGTACGG	14460
Db	14401	GACCCCCAAGACCAATCCATCATCGTTTACAGCGGTACGACGTCGTTGAAAACAACGTACGG	14460
QY	14461	CGCGACAGGTGTGCCAGAGTAACCTAGCCGCTTCCAAAGGACATTATCCCAAGCGGAAC	14520
Db	14461	CGCGACAGGTGTGCCAGAGTAACCTAGCCGCTTCCAAAGGACATTATCCCAAGCGGAAC	14520
QY	14521	GTGCTCAAGCTCTCTGGGGCGAAACGAGAGCGGACACAGCGTGTGGTGAACGTTCCGT	14580
Db	14521	GTGCTCAAGCTCTCTGGGGCGAAACGAGAGCGGACACAGCGTGTGGTGAACGTTCCGT	14580
QY	14581	CACACAGTATATTCTTACGCGAAGTTTCCAGCCGGCATTTAACGTACCCACATCTCTCCAG	14640
Db	14581	CACACAGTATATTCTTACGCGAAGTTTCCAGCCGGCATTTAACGTACCCACATCTCTCCAG	14640
QY	14641	CAGGCGCTCAAGAAACACAGACCGCGCGCTCGCGCTCTTCAGACCAAGAGAGTTGAAC	14700
Db	14641	CAGGCGCTCAAGAAACACAGACCGCGCGCTCGCGCTCTTCAGACCAAGAGAGTTGAAC	14700
QY	14701	AAAAGAAATTCATAAAGCCTAGAGCTCGCGAGACATCCCGTCACGGAATTCAGCTATCG	14760
Db	14701	AAAAGAAATTCATAAAGCCTAGAGCTCGCGAGACATCCCGTCACGGAATTCAGCTATCG	14760
QY	14761	TCCGGTTCATGCTCTCCACCCCTCAGACCCCGCTGTCGCGTGGGGGTGCCAGGTTTC	14820
Db	14761	TCCGGTTCATGCTCTCCACCCCTCAGACCCCGCTGTCGCGTGGGGGTGCCAGGTTTC	14820
QY	14821	GAGTCAAAAGCTGGAGCGCGTTGGCGGGTTCGTTTGGATCAGGGGTTTACACGTTTCGGG	14880
Db	14821	GAGTCAAAAGCTGGAGCGCGTTGGCGGGTTCGTTTGGATCAGGGGTTTACACGTTTCGGG	14880
QY	14881	TGGTACTCGTGGCGCGCGGCCACGCCCGCTGGCGGCGCAGAGATGCCAGGACGGCCCTG	14940
Db	14881	TGGTACTCGTGGCGCGCGGCCACGCCCGCTGGCGGCGCAGAGATGCCAGGACGGCCCTG	14940
QY	14941	GAGTTTGACTGCAGCTGGGAGGACCTCAGCGTTCAAGCGGACCGACGCACTGGCCCCG	15000
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QY	15001	TACCGCATCGTGGCGCTTTGATTTGACAGTGCACCTGGAGAGCGGGAAATTCGCGGCCACAG	15060
Db	15001	TACCGCATCGTGGCGCTTTGATTTGACAGTGCACCTGGAGAGCGGGAAATTCGCGGCCACAG	15060
QY	15061	CGCGACGGCGAGCGGGTGATCCAGATTCCTGCGTCTTACAGCAGCAAGGGAAGGCGGG	15120
Db	15061	CGCGACGGCGAGCGGGTGATCCAGATTCCTGCGTCTTACAGCAGCAAGGGAAGGCGGG	15120
QY	15121	CCCAATCCGCGCAACATACCTGTTCAAGCGTGGGACGTGCGACCCATCCCGGACACCGAC	15180
Db	15121	CCCAATCCGCGCAACATACCTGTTCAAGCGTGGGACGTGCGACCCATCCCGGACACCGAC	15180
QY	15181	GTTTTGGAGTTTCCGTCGGAATATACAGTCTGGTGTGTTTGGCCATGATCCGGGAC	15240
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21361 CCGCCAAAAGGGCGGGGAGACCCGTGGCGGCTCCCAAAATTTTACGCGCGGGGACAGTT 21420
21361 CCGCCAAAAGGGCGGGGAGACCCGTGGCGGCTCCCAAAATTTTACGCGCGGGGACAGTT 21420
21421 CCGTGAAGTGGTGGAGCCCTGTATTAACACAGCAACTCTCCAGAGCGCCCTCCAAA 21480
21421 CCGTGAAGTGGTGGAGCCCTGTATTAACACAGCAACTCTCCAGAGCGCCCTCCAAA 21480
21481 ACACCCCTTGTGTTAACAAGAGAAACTCGTCCCTGAGGTTATATCGGGCTGAAGCC 21540
21481 ACACCCCTTGTGTTAACAAGAGAAACTCGTCCCTGAGGTTATATCGGGCTGAAGCC 21540
21541 CGAACACGAGACCTGGTGGCCACGCGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 21600
21541 CGAACACGAGACCTGGTGGCCACGCGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 21600
21541 CGAACACGAGACCTGGTGGCCACGCGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 21600
21601 TTAATTCAGAGTGGCGCAAGTACTGCAAGTGGCGGAGTGGCGCGGACAGCGCAGCGGA 21660
21601 TTAATTCAGAGTGGCGCAAGTACTGCAAGTGGCGGAGTGGCGCGGACAGCGCAGCGGA 21660
21661 CCGCCGCGGACCTTCCTGGGGTGGGGAACCAACCGGAGTGGTGGCGCGGATTCAGACCA 21720
21661 CCGCCGCGGACCTTCCTGGGGTGGGGAACCAACCGGAGTGGTGGCGCGGATTCAGACCA 21720
21721 CCGAAACGGGTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 21780
21721 CCGAAACGGGTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 21780
21781 TTAACAACGAGGCTTTTCAACTATTAACGTTAAAGGGTGAAGAGCAAACTATTTTAA 21840
21781 TTAACAACGAGGCTTTTCAACTATTAACGTTAAAGGGTGAAGAGCAAACTATTTTAA 21840

QY	21841	AGCAGCTTGGGGGGGGCCGACACAGGCGCGGGCCGGCTGTTAGCGAGTAATAAACCA	21900
Db	21841	AGGCAGCTTGGGGGGGGCCGACACAGGCGCGGGCCGGCTGTTAGCGAGTAATAAACCA	21900
QY	21901	CGTGGTCTCCCAAGCGCTTCCCGAGCGTGAAGGTCTCCCAAGGCCAAACAAACAC	21960
Db	21901	CGTGGTCTCCCAAGCGCTTCCCGAGCGTGAAGGTCTCCCAAGGCCAAACAAACAC	21960
QY	21961	AGATAATAAATAATAATGTTATTTTATTAACCTTAACGGCGGATTAATGCTCTT	22020
Db	21961	AGATAATAAATAATAATAATGTTATTTTATTAACCTTAACGGCGGATTAATGCTCTT	22020
QY	22021	AACAGGGGCCAATGAAAGCAACGTCGAGGGCGGCATTGCGGCGCTCAAGAGCAACGCCAA	22080
Db	22021	AACAGGGGCCAATGAAAGCAACGTCGAGGGCGGCATTGCGGCGCTCAAGAGCAACGCCAA	22080
QY	22081	CACGGGGGCTCGTAACAGCGTTAAACAAACATTAAGCCATTGCTAACCGTTAAATCCA	22140
Db	22081	CACGGGGGCTCGTAACAGCGTTAAACAAACATTAAGCCATTGCTAACCGTTAAATCCA	22140
QY	22141	ACCCTTGTGCGTCCGAGACCAATTCGCGCAGCTGCTACGTCAAGGGTGTGTTTAAATGC	22200
Db	22141	ACCCTTGTGCGTCCGAGACCAATTCGCGCAGCTGCTACGTCAAGGGTGTGTTTAAATGC	22200
QY	22201	CATTTTGAGCCCTTGGACAGCGCGCGTCTGCGTTAATGTGTTTCTTAATCCGCTGCCA	22260
Db	22201	CATTTTGAGCCCTTGGACAGCGCGCGTCTGCGTTAATGTGTTTCTTAATCCGCTGCCA	22260
QY	22261	AGGCCCTCTTGGAATGTCATATAGCGCTGCGCGGGTCTTCTGCGCTTTTGGGACGC	22320
Db	22261	AGGCCCTCTTGGAATGTCATATAGCGCTGCGCGGGTCTTCTGCGCTTTTGGGACGC	22320
QY	22321	TTGTGCAACCGCGCTAAGCAGTTCCTTCTCACTGCGTGTCTCCCGGGATTTGGCACACAGTTT	22380
Db	22321	TTGTGCAACCGCGCTAAGCAGTTCCTTCTCACTGCGTGTCTCCCGGGATTTGGCACACAGTTT	22380
QY	22381	TTACCGGGGGAGTGTGTTAATATATCAGGCGCTCCACGACGACTGCGAGGTGTGGAG	22440
Db	22381	TTACCGGGGGAGTGTGTTAATATATCAGGCGCTCCACGACGACTGCGAGGTGTGGAG	22440
QY	22441	TAAAGACACATTAACCGGGGGGGGAGAGATGATTCATACCCCAACAGCAGAGTTCG	22500
Db	22441	TAAAGACACATTAACCGGGGGGGGAGAGATGATTCATACCCCAACAGCAGAGTTCG	22500
QY	22501	GGCGGGGTCGCTCATGAGGCCCATAGAAAGGCATTAATCACTACACACGGGAACAC	22560
Db	22501	GGCGGGGTCGCTCATGAGGCCCATAGAAAGGCATTAATCACTACACACGGGAACAC	22560
QY	22561	GCAAAAAAAGCAGCAGAAAGGCGCCCTCATGTGTGCAAAAAACAAACAAAGAGGG	22620
Db	22561	GCAAAAAAAGCAGCAGAAAGGCGCCCTCATGTGTGCAAAAAACAAACAAAGAGGG	22620
QY	22621	GTCGCTGTGCTGTGACACAGCGCAGCGCTGCGCGCTGCGGACAGGTTGAAGGGGTC	22680
Db	22621	GTCGCTGTGCTGTGACACAGCGCAGCGCTGCGCGCTGCGGACAGGTTGAAGGGGTC	22680
QY	22681	CATTAAATACCCGCGCGCGCGCTCGACGGAACACAGCGGTGTGTAACTACG	22740
Db	22681	CATTAAATACCCGCGCGCGCGCGCTCGACGGAACACAGCGGTGTGTAACTACG	22740
QY	22741	GCAGGTGCTTCCCTCCAGATGTGGCATGTGAGATCCCAAAAGGGGCTGTAACTACG	22800
Db	22741	GCAGGTGCTTCCCTCCAGATGTGGCATGTGAGATCCCAAAAGGGGCTGTAACTACG	22800
QY	22801	GTCGCGCGGGGTTCAAAAGAGGGGATTCGCCAAACAGTTAAAGCTTTTGTGCCAA	22860
Db	22801	GTCGCGCGGGGTTCAAAAGAGGGGATTCGCCAAACAGTTAAAGCTTTTGTGCCAA	22860
QY	22861	CAGAAAGCAACAGCAACCGAAAGAAATCTCCAAACAGCAGCAGGTCCTCCGCGCGCA	22920
Db	22861	CAGAAAGCAACAGCAACCGAAAGAAATCTCCAAACAGCAGCAGGTCCTCCGCGCGCA	22920

QY	22921	TAAAGGAAATTTCCCTCACCTTAACACACGCGCGCGGTAAAGCTTTAAACAGCGAAT	22980
Db	22921	TAAAGGAAATTTCCCTCACCTTAACACACGCGCGCGGTAAAGCTTTAAACAGCGAAT	22980
QY	22981	ACTTCCTAGGCTGTGTTAATAAACACACAGGCTGTAAATTCGCGGGGCCCTTTGG	23040
Db	22981	ACTTCCTAGGCTGTGTTAATAATAACACACAGGCTGTAAATTCGCGGGGCCCTTTGG	23040
QY	23041	GCCCGCGCGTGTGGGGGTGCGTGTCTGCTGTGTGCGAATCACCACCCGCTGCC	23100
Db	23041	GCCCGCGCGTGTGGGGGTGCGTGTCTGCTGTGTGCGAATCACCACCCGCTGCC	23100
QY	23101	CGAAAAAGGCGACACACCCCTGCGCTAGTTTTTTTAAAACTTAACACCGGCAAGGGA	23160
Db	23101	CGAAAAAGGCGACACACCCCTGCGCTAGTTTTTTTAAAACTTAACACCGGCAAGGGA	23160
QY	23161	GAGGGGAAAGGGGTGCGCTAAATGCGCTTTAGAGCAACCGGACGCGGGGAAAAAGG	23220
Db	23161	GAGGGGAAAGGGGTGCGCTAAATGCGCTTTAGAGCAACCGGACGCGGGGAAAAAGG	23220
QY	23221	GGGCAAAACCGCGGTTAACACAAACAGCAACAGCGGCCAACCAATTAACACAGCA	23280
Db	23221	GGGCAAAACCGCGGTTAACACAAACAGCAACAGCGGCCAACCAATTAACACAGCA	23280
QY	23281	TATTCCTGTGTTTGGCGGGCGCGGTGCTAACCGCTTAACCGCTTGGCGTTTGCA	23340
Db	23281	TATTCCTGTGTTTGGCGGGCGCGGTGCTAACCGCTTAACCGCTTGGCGTTTGCA	23340
QY	23341	AGCAGCGCCCGCGCTGACACCGCGGCTCCCGGAGTACAGAAAGGTTCAGAAACATGAT	23400
Db	23341	AGCAGCGCCCGCGCTGACACCGCGGCTCCCGGAGTACAGAAAGGTTCAGAAACATGAT	23400
QY	23401	TTACAGGTCGCGAGTGCAGCGCGGCTGGCAACATCTTTGCGTCCCTCCGAAACCGGAA	23460
Db	23401	TTACAGGTCGCGAGTGCAGCGCGGCTGGCAACATCTTTGCGTCCCTCCGAAACCGGAA	23460
QY	23461	AAATCCCGCGCGCGCGGGTGTTCGAGAGGACCGAAAGATATCCCAACGCACTA	23520
Db	23461	AAATCCCGCGCGCGCGGGTGTTCGAGAGGACCGAAAGATATCCCAACGCACTA	23520
QY	23521	AAGCATATGTTTGGGGTTTTCGTATACGCGCGCCGACAGAGAGCGCGGTGTGGCGCTGG	23580
Db	23521	AAGCATATGTTTGGGGTTTTCGTATACGCGCGCCGACAGAGAGCGCGGTGTGGCGCTGG	23580
QY	23581	CGAAGATAGTGGCGCGACAGCAGGCTTTCGATGACGCGCTGACGCGCTGCACCT	23640
Db	23581	CGAAGATAGTGGCGCGACAGCAGGCTTTCGATGACGCGCTGACGCGCTGCACCT	23640
QY	23641	GGCAGCAGGCGCAAAAACACGGGCGCGGAGCGCGGAGGAGTGGCGCGCTTCCCG	23700
Db	23641	GGCAGCAGGCGCAAAAACACGGGCGCGGAGCGCGGAGGAGTGGCGCGCTTCCCG	23700
QY	23701	CACGCGCGATTTGGCAAAATAGCGAGCGCGGAGCGCGTTGGAACGCGCGGACGTCA	23760
Db	23701	CACGCGCGATTTGGCAAAATAGCGAGCGCGGAGCGCGGTTGGAACGCGCGGACGTCA	23760
QY	23761	TCACGACGAGAGAAAGCGAGTGTGCTAGTTTCCCGTCAATCACCGAGGCGCGCGCG	23820
Db	23761	TCACGACGAGAGAAAGCGAGTGTGCTAGTTTCCCGTCAATCACCGAGGCGCGCGCG	23820
QY	23821	TTGGGGGATTAATTAACACCGCGCGGGGCAATTTGGACGCTGGCGGACCAATGGCGCGT	23880
Db	23821	TTGGGGGATTAATTAACACCGCGCGGGGCAATTTGGACGCTGGCGGACCAATGGCGCGT	23880
QY	23881	TGGGTTTGTTTACAGTTCCTATATATATATATATATATATATATATATATATATATAT	23940
Db	23881	TGGGTTTGTTTACAGTTCCTATATATATATATATATATATATATATATATATATATAT	23940
QY	23941	CCATGTTCTTAATCTAATCAGCTGGGTTATATATTAATTAATTAATTAATTAATTAAT	24000
Db	23941	CCATGTTCTTAATCTAATCAGCTGGGTTATATATTAATTAATTAATTAATTAATTAAT	24000
QY	24001	TACTGATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	24060

[illegible]

Qy	26221	CCCCGAGGATCCCCGGCTCCCGTCCCGAGGGTCCGGGCTCCCGTTCCCGAGGT	26280
Db	26222	CCCCGAGGATCCCCGGGCTCCCGTCCCGAGGGTCCGGGCTCCCGTTCCCGAGGT	26280
Qy	26281	CCCCGGCTCCCGTCCCGAGGGTCCGGGCTCCCGTTCCCGAGGGTCCGGGCTCC	26340
Db	26281	CCCCGGCTCCCGTCCCGAGGGTCCGGGCTCCCGTTCCCGAGGGTCCGGGCTCC	26340
Qy	26341	CCGTTCCCGAGGGTCCCGGCTCCCGTTCCCGAGGGTCCGGGCTCCCGTTCCCG	26400
Db	26341	CCGTTCCCGAGGGTCCCGGCTCCCGTTCCCGAGGGTCCGGGCTCCCGTTCCCG	26400
Qy	26401	AGGGTCCCGGCTCCCGTCCCGAGGGTCCGGGCTCCCGTTCCCGAGGGTCCCG	26460
Db	26401	AGGGTCCCGGCTCCCGTCCCGAGGGTCCGGGCTCCCGTTCCCGAGGGTCCCG	26460
Qy	26461	GCTCCCGGTTCCCGAGGGTCCGGGCTCCCGTTCCCGAGGGTCCGGGCTCCCG	26520
Db	26461	GCTCCCGGTTCCCGAGGGTCCGGGCTCCCGTTCCCGAGGGTCCGGGCTCCCG	26520
Qy	26521	CCCGATTCACGTTAAGTGTATTAGCAAAACAGTTTTCGCGGTTGGG	26580
Db	26521	CCCGATTCACGTTAAGTGTATTAGCAAAACAGTTTTCGCGGTTGGG	26580
Qy	26581	TTGTACATACACGCGGTCGTCATTTGCGCCGATCAAAAATAACGTTGGGTTCC	26640
Db	26581	TTGTACATACACGCGGTCGTCATTTGCGCCGATCAAAAATAACGTTGGGTTCC	26640
Qy	26641	GAACCGGTAAGTGTATTAGTGTTCATGCAACGTTTTCGTCACGTAAGAGTGT	26700
Db	26641	GAACCGGTAAGTGTATTAGTGTTCATGCAACGTTTTCGTCACGTAAGAGTGT	26700
Qy	26701	GTTTGTGAGGAATGCAACGAGTACGTCGCTACCGGGAAGGAACGTTTAA	26760
Db	26701	GTTTGTGAGGAATGCAACGAGTACGTCGCTACCGGGAAGGAACGTTTAA	26760
Qy	26761	CCGAGTGTACCGCGTCGCGCATAGGTTTAACTGCAACTCCGTCGCGCGCTGG	26820
Db	26761	CCGAGTGTACCGCGTCGCGCATAGGTTTAACTGCAACTCCGTCGCGCGCTGG	26820
Qy	26821	TACCTTAAGTTTACGTAACATTAATGCGGCTGTTACAGGCTCCCGCCCTGA	26880
Db	26821	TACCTTAAGTTTACGTAACATTAATGCGGCTGTTACAGGCTCCCGCCCTGA	26880
Qy	26881	GGAAGAAATGAATAATCTTGGCAGTTGAGTTTATGCTATAGAGGCACTTCTTTA	26940
Db	26881	GGAAGAAATGAATAATCTTGGCAGTTGAGTTTATGCTATAGAGGCACTTCTTTA	26940
Qy	26941	CTGTGGCTCGGCGAGCGAGTACTTGACACATCCGTTTAAAGCCCTATTAAAGATT	27000
Db	26941	CTGTGGCTCGGCGAGCGAGTACTTGACACATCCGTTTAAAGCCCTATTAAAGATT	27000
Qy	27001	TATCAGCGCTTCTCAAGACACGCTCGCTTACGAGAGCTTTGGCCACACCGA	27060
Db	27001	TATCAGCGCTTCTCTCAAGACACGCTCGCTTACGAGAGCTTTGGCCACACCGA	27060
Qy	27061	TTACCGCTCTGCGGGAGCTAAACGCGCATAGGCCAGAGGATGCTGCAATAAACACGGA	27120
Db	27061	TTACCGCTCTGCGGGAGCTAAACGCGCATAGGCCAGAGGATGCTGCAATAAACACGGA	27120
Qy	27121	CGGACGCGACACTGGGCTGGCGTTTGGCGTTTGGTGTGGTATGAGTGA	27180
Db	27121	CGGACGCGACACTGGGCTGGCGTTTGGCGTTTGGTGTGGTATGAGTGA	27180
Qy	27181	TAAAGTTAAAGACGACGCTTTTAAAGTTGCGCATAGCCGTTTACCCGTAAGC	27240
Db	27181	TAAAGTTAAAGACGACGCTTTTAAAGTTGCGCATAGCCGTTTACCCGTAAGC	27240
Qy	27241	GTAAGAGGCTGAGTCTAGTGTTCGTTACAGGCGAATGGAAGGACACAGAA	27300
Db	27241	GTAAGAGGCTGAGTCTAGTGTTCGTTACAGGCGAATGGAAGGACACAGAA	27300
Qy	27301	TTACTGAGACGATAGGATCGCCGCAACGCGAGAGACACATGTCTACGAGT	27360
Db	27301	TTACTGAGACGATAGGATCGCCGCAACGCGAGAGACACATGTCTACGAGT	27360
Qy	27361	TGCGGCTGTCTTCTGCGCTAGTGGCTGTTTGCATCAGCGGATAGTGTCTTTA	27420
Db	27361	TGCGGCTGTCTTCTGCGCTAGTGGCTGTTTGCATCAGCGGATAGTGTCTTTA	27420
Qy	27421	ACCGGATTTCCCGACCTGACCTTAAGAGGCGATTTGATATGAGCAATAAACA	27480
Db	27421	ACCGGATTTCCCGACCTGACCTTAAGAGGCGATTTGATATGAGCAATAAACA	27480
Qy	27481	AAACAACTAAGCTGATTCGTTTGAACAATTTTATTTAGACAGTTCCCGAGACA	27540
Db	27481	AAACAACTAAGCTGATTCGTTTGAACAATTTTATTTAGACAGTTCCCGAGACA	27540
Qy	27541	TTTTTTTATCTGTGACACGCGGCTGTGCTGCTCCACCGGCGCGCGG	27600
Db	27541	TTTTTTTATCTGTGACACGCGGCTGTGCTGCTCCACCGGCGCGCGCGG	27600
Qy	27601	ACTGCGCATTCGATCGAGGGGCGGACGCGCCAGCGGGGGGAGAGGCTGAG	27660
Db	27601	ACTGCGCATTCGATCGAGGGGCGGACGCGCCAGCGGGGGGAGAGGCTGAG	27660
Qy	27661	GAATGCGGTTGACATTACAGATTCTTGGCGCGCGGCGCTGAGTTGCCGCTGCG	27720
Db	27661	GAATGCGGTTGACATTACAGATTCTTGGCGCGCGGCGCTGAGTTGCCGCTGCG	27720
Qy	27721	CGAGCGGCGTGGTGGCTCGCGGCTCGCGGGGCGGTGGTGGCTTGGATGGCCT	27780
Db	27721	CGAGCGGCGTGGTGGCTCGCGGCTCGCGGGGCGGTGGTGGCTTGGATGGCCT	27780
Qy	27781	GCGGCTCTGCTGATCGGCTGTGGGCGTGGAGATGGGTGTCGCGGAATACACAGCG	27840
Db	27781	GCGGCTCTGCTGATCGGCTGTGGGCGTGGAGATGGGTGTCGCGGAATACACAGCG	27840
Qy	27841	GCTGTACGCTAGGTAGGTCAGGCGCAGACGCTAGGTCTGTGCGCACAGAACTGAACGGGCG	27900
Db	27841	GCTGTACGCTAGGTAGGTCAGGCGCAGACGCTAGGTCTGTGCGCACAGAACTGAACGGGCG	27900
Qy	27901	GTTGTTGCGGCTGTGGTCCGCTGTCTGTGTGGCGGAGGTGTGCGACGCGCTGTTTA	27960
Db	27901	GTTGTTGCGGCTGTGGTCCGCTGTCTGTGTGGCGGAGGTGTGCGACGCGCTGTTTA	27960
Qy	27961	GGTCCCTCAGATCCGCTGAAATGTCAATATTTTGGACAGCGCATGACGTCTGT	28020
Db	27961	GGTCCCTCAGATCCGCTGAAATGTCAATATTTTGGACAGCGCATGACGTCTGT	28020
Qy	28021	GATGCGGACCTCTCGCTGGAACAACGCGCTGTGGAAGCTCCACGTCCTGTTGC	28080
Db	28021	GATGCGGACCTCTCGCTGGAACAACGCGCTGTGGAAGCTCCACGTCCTGTTGC	28080
Qy	28081	GCTTCTGTGGCGAGAGGTCGCGGACGCTAGCCGTACGTGTGGAATATAGTACGTGCGG	28140
Db	28081	GCTTCTGTGGCGAGAGGTCGCGGACGCTAGCCGTACGTGTGGAATATAGTACGTGCGG	28140
Qy	28141	CATACGGAAGGTTGGGGGCAAAACGCGACTGGAAGGAAAGGATGCGCGAGCGGCG	28200
Db	28141	CATACGGAAGGTTGGGGGCAAAACGCGACTGGAAGGAAAGGATGCGCGAGCGGCG	28200
Qy	28201	GTCGCTACGATGGAGCGTACGTCAGCGGCGGTATCCAGATGATACGCGCGTTG	28260
Db	28201	GTCGCTACGATGGAGCGTACGTCAGCGGCGGTATCCAGATGATACGCGCGTTG	28260
Qy	28261	CCGCGATCAGAGGTGGCGCAGAAACGTAAGTGTGGCTGCTGTGCGATATTCGA	28320
Db	28261	CCGCGATCAGAGGTGGCGCAGAAACGTAAGTGTGGCTGCTGTGCGATATTCGA	28320
Qy	28321	GACTGCTGTGACCATATGCTCAGAAAGTGTCTTGGAAATGTATGTTCCTCCGGA	28380
Db	28321	GACTGCTGTGACCATATGCTCAGAAAGTGTCTTGGAAATGTATGTTCCTCCGGA	28380
Qy	28381	GGCGCTCATGCTTCCGGGTGTCCGCTTACCGCAGTGTGACCGAGGAACCTGGCTTG	28440

D	28381	GGGCGCTCAGGTGTGGGTGTGCGGGTATCCCGAGTGTGAGCGGAGGAACTGGCTTG		28440
Q	28441	CCTTTAAATACGTACTTCTCGGAGACTGGCCAGCGCTTATCTGTTTGAGCAGGTCTG		28500
D	28441	CGTTTAAATACGTACTTCTCGGAGACTGGCCAGCGCTTATCTGTTTGAGCAGGTCTG		28500
Q	28501	TGCGATCTCGGATTAATCCGGCGTCGATGCGCTTGCGCATCAGTGTCTCAAGAGGGCGG		28560
D	28501	TGCGATCTCGGATTAATCCGGCGTCGATGCGCTTGCGCATCAGTGTCTCAAGAGGGCGG		28560
Q	28561	GCAATTCTGGCGGTGCACCTCAGCTTCCCAAGATCTAAACATTTGACCTTATTTTAC		28620
D	28561	GCAATTCTGGCGGTGCACCTCAGCTTCCCAAGATCTAAACATTTGACCTTATTTTAC		28620
Q	28621	CGGCTTCTCTCGCGTAAGAGATCAAACTTGAGAGCAGCCATGTAGGGTCTGGTCCGT		28680
D	28621	CGGCTTCTCTCGCGTAAGAGATCAAACTTGAGAGCAGCCATGTAGGGTCTGGTCCGT		28680
Q	28681	AAACGGCGATTAACCCCTACGCTCCCGACAGTGCACAGAGAGACGTGCTGAACGCGG		28740
D	28681	AAACGGCGATTAACCCCTACGCTCCCGACAGTGCACAGAGAGACGTGCTGAACGCGG		28740
Q	28741	GTGGGATTTGGGGTCTTGCACCTCTCTGGGTGGAGGAGACGAGAGGAGACTCCGGGA		28800
D	28741	GTGGGATTTGGGGTCTTGCACCTCTCTGGGTGGAGGAGACGAGAGGAGACTCCGGGA		28800
Q	28801	GCCATGTGTATTAACATCTTCCACAGGGGGTCCCGAGGCAATGGGGTTTACCTGATCTGG		28860
D	28801	GCCATGTGTATTAACATCTTCCACAGGGGGTCCCGAGGCAATGGGGTTTACCTGATCTGG		28860
Q	28861	CCGCTCGCGAGTCCCGCGGAGCGCTGACGCCAGGGCCAAAGAACTGTGGCTGTAGCT		28920
D	28861	CCGCTCGCGAGTCCCGCGGAGCGCTGACGCCAGGGCCAAAGAACTGTGGCTGTAGCT		28920
Q	28921	TGCCAGGCAAAATATCCCGTGTACTTGGAGAGACGCAATGTGTGACCTAGCTGGG		28980
D	28921	TGCCAGGCAAAATATCCCGTGTACTTGGAGAGACGCAATGTGTGACCTAGCTGGG		28980
Q	28981	CTTCCGGGAGCTGCTATGTTTATCGTAGAGGGTCCGTATACGGGAGACAGGTCCCA		29040
D	28981	CTTCCGGGAGCTGCTATGTTTATCGTAGAGGGTCCGTATACGGGAGACAGGTCCCA		29040
Q	29041	CGATTGAGGGCTCTAAATACACCTCTTCTATCTTGGTAGCGTACACGTCCACCT		29100
D	29041	CGATTGAGGGCTCTAAATACACCTCTTCTATCTTGGTAGCGTACACGTCCACCT		29100
Q	29101	ATCCCCCAACGTACACGGGAGTCAATGTTGGGTGCGTGTGAGATTTTAAATAGCTTTC		29160
D	29101	ATCCCCCAACGTACACGGGAGTCAATGTTGGGTGCGTGTGAGATTTTAAATAGCTTTC		29160
Q	29161	GGCGCGTCTTCGGGGGCTGATGTGGCGGCTTATCCGTTGTGAGATTTTAAATAGCTTTC		29220
D	29161	GGCGCGTCTTCGGGGGCTGATGTGGCGGCTTATCCGTTGTGAGATTTTAAATAGCTTTC		29220
Q	29221	TCCCTGGGAGCTCAGGTTTCTTCACTGTGTCTGTGCAATGTACACTACGCTCTTA		29280
D	29221	TCCCTGGGAGCTCAGGTTTCTTCACTGTGTCTGTGCAATGTACACTACGCTCTTA		29280
Q	29281	ACGTATACCTTCTGAAGGAGGCAATTCGCAATACCGGAACGAGGAGCGATATTGTCTCG		29340
D	29281	ACGTATACCTTCTGAAGGAGGCAATTCGCAATACCGGAACGAGGAGCGATATTGTCTCG		29340
Q	29341	GGCGTAAGGTTCCGGTGAAGTCTGGAATAATGTTTACGATGGTTAAAGAGATGGGGG		29400
D	29341	GGCGTAAGGTTCCGGTGAAGTCTGGAATAATGTTTACGATGGTTAAAGAGATGGGGG		29400
Q	29401	TTTCTGAGGCAACGTTGCTCTTGAACCAAAAGGGGCTGTGTGGCTTACTTCAACG		29460
D	29401	TTTCTGAGGCAACGTTGCTCTTGAACCAAAAGGGGCTGTGTGGCTTACTTCAACG		29460
Q	29461	GGCGTCCGCTGTAAAGGCTAGGAGACTAGTTTGTGCAACGTGGGGTTAAGCC		29520
D	29461	GGCGTCCGCTGTAAAGGCTAGGAGACTAGTTTGTGCAACGTGGGGTTAAGCC		29520
D	29461	GGCGTCCGCTGTAAAGGCTAGGAGACTAGTTTGTGCAACGTGGGGTTAAGCC		29520
Q	29521	ACAGCGTACGCGTGTGCCGAAAAACCTAACGGATGGAAATTAATCTATAACCTAGGCA		29580
D	29521	ACAGCGTACGCGTGTGCCGAAAAACCTAACGGATGGAAATTAATCTATAACCTAGGCA		29580
Q	29581	GGCTATACCATGTGCGCTGCTTGTGGCACTGAGCTACTGTTTGGCGTTTGGGGGACG		29640
D	29581	GGCTATACCATGTGCGCTGCTTGTGGCACTGAGCTACTGTTTGGCGTTTGGGGGACG		29640
Q	29641	CTGACAGGAGCCGTGGGTCAAGTTGTGGCGGCAAGATTTTATCTACTTAATAATA		29700
D	29641	CTGACAGGAGCCCTGGGTCAAGTTGTGGCGGCAAGATTTTATCTACTTAATAATA		29700
Q	29701	TTTCCGGCCACATTAATGACAGGAAGTCAATCTTAGAACAGGTGGGAACGTCCGGGTAG		29760
D	29701	TTTCCGGCCACATTAATGACAGGAAGTCAATCTTAGAACAGGTGGGAACGTCCGGGTAG		29760
Q	29761	GTGGCTTGTGAGGAGTGTGTGCGGATGTTTCCGGCGGTACACGGGATTCGGCGTGG		29820
D	29761	GTGGCTTGTGAGGAGTGTGTGCGGATGTTTCCGGCGGTACACGGGATTCGGCGTGG		29820
Q	29821	ATTTGGCGTCCGGGCTCCGGGTTAAGCTCTCAACAGAGGAGTACTGTTGGGTGA		29880
D	29821	ATTTGGCGTCCGGGCTCCGGGTTAAGCTCTCAACAGAGGAGTACTGTTGGGTGA		29880
Q	29881	ATTAACAGCTAGTATGAGGTGCGCTCACACTACCGACGTGGCGAGCGGAGTATCCAG		29940
D	29881	ATTAACAGCTAGTATGAGGTGCGCTCACACTACCGACGTGGCGAGCGGAGTATCCAG		29940
Q	29941	GACCAAAAAATTAACCTCTGTCTAGTGTGCTGTAACTCCGATTTGGCTTTTATATATC		30000
D	29941	GACCAAAAAATTAACCTCTGTCTAGTGTGCTGTAACTCCGATTTGGCTTTTATATATC		30000
Q	30001	GTGTGCAACAGCGGGGGGAGTGGGCGCAAGAGATGGGGCGAGGCTTCTCCGGCGT		30060
D	30001	GTGTGCAACAGCGGGGGGAGTGGGCGCAAGAGATGGGGCGAGGCTTCTCCGGCGT		30060
Q	30061	TAAACGTACGACGTTTGAACCTGAATCAGGCTGCACGCTCCGTGAACGTAGCTTTTG		30120
D	30061	TAAACGTACGACGTTTGAACCTGAATCAGGCTGCACGCTCCGTGAACGTAGCTTTTG		30120
Q	30121	GTTCAAGATGTAAAGATTTGCTTAAATCTGGAACCGGTACAGTTGAGCAAGGACGAT		30180
D	30121	GTTCAAGATGTAAAGATTTGCTTAAATCTGGAACCGGTACAGTTGAGCAAGGACGAT		30180
Q	30181	GTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG		30240
D	30181	GTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG		30240
Q	30241	AAACGACGTGGGGGCTGTGCGCGCGCAAAAGAAATGGGAGATGTAAATTTCTGTCA		30300
D	30241	AAACGACGTGGGGGCTGTGCGCGCGCAAAAGAAATGGGAGATGTAAATTTCTGTCA		30300
Q	30301	GAAATCAAAAAATTTGCTTCTTAAAGATTTTGAACCGGAGGGGTCTTACCTT		30360
D	30301	GAAATCAAAAAATTTGCTTCTTAAAGATTTTGAACCGGAGGGGTCTTACCTT		30360
Q	30361	GGAATAATCTCCACCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG		30420
D	30361	GGAATAATCTCCACCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG		30420
Q	30421	GATTTGGGCGACGCTCCCAATAGCAGTAAACCAAACTAAGCCTAGTCCGAGAGGCC		30480
D	30421	GATTTGGGCGACGCTCCCAATAGCAGTAAACCAAACTAAGCCTAGTCCGAGAGGCC		30480
Q	30481	GGCTCGGAGTTCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG		30540
D	30481	GGCTCGGAGTTCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG		30540
Q	30541	CGCAAGATGTATACGAGATCTGTGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT		30600
D	30541	CGCAAGATGTATACGAGATCTGTGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT		30600

QY	30601	GGGTAGCAGTCCGCTGTGTGCCAACGTCGGCTATATACGTGGTTTGTAAAGAGTCCGC	30650
Db	30601	GGGTAGCAGTCCGCTGTGTGCCAACGTCGGCTATATACGTGGTTTGTAAAGAGTCCGC	30660
QY	30661	GTGTACTTTGTTCTTTGTTTAGGGCGCTAGAGAGGGCGCTGCTCGGATTTGGAATA	30720
Db	30661	GTGTACTTTGTTCTTTGTTTAGGGCGCTAGAGAGGGCGCTGCTCGGATTTGGAATA	30720
QY	30721	TGTAAACTCGAAACCCAGGCGCTTGTGTGTTTTTTAGGTGAGACACAAGGTCGCCAG	30780
Db	30721	TGTAAACTCGAAACCCAGGCGCTTGTGTGTTTTTTAGGTGAGACACAAGGTCGCCAG	30780
QY	30781	CTTTGTGCCGAGGTTATCCAGAGCGGCTTTCGAGTTGGCGCACGGGGTACCTGTCCG	30840
Db	30781	CTTTGTGCCGAGGTTATCCAGAGCGGCTTTCGAGTTGGCGCACGGGGTACCTGTCCG	30840
QY	30841	GTGACAGTAGACCCGTTGAGGAGGCGACAGCGGGCGCTGTGTCGATACGTTGGCGAC	30900
Db	30841	GTGACAGTAGACCCGTTGAGGAGGCGACAGCGGGCGCTGTGTCGATACGTTGGCGAC	30900
QY	30901	ATCCGCGTAAAGTCTTGTGTATCGAGGCGGCTGTTGAGATTACGGCAGACATTAGCTT	30960
Db	30901	ATCCGCGTAAAGTCTTGTGTATCGAGGCGGCTGTTGAGATTACGGCAGACATTAGCTT	30960
QY	30961	TAGAGACGTGAGTTTGAAGAATTTGTGTGCTCCGAAATCTCTGGGACACCTCGCG	31020
Db	30961	TAGAGACGTGAGTTTGAAGAATTTGTGTGCTCCGAAATCTCTGGGACACCTCGCG	31020
QY	31021	TTGCATGGCGTATCTGTGAGGCTACGTATCCAGCGCGCTATTTGGAGGCATTGGTT	31080
Db	31021	TTGCATGGCGTATCTGTGAGGCTACGTATCCAGCGCGCTATTTGGAGGCATTGGTT	31080
QY	31081	TTGGTTCATGTACAGGCTTGGCAGAGAGCTCCAGACGAGATCTGTGTTTACCGTGAATCC	31140
Db	31081	TTGGTTCATGTACAGGCTTGGCAGAGAGCTCCAGACGAGATCTGTGTTTACCGTGAATCC	31140
QY	31141	CGGGTCTCCGGGGGCTATTTGTGACACAGAACGCGTCTCCATGTGTCTGGGGGCGATT	31200
Db	31141	CGGGTCTCCGGGGGCTATTTGTGACACAGAACGCGTCTCCATGTGTCTGGGGGCGATT	31200
QY	31201	GGGTGGGGGTTTAGTATGTTTGGGCAATGGCGGTTCCCTCCCGGGGACCGCAGATC	31260
Db	31201	GGGTGGGGGTTTAGTATGTTTGGGCAATGGCGGTTCCCTCCCGGGGACCGCAGATC	31260
QY	31261	CCGACCATGTTTGAATGTTTCTAGTGGCGCATGACACATCTGTGTTCCGTTGGGTG	31320
Db	31261	CCGACCATGTTTGAATGTTTCTAGTGGCGCATGACACATCTGTGTTCCGTTGGGTG	31320
QY	31321	CGTTTGGAGCAGCTTGTCTAGTCTTACCCGGAGCAGGTTTTTTCGAGGCTGTGAACCT	31380
Db	31321	CGTTTGGAGCAGCTTGTCTAGTCTTACCCGGAGCAGGTTTTTTCGAGGCTGTGAACCT	31380
QY	31381	TAGCGCAGCGTGTGATTTGCGATCACAAACGCGTTCTCTTCTTATCAGAGATGG	31440
Db	31381	TAGCGCAGCGTGTGATTTGCGATCACAAACGCGTTCTCTTCTTATCAGAGATGG	31440
QY	31441	TTTGTGAATAAACAAGACGTTGTTGGATGGGGGCCCAAAAAGTTGCGTAATTTGCCG	31500
Db	31441	TTTGTGAATAAACAAGACGTTGTTGGATGGGGGCCCAAAAAGTTGCGTAATTTGCCG	31500
QY	31501	CGGTGGTTTTCTGGGGTATCTCATACAGCATTTTTTCTGACGTGCGATCTTCCCATTTGGC	31560
Db	31501	CGGTGGTTTTCTGGGGTATCTCATACAGCATTTTTTCTGACGTGCGATCTTCCCATTTGGC	31560
QY	31561	TAAAAAACCCGTTTAGCGCGCGCAGCTGCTTGTGATAAATGAGCGGAAACGCTGATG	31620
Db	31561	TAAAAAACCCGTTTAGCGCGCGCAGCTGCTTGTGATAAATGAGCGGAAACGCTGATG	31620
QY	31621	ACTCAGTATGAAATGTTTAAAGTGTGTTTCTGTGTTCTTAAATATACACAGGCGCTTACCG	31680
Db	31621	ACTCAGTATGAAATGTTTAAAGTGTGTTTCTGTGTTCTTAAATATACACAGGCGCTTACCG	31680
QY	31681	ACCAAGTTTGGTGTCTTGTGAGGCGCGCTGTGCTATATATGCAAGGAAATGTTCAGTT	31740
Db	31681	ACCAAGTTTGGTGTCTTGTGAGGCGCGCTGTGCTATATATGCAAGGAAATGTTCAGTT	31740
QY	31741	GGTGTAGCCCTGGCATCGCTGTGATATTTTTTATCGTTGGCGGGAATATACGCCGCC	31800
Db	31741	GGTGTAGCCCTGGCATCGCTGTGATATTTTTTATCGTTGGCGGGAATATACGCCGCC	31800
QY	31801	TTAGGCACGTTGTAGTTCAATTACGTAGCAGCTTTTTTGTATGTTGCTATTACGGTAA	31860
Db	31801	TTAGGCACGTTGTAGTTCAATTACGTAGCAGCTTTTTTGTATGTTGCTATTACGGTAA	31860
QY	31861	GCACACATCTGCTATTTCCGCTACCTTAGGAAACCTCGAAAAAATCCTTAATTTTACGT	31920
Db	31861	GCACACATCTGCTATTTCCGCTACCTTAGGAAACCTCGAAAAAATCCTTAATTTTACGT	31920
QY	31921	TTTTGTGCTCCGTAGAGTTTGGGCGAATTTGAAAGAACTTTAAATATCATCACGACAC	31980
Db	31921	TTTTGTGCTCCGTAGAGTTTGGGCGAATTTGAAAGAACTTTAAATATCATCACGACAC	31980
QY	31981	GGTGTGATTAACCGTGTATCTAGTAAAGTGGGCGGAGTTCCAGCGCGTTTGGCGTG	32040
Db	31981	GGTGTGATTAACCGTGTGTATCTAGTAAAGTGGGCGGAGTTCCAGCGCGTTTGGCGTG	32040
QY	32041	AGCGCGGAAGGCTTTCAGAGGTTGGCAGACGTGCTTACATTGATTTGCAACGGCATGGCG	32100
Db	32041	AGCGCGGAAGGCTTTCAGAGGTTGGCAGACGTGCTTACATTGATTTGCAACGGCATGGCG	32100
QY	32101	AAGGAGGTTGAGCTTGGGTCGAGAGAGCTTGTCCGTAGATGCGGATTCGGAAGCCTAGAT	32160
Db	32101	AAGGAGGTTGAGCTTGGGTCGAGAGAGCTTGTCCGTAGATGCGGATTCGGAAGCCTAGAT	32160
QY	32161	GGGACGAGTCTTCCGACGATCTGATGACGCGGTTTAAAGGAGCTTGTGAGTATG	32220
Db	32161	GGGACGAGTCTTCCGACGATCTGATGACGCGGTTTAAAGGAGCTTGTGAGTATG	32220
QY	32221	ATGATGTGTTCCCGGTGTAGATACGACGCGCTTAAAGGCGCTGGAACCTGAAACTATG	32280
Db	32221	ATGATGTGTTCCCGGTGTAGATACGACGCGCTTAAAGGCGCTGGAACCTGAAACTATG	32280
QY	32281	ACGTACCCAGTCTCCCTCCGGAAGCGGCTGTGGAATTTACTGCACCCGACGCGCTGTATG	32340
Db	32281	ACGTACCCAGTCTCCCTCCGGAAGCGGCTGTGGAATTTACTGCACCCGACGCGCTGTATG	32340
QY	32341	CACATCCGAGGTCCCGCCTTAAAGGGCGGTGTGCCGGCGGTGGCGGCTGCCAAGC	32400
Db	32341	CACATCCGAGGTCCCGCCTTAAAGGGCGGTGTGCCGGCGGTGGCGGCTGCCAAGC	32400
QY	32401	TGTCGGGTTCTGGGCTAGACTTCATATGTTGAGACAGAGATTTTGGGGATATGAGAA	32460
Db	32401	TGTCGGGTTCTGGGCTAGACTTCATATGTTGAGACAGAGATTTTGGGGATATGAGAA	32460
QY	32461	CGCGGACAGCTTACCGGGGCGTCACTTTTCTTCCAGAGCGACGACGAAATATGGCGAAATAC	32520
Db	32461	CGCGGACAGCTTACCGGGGCGTCACTTTTCTTCCAGAGCGACGACGAAATATGGCGAAATAC	32520
QY	32521	CGGAGCGTACTATACAGCGCCCGGTTGAAAGCGGTGACAGAGAAATTTTACCTCCGGGC	32580
Db	32521	CGGAGCGTACTATACAGCGCCCGGTTGAAAGCGGTGACAGAGAAATTTTACCTCCGGGC	32580
QY	32581	GTAGGGGTGCAATCTGGGGACCGCTCGTCGACAAACCTATGTCAGGTGGGGGTTTAACAC	32640
Db	32581	GTAGGGGTGCAATCTGGGGACCGCTCGTCGACAAACCTATGTCAGGTGGGGGTTTAACAC	32640
QY	32641	GTAAGACTTAAACGTCCTCATAGTATTAGTCTTAAACCTTGTCGCGATTAAGAGCAGATG	32700
Db	32641	GTAAGACTTAAACGTCCTCATAGTATTAGTCTTAAACCTTGTCGCGATTAAGAGCAGATG	32700
QY	32701	ATGCTTAAGTGTAGTATCCAGGCGCGGTTTACCTGCGGGTTATCTCATGACGCGGCATC	32760
Db	32701	ATGCTTAAGTGTAGTATCCAGGCGCGGTTTACCTGCGGGTTATCTCATGACGCGGCATC	32760
QY	32761	CTATGAGGGAATATAGAAATGCGCTTTTATCTATCTAGAGGGGGGTCATGSGGTGTTGSA	32820

QY	31981	ACCAATTTCCTGCTCCTTGGCGGCGCTTCGCTATATATGCGCAAGAAATCTGCACTT	31740
QY	31741	GGTGAACCCCTGCCATGCATGTGTATTTTATATGCGTCCGGGAATATACGCGGC	31800
Db	31741	GGTGAACCCCTGCCATGCATGTGTATTTTATATGCGTCCGGGAATATACGCGGC	31800
QY	31741	GGTGAACCCCTGCCATGCATGTGTATTTTATATGCGTCCGGGAATATACGCGGC	31800
QY	31801	TTAGCAGCTGTGATTCATTTACGTAGCACGTTTTTGTATGTTCGCTATTACGGTAA	31860
Db	31801	TTAGCAGCTGTGATTCATTTACGTAGCACGTTTTTGTATGTTCGCTATTACGGTAA	31860
QY	31861	GCACACATCTGCTATTTCGCTACTACGGAAACCTCGAAAAAATCTCTAAATTTAAGT	31920
Db	31861	GCACACATCTGCTATTTCGCTACTACGGAAACCTCGAAAAAATCTCTAAATTTAAGT	31920
QY	31921	TTTTGCTTGCCTGTGATTTGGGCGAAATTTGAAAGAACTTTAAATATCATCAACGACC	31980
Db	31921	TTTTGCTTGCCTGTGATTTGGGCGAAATTTGAAAGAACTTTAAATATCATCAACGACC	31980
QY	31981	GGTGTATTATTAACCGCTGATATCTATAGTGTGGCGCGAGTTCACGCCGTTTGGCGTG	32040
Db	31981	GGTGTATTATTAACCGCTGATATCTATAGTGTGGCGCGAGTTCACGCCGTTTGGCGTG	32040
QY	32041	AGCCCGGAAGGCTTCGAGAGGTGGGAGTGGTTACATTGATTTTGCAAAACGCAAGGCGC	32100
Db	32041	AGCCCGGAAGGCTTCGAGAGGTGGGAGTGGTTACATTGATTTTGCAAAACGCAAGGCGC	32100
QY	32101	AAGGAGGCTTGCGCTTTGGCGACGAGTTCGCTCAGATGCGGGATCGGAAGCTTAGAT	32160
Db	32101	AAGGAGGCTTGCGCTTTGGCGACGAGTTCGCTCAGATGCGGGATCGGAAGCTTAGAT	32160
QY	32161	GGGACGAGTCTTCGACGATACTGATGACGTTGACACCGAAACGACCGATCTTGGATATG	32220
Db	32161	GGGACGAGTCTTCGACGATACTGATGACGTTGACACCGAAACGACCGATCTTGGATATG	32220
QY	32221	ATGATGTTCCTCCGCTGGTATATAGCAAGGCTTATAGCCCTCGAAAGTCAAACTATAG	32280
Db	32221	ATGATGTTCCTCCGCTGGTATATAGCAAGGCTTATAGCCCTCGAAAGTCAAACTATAG	32280
QY	32281	ACGTACCCACGCTCTCGTCCGGAACCGCGTGGGAATTAATCGACCCGCGACGCTGTATG	32340
Db	32281	ACGTACCCACGCTCTCGTCCGGAACCGCGTGGGAATTAATCGACCCGCGACGCTGTATG	32340
QY	32341	CACATTCGAGGTGCCCGCTTAAAGGGGGGTGTGCTCGGGCGGTGGCGGCTCCCAAGG	32400
Db	32341	CACATTCGAGGTGCCCGCTTAAAGGGGGGTGTGCTCGGGCGGTGGCGGCTCCCAAGG	32400
QY	32401	TGTCGGGCTTCGCGCTAGACTTCAATATGTGGACGACAGAGTTTGGGGATPACAGAGA	32460
Db	32401	TGTCGGGCTTCGCGCTAGACTTCAATATGTGGACGACAGAGTTTGGGGATPACAGAGA	32460
QY	32461	CGCGGACGCTTACCGGGGCTCAGTTTCTTCGGAAGGAGGACGACGAATATGCGGAATATC	32520
Db	32461	CGCGGACGCTTACCGGGGCTCAGTTTCTTCGGAAGGAGGACGACGAATATGCGGAATATC	32520
QY	32521	CGGACGCTACTACTACAGCGCCGGTGTGAAAGCGGTGACAAAGGAATTTTCACTCCGGGC	32580
Db	32521	CGGACGCTACTACTACAGCGCCGGTGTGAAAGCGGTGACAAAGGAATTTTCACTCCGGGC	32580
QY	32581	GTAAGGGGTGCAATCTCGGAGACCTGTGTGACAAACCTATAGTCAGCGTGGGGTTAAAC	32640
Db	32581	GTAAGGGGTGCAATCTCGGAGACCTGTGTGACAAACCTATAGTCAGCGTGGGGTTAAAC	32640
QY	32641	GTAAGACATAAAACGTCGCTGATGTATTAGTCTTAAACCTTGGTGGGATTAAGGACGATG	32700
Db	32641	GTAAGACATAAAACGTCGCTGATGTATTAGTCTTAAACCTTGGTGGGATTAAGGACGATG	32700
QY	32701	ATGCTTAAGGTGATATACCGAGGCGGTTACCGTCCGTTATCTCATGACGCGCATC	32760
Db	32701	ATGCTTAAGGTGATATACCGAGGCGGTTACCGTCCGTTATCTCATGACGCGCATC	32760
QY	32761	CTATACGGAATATATGAATGCTTTTAAATATATCTATGAGGGGGGTATGGATGTGGAA	32820

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32761 CTAATGCGAATATATGAAATGCTTTTATCTATCTATAGAGGGGCGCATGGGCTTGGAA 32820
QY 32821 AAACAACGCTATTTGAATTCATGACAGGATGCTGGCGAGAAAACGTTAAAGCTGAC 32880
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Db 32821 AAACAACGCTATTTGAATTCATGACAGGATGCTGGCGAGAAAACGTTAAAGCTGAC 32880
QY 32881 CCGAGCCCATGAAATTTTGACGCTGTGTTTATTCAAATTCCTTAAAGAACGCGAGCA 32940
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Db 32881 CCGAGCCCATGAAATTTTGACGCTGTGTTTATTCAAATTCCTTAAAGAACGCGAGCA 32940
QY 32941 TATGTTAGCAAGGACCCGAGGAAATTTATCATCTCTGCTGCGCATATACGGCTGACAA 33000
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Db 32941 TATGTTAGCAAGGACCCGAGGAAATTTATCATCTCTGCTGCGCATATACGGCTGACAA 33000
QY 33001 GCAAGTTTGGCTACCGTTTCTGCGACAGCCGCGCATGCGTCCCAACCTGCAACCGT 33060
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Db 33001 GCAAGTTTGGCTACCGTTTCTGCGACAGCCGCGCATGCGTCCCAACCTGCAACCGT 33060
QY 33061 GCGTGGTGGGAAACGGTAGCACAAAGCCAGCAATTTGATTTTGAACAGACCTTAC 33120
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Db 33061 GCGTGGTGGGAAACGGTAGCACAAAGCCAGCAATTTGATTTTGAACAGACCTTAC 33120
QY 33121 TGTCCGCAACGGTGGTTTTCGGCTGCTCAGTTAAGTACAACAGCCTAACGCGGATC 33180
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Db 33121 TGTCCGCAACGGTGGTTTTCGGCTGCTCAGTTAAGTACAACAGCCTAACGCGGATC 33180
QY 33181 ATCTGTTTCAAAATCTATCTCTTCTTCGCGACAGCAGCGCATGCTGCTTTCCTAA 33240
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Db 33181 ATCTGTTTCAAAATCTATCTCTTCTTCGCGACAGCAGCGCATGCTGCTTTCCTAA 33240
QY 33241 CGCTCAACAGTTTGGAGGCGCACAGGCGCATTCAAAGTGGAGCCCTAAAGAAAGAAAG 33300
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Db 33241 CGCTCAACAGTTTGGAGGCGCACAGGCGCATTCAAAGTGGAGCCCTAAAGAAAGAAAG 33300
QY 33301 GAATCAACGCAAACTACTTGCACAGATGACGCGGAGGCGTACCATGCGCTGCTGACGT 33360
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Db 33301 GAATCAACGCAAACTACTTGCACAGATGACGCGGAGGCGTACCATGCGCTGCTGACGT 33360
QY 33361 GGGTGTATGATGCAATATCTCACACCGAGCAAAATGGTTGAGTGTGTAACAACGTGT 33420
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Db 33361 GGGTGTATGATGCAATATCTCACACCGAGCAAAATGGTTGAGTGTGTAACAACGTGT 33420
QY 33421 CCATAGAGAGCATATGCAATATGCAATTCGAGATGACTATGCTTCTTCAACCTTACAA 33480
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Db 33421 CCATAGAGAGCATATGCAATATGCAATTCGAGATGACTATGCTTCTTCAACCTTACAA 33480
QY 33481 AACTACATGAACAGAGATGATACCATGCTGAGCAAAATGTTAGTATGTTTAAAGAAC 33540
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Db 33481 AACTACATGAACAGAGATGATACCATGCTGAGCAAAATGTTAGTATGTTTAAAGAAC 33540
QY 33541 ACGTGAACCTTAAATGAGGCTGTGTTGGACCTTTTAAAGAGCTAGCAAAAGCTTCAATTT 33600
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Db 33541 ACGTGAACCTTAAATGAGGCTGTGTTGGACCTTTTAAAGAGCTAGCAAAAGCTTCAATTT 33600
QY 33601 TTAATGTTGACAGCAGAGAAACATCTAGATGATGCGGTGGCTGTGGGAAATATTTATG 33660
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Db 33601 TTAATGTTGACAGCAGAGAAACATCTAGATGATGCGGTGGCTGTGGGAAATATTTATG 33660
QY 33661 GGCAGGTGATGTCAAATGAGGTATTTAAACAGAGCAATGAACTGCGGCAAGCTTTGAAA 33720
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Db 33661 GGCAGGTGATGTCAAATGAGGTATTTAAACAGAGCAATGAACTGCGGCAAGCTTTGAAA 33720
QY 33721 GCTACATTCAAACGCTAACCAATTTGAAAGGCAATGGCGCTATTTATTTATTTT 33780
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Db 33721 GCTACATTCAAACGCTAACCAATTTGAAAGGCAATGGCGCTATTTATTTATTTT 33780
QY 33781 TTTACTATTAATAGGTGTTCTGTAACGCAAAATACGTTATGATGAAATCAAAATGTA 33840
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Db 33781 TTTACTATTAATAGGTGTTCTGTAACGCAAAATACGTTATGATGAAATCAAAATGTA 33840
QY 33841 GAGTGGATTTAAATGGAACATTTTACCAATTTATTTGAGAAAGGTAAAGCAAAATTA 33900
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33841 GAGTTGGAATTTAATGGAACATTTTACCAATTTAATGGAGAAACGTAAGCAAAATTA 33900
QY 33901 ACATCTATTTGTAATGGAATGCGTGTGATGATTTCTTACTGCTGGAACATTTCTGTG 33960
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Db 33901 ACATCTATTTGTAATGGAATGCGTGTGATGATTTCTTACTGCTGGAACATTTCTGTG 33960
QY 33961 ACTTTGGAAAAAGAAAAAGTTTCTGCGATCAGATATAGTTATATGCTATATATGAC 34020
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Db 33961 ACTTTGGAAAAAGAAAAAGTTTCTGCGATCAGATATAGTTATATGCTATATATGAC 34020
QY 34021 TATACATTTTGTAAATCTTCAAGTGCACATGTAATTAACCTTACGGTGGATTTTATAC 34080
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QY 34081 AGTTCTTCCAGGTTTACTGGAAATTTTAAATGTAATGACATGCTTTTAAACAGAGC 34140
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Db 34081 AGTTCTTCCAGGTTTACTGGAAATTTTAAATGTAATGACATGCTTTTAAACAGAGC 34140
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Db 34141 GTTTATTTAAGCAACGTAATTTATTTACCACTCAACAACTTATGATCTTTTTC 34200
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Db 34201 GCGGAAAAATTAATGCAAAATGTTCAAGATTTACTTTGATTTTCCAAATGTAATTT 34260
QY 34261 TCCGGCATTTAACAGAAATTTGATATGATATGATATGATATGATATGATATGATATG 34320
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Db 34261 TCCGGCATTTAACAGAAATTTGATATGATATGATATGATATGATATGATATGATATG 34320
QY 34321 AATATGCAATGTTGCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 34380
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Db 34321 AATATGCAATGTTGCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 34380
QY 34381 TATGATCTTATGCTGATTTATGTCGCTTAAATAATTCAAATATGCTGCTGCTGTAAT 34440
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Db 34381 TATGATCTTATGCTGATTTATGTCGCTTAAATAATTCAAATATGCTGCTGCTGTAAT 34440
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Db 34501 TTTGTTTCAATATGATATGTCGCTTATGCTATGATTTATCTCAAAAGAAACCTTTG 34560
QY 34561 GCTATTTGAAGCAAAAGGTCCTGTCNAATTCCTTCAAAATGAAATGATATCTTATCTTTC 34620
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Db 34561 GCTATTTGAAGCAAAAGGTCCTGTCNAATTCCTTCAAAATGAAATGATATCTTATCTTTC 34620
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Db 34621 TTTTGTGAAGTATCTGCAATAATTTTATTTTAAATAAACTTCAAAAGCAGCAATTA 34680
QY 34681 GTTAACGTTGGGTGTGTTTACGCAATGTTTGAAGGTTTGAAGTTTATGATTTATTA 34740
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Db 34681 GTTAACGTTGGGTGTGTTTACGCAATGTTTGAAGGTTTGAAGTTTATGATTTATTA 34740
QY 34741 AGGCTCTGTACCAACGTTTATGATTTATGAGCTTAAATTTGAAACGTTTGCAGATAT 34800
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Db 34741 AGGCTCTGTACCAACGTTTATGATTTATGAGCTTAAATTTGAAACGTTTGCAGATAT 34800
QY 34801 GCAAGTCCAGGTTTAACTTTCGCGGCAAAATGACATGTTATCTTTTACATTAATGAT 34860
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Db 34801 GCAAGTCCAGGTTTAACTTTCGCGGCAAAATGACATGTTATCTTTTACATTAATGAT 34860
QY 34861 CAAGAGTCCATTTTCAATGTTTAAATTTGATTTAAATGACCTTAAAGGTTGCTGTA 34920
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Db 34861 CAAGAGTCCATTTTCAATGTTTAAATTTGATTTAAATGACCTTAAAGGTTGCTGTA 34920
QY 34921 ATTCTAAAGCAATTTGATATTTACTATTTCAATGATACCAAAATACAGTAAATTTAT 34980
|||||
Db 34921 ATTCTAAAGCAATTTGATATTTACTATTTCAATGATACCAAAATACAGTAAATTTAT 34980

OY	34981	CAGTAAACCAACACATTTAGCGGAGATGTAATGAACATGTATGAAGTTTAAACAATT	35040
Db	34981		
OY	35041	AAATTTAAAGTCACAGATTCCTGTGTGTTTATCCGTAATATTTGTTCACATCCATGTGT	35100
Db	35041		
OY	35101	AATATGTAGATATCATATATGTATTAATGAAGAAAGCCGATGACATCCACATA	35160
Db	35101		
OY	35161	TTTCGCGTGTTCGCTGTGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTT	35220
Db	35161		
OY	35221	CGATCCGACGACCGCAGACGTCAAAAGAACCGGCTCGGAACCTGGCAACAGAGCGTCT	35280
Db	35221		
OY	35281	GCTTTTGGCGGCTTTCACAGCTTTTACAGCCAGCGCTATTAACGAGTTTTCATCATATA	35340
Db	35281		
OY	35341	AATTTACACAGCTGCATGGAAGCAAGTAACCGGCTGATCCGCTTACGAACATCCAG	35400
Db	35341		
OY	35401	TACGTCATAGCTCCGTCGCGCCCTGATACAGCTCCGCTTACGAGTTTCGAGAGTGTTC	35460
Db	35401		
OY	35461	CTTAACACCGGAGATTTGTCTCGGCGCTTATCCAAATGTCTCATTTTACACCGCC	35520
Db	35461		
OY	35521	GATACCGGCTTACACATTCGATATGTAATACCTTTCCGCGCCGAGGATAGATGTCCG	35580
Db	35521		
OY	35581	CTGTGTGATTCGATTTGTTTGAAGTATGATGAGAACAGGACTACAGACCATGATGTAC	35640
Db	35581		
OY	35641	GTGTCAAAACCCACAGTTCAGCCACTGTTTCCCGTATTCCTTCTTTTACACAC	35700
Db	35641		
OY	35701	GATATTTTCAATATCATTTATTTGTTTAAAGTAATGAACAAGGATACGCTTGTGAATTCGG	35760
Db	35701		
OY	35761	GGATTTGTACAGAAAGACGACACTGATGCTATGATAGTATTTGCTTTTATGGAACA	35820
Db	35761		
OY	35821	ATGTCTGCTGTATTTCTGTCTGTTTAAAGTGTTCATTCCTGCTTAACTGTATATAA	35880
Db	35821		
OY	35881	GGCTAAACCTTTAAAGTTGTTTCCGTTTCTTTTGGATGTTTACGCGGGAGCTGAGA	35940
Db	35881		
OY	35941	TTAGGAGAACCTCGGATAGAGCGTGCCTACATATTTGATTCATCACTCTCGCCA	36000
Db	35941		
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VERSION AF210726.1 GI:7329990
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AUTHORS Alexander, L., Denekamp, L., Knapp, A., Auerbach, M.R., Damania, B. and
Desrosiers, R.C.
TITLE The primary sequence of rhesus monkey rhadinovirus isolate 26-95:
sequence similarities to Kaposi's sarcoma-associated herpesvirus
and rhesus monkey rhadinovirus isolate 17577
JOURNAL J. Virol. 74 (7), 3388-3398 (2000)
MEDLINE 20173730
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REFERENCES 2 (bases 1 to 130733)
AUTHORS Alexander, L., Denekamp, L.M., Knapp, A., Auerbach, M., Czajak, S.,
Damania, B. and Desrosiers, R.C.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1999) Microbiology, New England Regional Primate
Research Center, One Pinehill Dr, Southborough, MA 01772, USA

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Query Match 26.9%; Score 10772; DB 1; Length 130733;
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Db	13017	TCGTTCTGGAATCACAGGGTTTACCAGCTTGGGGTGTACTCGTGGCCGCGCGCCACGCCCC	13076
OY	14909	GCCTGGCGGGCCACAGATGCCAGGAGGGCCCTGGAGTTTACATGCAAGCTGGAGGACCTCA	14968
Db	13077	GCCTGGCGGGCCACAGATGCCAGGAGGGCCCTGGAGTTTACATGCAAGCTGGAGGACCTCA	13136
OY	14969	GCCTTCAAGCGGACCCGACGAGCATGGGCCCCCGTACGCATTCGTGGCCCTTGTATGAGT	15028
Db	13137	GCCTTCAAGCGGACCCGACGAGCATGGGCCCCCGTACGCATTCGTGGCCCTTGTATGAGT	13196
OY	15029	GCACGTGAGAGCGCGGATTTCCGTGCGCACGCGCGACGGCGACGCGCGGTGATCTCAGATCT	15088
Db	13197	GCACGTGAGAGCGCGGATTTCCGTGCGCACGCGCGACGGCGACGCGCGGTGATCTCAGATCT	13256
OY	15089	CGTGCCTCTCTACAGACAGGAGGAGCGGCCCAATCCGGCAAAACATCTGTTACACG	15148
Db	13257	CGTGCCTCTCTACAGACAGGAGGAGCGGCCCAATCCGGCAAAACATCTGTTACACG	13316
OY	15149	TCGGGAGCGTCGACACCCCATCCCGACACCGACGTTTTGGATTTCCGTGCGAAATGTGACA	15208
Db	13317	TCGGGAGCGTCGACACCCCATCCCGACACCGACGTTTTGGATTTCCGTGCGAAATGTGACA	13376
OY	15209	TGCTGTGTCTGCTTCGCGCATGATCCGCGACTTCGAGGTGACGTTTTTAAACGGCTATA	15268
Db	13377	TGCTGTGTGTCTTCGCGCATGATCCGCGACTTCGAGGTGACGTTTTTAAACGGCTATA	13436
OY	15269	ACATCTCAAACTTCGATCTCCGCTACTTAAATACCGGACCGTCCGACGCTGTACAACCTTC	15328
Db	13437	ACATCTCAAACTTCGATCTCCGCTACTTAAATACCGGACCGTCCGACGCTGTACAACCTTC	13496
OY	15329	GATTTAAACGAATACACAAAATTAATAACCGGCTCATCTTTAAAGTTACAGAGCCCGCTG	15388
Db	13497	GATTTAAACGAATACACAAAATTAATAACCGGCTCATCTTTAAAGTTACAGAGCCCGCTG	13556
OY	15389	GCGGGGAGGGGGGGTTCATGAGTGGGTCTCAAAATTAATAATAGCGGCATCTGCCCA	15448
Db	13557	GCGGGGAGGGGGGGTTCATGAGTGGGTCTCAAAATTAATAATAGCGGCATCTGCCCA	13616
OY	15449	TAGCATGTACCAAGGAGTGTCCGGAAAGTCAAGCTTCGCACTACAACGTGGACACGG	15508
Db	13617	TAGCATGTACCAAGGAGTGTCCGGAAAGTCAAGCTTCGCACTACAACGTGGACACGG	13676
OY	15509	TGGCCAGGACGATCTGGGGTGGGAAAAAAGAGACGTATCGTACAAGACATTCGCCCTC	15568
Db	13677	TGGCCAGGACGATCTGGGGTGGGAAAAAAGAGACGTATCGTACAAGACATTCGCCCTC	13736
OY	15569	TGTTTTGCCTAGAGTCCGGGCGCGAGGGGCTAAGGTGGGACGATATTGCGTGATGGACTGG	15628
Db	13737	TGTTTTGCCTAGAGTCCGGGCGCGAGGGGCTAAGGTGGGACGATATTGCGTGATGGACTGG	13796
OY	15629	TCCCTGGGATGAGCACTCTTAAAAATGTTTATGATACCTGGAGATTTCCGGAGATAGCCA	15688
Db	13797	TCCCTGGGATGAGCACTCTTAAAAATGTTTATGATACCTGGAGATTTCCGGAGATAGCCA	13856
OY	15689	AGCTGGCCAAAGATTCAAGGCCAGGCGCGTCTGACGGACGGCAACAGCTCCGCGATTCT	15748
Db	13857	AGCTGGCCAAAGATTCAAGGCCAGGCGCGTCTGACGGACGGCAACAGCTCCGCGATTCT	13916
OY	15749	CTGTCCCTGTGAGAGCGCCGGGGCCAGGAGAACTTTATCTCTCCCGGTTCCAAAGCCCGGAG	15808
Db	13917	CTGTCCCTGTGAGAGCGCCGGGGCCAGGAGAACTTTATCTCTCCCGGTTCCAAAGCCCGGAG	13976
OY	15809	GACAGGGGGGCTATCAAGGGGCGACAGTATCAACCCATTCGCGGGGTTTTACAGCAGAC	15868
Db	13977	GACAGGGGGGCTATCAAGGGGCGACAGTATCAACCCATTCGCGGGGTTTTACAGCAGAC	14036
OY	15869	CGGTCTGTGTGATTTTTCAGGCTGTACCCGACATTCACAGGCGCAACACTGT	15928
Db	14037	CGGTCTGTGTGATTTTTCAGGCTGTACCCGACCTTACCCGACATTCACAGGCGCAACACTGT	14096

OY	15525	GCTACTCCACCATGATATACAGGACGAGACTGCACTCGACCCCAACTGACGCGGGACG	159888
Db	14097	GCTACTCCACCATGATATACAGGACGAGACTGCACTCGACCCCAACTGACGCGGGACG	141566
OY	15989	ACTACGAGAGCTTCGCTCTGAGGGGGGACCGGCTACATTTTGTAAAAAACAAGCGGG	160488
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OY	16049	AGTCTCTGCTGGGAAAGACTGCTAAACGCTGTGTGTAGAAAAAGCGAAGGGGATCCGGCGCA	161088
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OY	16109	CCCTGGCGGCGCTGCGATGACCCGCTCGCTAAAAACATCTTAGATAAACACAGCTGGCCA	161688
Db	14277	CCCTGGCGGCGCTGCGATGACCCGCTCGCTAAAAACATCTTAGATAAACACAGCTGGCCA	143366
OY	16169	TCGAAGTACATGTAACGCGGTTTACCGGGGTTCACCGGGGGGCGACGGGCTCTCCCAT	162288
Db	14337	TCGAAGTACATGTAACGCGGTTTACCGGGGTTCACCGGGGGGCGACGGGCTCTCCCAT	143988
OY	16229	GCATTTAACATAGCGGAAACCGTACACGCTCCGGGGGGCGCAAGATGTGAGATGTCAAGT	162888
Db	14397	GCATTTAACATAGCGGAAACCGTACACGCTCCGGGGGGCGCAAGATGTGAGATGTCAAGT	144566
OY	16289	CTTACGTGTGAGGCCCTTGACGAGCGAAGACCTGCGAACCGCTCTCGGTGCGAGGTGACCG	163488
Db	14457	CTTACGTGTGAGGCCCTTGACGAGCGAAGACCTGCGAACCGCTCTCGGTGCGAGGTGACCG	145188
OY	16349	CCCTGTACAGGCGGGCGGTTTTCGGGTGCTACGGGTGACACACGACTCCCTTTATTCGGCT	164088
Db	14517	CCCTGTACAGGCGGGCGGTTTTCGGGTGCTACGGGTGACACACGACTCCCTTTATTCGGCT	145766
OY	16409	GCGACGGTTTATTCGCGCGAAGACCGTTTCCGCTTTCTGTGACATCTGGCGCGCAGGATCA	164688
Db	14577	GCGACGGTTTATTCGCGCGAAGACCGTTTCCGCTTTCTGTGACATCTGGCGCGCAGGATCA	146388
OY	16469	CTGGCGACCTGTTCCGCCCAACCCCATTAAGCTAGAGCGGAAAAAGACGTTTCAAGTGTCTGC	165288
Db	14637	CTGGCGACCTGTTCCGCCCAACCCCATTAAGCTAGAGCGGAAAAAGACGTTTCAAGTGTCTGC	146988
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Db	14697	TGCTGTGTACGAAAAACGGGTACATCGGGGTCTCTATTGAAACGCAAAATGTGTCATGAAG	147566
OY	16589	GGGTGCACTCATTTCCGAAAAACGGCGTCAAGTTTGTCCAGAGCATGCGCGGCATCTC	166488
Db	14757	GGGTGCACTCATTTCCGAAAAACGGCGTCAAGTTTGTCCAGAGCATGCGCGGCATCTC	148188
OY	16649	TGGAACCTGTGTCTCCAGATCCGAGAGTCAAGGCTCGGGCGCGGCTGTTGTGCAAGCGGC	167088
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OY	16709	CGCGGACCGGGTATACGAGAGAGGGCTGCGGGCTGGCTTTTATAAAAATCTGTAGAGTGC	167688
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Db	15057	TGTACCAAAAGCTGTGGAGAGAGTGGAGAGAGTGGCCCAAGTGTGACATTAAGATCCCT	151166
OY	16949	ACGCTGTTCTGTGAGCGCGCGGGTCCCTTAAAGTCGAGACTGGCGCAACACCGGATTTACG	170088
Db	15117	ACGCTGTTCTGTGAGCGCGCGGGTCCCTTAAAGTCGAGACTGGCGCAACACCGGATTTACG	151766
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RESULT 3	
AF029302	10595 bp DNA linear VRL 21-NOV-1997
LOCUS	Rhesus monkey rhadinovirus H26-95 glycoprotein B, DNA polymerase, and interleukin-6 homolog genes, complete cds; and thymidylate synthase homolog gene, partial cds.
DEFINITION	
AF029302	AF029302.1 GI:2625041
ACCESSION	
VERSION	
KEYWORDS	Rhesus monkey rhadinovirus H26-95
SOURCE	Rhesus monkey rhadinovirus H26-95
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
REFERENCE	1 (bases 1 to 10595)
AUTHORS	Desrosiers, R.C., Sasseville, V.G., Czajak, S.C., Zhang, X., Mansfield, R.G., Kaur, A., Johnson, R.P., Lackner, A.A. and Jung, J.U.
TITLE	A herpesvirus of rhesus monkeys related to the human Kaposi's sarcoma-associated herpesvirus
JOURNAL	J. Virol. 71 (12), 9764-9769 (1997)
MEDLINE	98037693
PUBMED	9371642
REFERENCE	2 (bases 1 to 10595)
AUTHORS	Desrosiers, R.C., Sasseville, V.G., Czajak, S.C., Zhang, X., Mansfield, R.G., Kaur, A., Johnson, R.P., Lackner, A.A. and Jung, J.U.
TITLE	Direct Submission
JOURNAL	Submitted (08-Oct-1997) Microbiology, New England Regional Primate Research Center, 1 Pine Hill Drive, Southborough, MA 01772-9102, USA
FEATURES	
source	Location/Qualifiers 1..10595 /organism="rhesus monkey rhadinovirus H26-95" /mol_type="genomic DNA" /isolate="H26-95" /db_xref="taxon:69256" /note="related to Kaposi's sarcoma-associated herpesvirus (KSHV or human herpesvirus-8)" 1..498 /note="ORF 7" /codon_start=1 /product="unknown protein" /protein_id="AAC58685.1" /db_xref="GI:2625042" /translation="QFGLITPPLTRQSLDFPGPANVLAQCFEAGMLPHKMLYSEMTWPIQPKWDIDQTFNRFYQLPEGLNVAOKSAMCFIRELVSAVLNRTWEKTLRIEFLAREKLSISMVKGILSGLYTEQDAPLVLSQNTGMIFKDLVLLYHLQLSDGHDDN" 485..2974 /note="ORF 8; similar to human herpesvirus-8 (HHV-8) glycoprotein B" /codon_start=1 /product="glycoprotein B" /protein_id="AAC58686.1" /db_xref="GI:2625043" /translation="MMITNRRRLRLRAWVLIATIGAVGENTYTPKGATTKPPGSPTRPENPRAEAFKFRYCSASATGELFRFLNEKTCPECTEDKTHQEGILMPKKNIYPIIKVRRKRAIVSYIRKWTETAVTEKQEVINRPOYELNHDTYOCSSKRNANGIVNYTDROFTNQVFLQPEGLTNIQRYFSQPVLYTTPGMPGIVRYRTVNCLEIVDIARSAEYSYFVALGDTVEVSPCHNDSTCSVAEKTENGILGAIVRNTYMDFAIRAPTEETRVFADSGEYVEMKAEDPSKAVCALTKMTFPRAIOTHEASVYEVAN DYATFTSPLEISLVANGTYSCLDEIOKTLDDTKIKLSDTHVNGSAQYVTEGGLLMOPLPLSLYDVMKGLNGTTPAPPATTSYTSRRRSVNTNEQATNDIAAQLQFAYDKLRASINKVLELSRWCRQEVRODTYMYELSKINPSVMAIIGRPVSAFVGDAISYTDVAVDAQSVSIHSLRTSTPGMCSRPVTFRLNSTLIFGOLGSAFNEIILTDNVEACKETCEHYFIASNYVYKDYVEFKINTSEISLTGFIALNSFIENIDERVIELYSAREKLSGSVEDETMRREYNYTORLAGLREDIDTIDINRODLARDLSEIYADLGVGRVYVNVASVITLSEGISGFINEFKSPFGMLMLIVAYVLYFALANRRTNALADAPITRMITPIDIKMQPSGKVVDDQIKNIIAGMHQLQOEERRRLDEQORSAPSLEFRASDGLKRRFRKGYKPLENEAQEYEMSK" 3092..6136 /note="ORF 9; similar to human herpesvirus-8 (HHV-8) DNA polymerase" /codon_start=1 /product="DNA polymerase"
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BASE COUNT	2307 a 3372 c 2971 g 1945 t

ORIGIN

Query Match	19.9%	Score 7957;	DB 1;	Length 10595;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 8257;	Conservative	0;	Mismatches 6;	Indels 0;
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 RESULT 4
 AF087411 3804 bp DNA linear VRL 04-NOV-1999
 LOCUS
 DEFINITION Rhesus macaque rhadinovirus R2 protein, thymidylate synthase, and
 R3 protein genes, complete cds.
 ACCESSION AF087411
 VERSION AF087411.1 GI:5823013
 KEYWORDS
 SOURCE
 ORGANISM
 Cercopithecine herpesvirus 17
 Cercopithecine herpesvirus 17
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae; Rhadinovirus.
 REFERENCE 1 (bases 1 to 3804)
 Wong,S.W., Bergquam,E.P., Swanson,R.M., Lee,F.W., Shigtl,S.M.,
 Avery,N.A., Pantou,V.W. and Axthelm,M.K.
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 virus-infected rhesus macaques with the simian homologue of
 Kaposi's sarcoma-associated herpesvirus
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 MEDLINE 99429887
 PUBMED 10499921
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 Wong,S.W., Bergquam,E.P., Swanson,R.M., Lee,F.W., Shigtl,S.M.,
 Avery,N.A. and Axthelm,M.K.
 Direct Submission

20903 GGTCTCCGCACTAAGCAGAGGAGATCAACGTGTTGTTAAAGCTGGGCTCACC 20962
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Db 1501 GGTCTCCGCACTAAGCAGAGGAGATCAACGTGTTGTTAAAGCTGGGCTCACC 1560
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Db 3781 ATGGGCTGTAGACGCCAACCGCA 3804

RESULT 5
AF159033 475 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca mulatta gamma virus DNA
DEFINITION polymerase (pol) gene, partial cds.
ACCESSION AF159033
VERSION AF159033.1 GI:6671074
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
J Clin. Virol. 16 (3), 253-269 (2000)

JOURNAL MEDLINE 20204465
PUBMED 10738144

REFERENCE 2 (bases 1 to 475)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
SUBMITTED (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
LOCATION/Qualifiers
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/codon_start=2
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/db_xref="GI:6671075"
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KHRESLIGRLTVLEKRAIRRTLAACDDPSLKTLDKOLAIXYTCNAVVGFTGV
ASGLPCINAEIVTLRGRTMLEMSKSYVALTDELRTLRGKRVTAHRAARRRVV"

BASE COUNT 110 a 141 c 143 g 81 t

ORIGIN

Query Match 1.2%; Score 475; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 4, Be-268;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 AGAAAACGGAAGGCGATCCGCGCACCCCTGGCGGCTGGGATGACCCGTGCTAAAAAC 240

QY 16143 CATCTTAGATAAACACAGCTGGCCATCAGAGTGACATGTAAACCGGTTTACGGCTCAC 16202

Db 241 CATCTTAGATAAACACAGCTGGCCATCAGAGTGACATGTAAACCGGTTTACGGCTCAC 300

QY 16203 CGGGGTGGCAGCGGCTCCCTCCATGATTAACATAGCGGAACCGTGAAGCTCCGGG 16262

Db 301 CGGGGTGGCAGCGGCTCCCTCCATGATTAACATAGCGGAACCGTGAAGCTCCGGG 360

QY 16263 GCGCAGCATCTGGAGATGTCAAGTCTACGTGAGAGCCCTGACGACGGAAGACCTGCG 16322

Db 361 GCGCAGCATCTGGAGATGTCAAGTCTACGTGAGAGCCCTGACGACGGAAGACCTGCG 420

QY 16323 AACCGTCTGGTCCGACAGTGAACCGGCGGCGGCGGCTTGGCGCTGTC 16377

Db 421 AACCGTCTGGTCCGACAGTGAACCGGCGGCGGCGGCTTGGCGCTGTC 475

RESULT 6
AF159041 395 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca mulatta gamma virus glycoprotein
DEFINITION B (gB) gene, partial cds.
ACCESSION AF159041
VERSION AF159041.1 GI:6671090
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

REFERENCE 1 (bases 1 to 395)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
J Clin. Virol. 16 (3), 253-269 (2000)

JOURNAL MEDLINE 20204465
PUBMED 10738144

REFERENCE 2 (bases 1 to 395)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
SUBMITTED (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
LOCATION/Qualifiers
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BASE COUNT 106 a 113 c 108 g 68 t

ORIGIN

Query Match 0.8%; Score 331; DB 1; Length 395;
Best Local Similarity 99.7%; Pred. No. 3, 36-183;
Matches 381; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11759 CGGGCAGCGAGACACGACACCAAGGATCTGATGTGTTTAAAAAATATATG 11818

Db 1 CGGGCAGCGAGACACGACACCAAGGATCTGATGTGTTTAAAAAATATATG 60

QY	11834	AGGTCANAGCGGTACCGCAAGGTGGCCACTTCGTGGTACACCGTCTATCCAGAGGTTGACCCGAGA	1189
Db	1	AGGTCANAGCGGTACCGCAAGGTGGCCACTTCGTGGTACACCGTCTATCCAGAGGTTGACCCGAGA	60
QY	11894	CCGCGCGGACCGGCAAGCAAGAGGTCTATCCGACCGGTGGCCGACGTACGATCAACCA	1195
Db	61	CCGCGCGGACCGGCAAGCAAGAGGTCTATCCGACCGGTGGCCGACGTACGATCAACCA	120
QY	11954	TGGACACGACCTACCACTGTTTCAGCTTCATGGCGGT	11990
Db	121	TGGACACGACCTACCACTGTTTCAGCTTCATGGCGGT	157
RESULT 8			
AF204167			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
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FEATURES			
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Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15703 CAGCCAGGCGCGCTGACGAGCGCCACAGCTCCGCGTGTCTCTCTGCTGAG 15762
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Db 1126 CAGCCAGGCGCGCTGACGAGCGCCACAGCTCCGCGTGTCTCTCTGCTGAG 1185
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Oy 15763 GCGCGGCGGAGGAGACTT 15782
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Db 1186 GCGCGGCGGAGGAGACTT 1205
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RESULT 9
AF159031 475 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca nemestrina gamma virus DNA
DEFINITION polymerase (pol) gene, partial cds.
ACCESSION AF159031
VERSION AF159031.1 GI:6671070
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thouless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLES Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
2 (bases 1 to 475)
REFERENCE Strand,K.B. and Bosch,M.L.
AUTHORS Direct Submission
TITLES Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
JOURNAL 357238, Seattle, WA 98125, USA
FEATURES
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BASE COUNT 100 a 147 c 152 g 76 t
ORIGIN

Query Match 0.2%; Score 71; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.2e-30;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15903 GAGCATCATCAGGCGGACACCTGTCTACTCCACCATGATACGAGGAGACTTGA 15962
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Db 1 GAGCATCATCAGGCGGACACCTGTCTACTCCACCATGATACGAGGAGACTTGA 60
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Oy 15963 CCTGCACCCCA 15973

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DB 61 CCTGCACCCCA 71
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RESULT 10
AF159034 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca nemestrina 116 gamma virus DNA
DEFINITION polymerase (pol) gene, partial cds.
ACCESSION AF159034
VERSION AF159034.1 GI:6671076
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thouless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLES Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
2 (bases 1 to 336)
REFERENCE Strand,K.B. and Bosch,M.L.
AUTHORS Direct Submission
TITLES Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
JOURNAL 357238, Seattle, WA 98125, USA
FEATURES
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BASE COUNT 75 a 103 c 105 g 53 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15976 CTGACGCGGACGACTACGAGACGTTGCTGACGCGGACGCGTACATTTC 16031
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Db 41 CTGACGCGGACGACTACGAGACGTTGCTGACGCGGACGCGTACATTTC 96
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RESULT 11
AF159032 475 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis gamma virus DNA
DEFINITION polymerase (pol) gene, partial cds.
ACCESSION AF159032
VERSION AF159032.1 GI:6671072
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thouless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.

```

TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kaposi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
PUBMED 20204465
10738144

REFERENCE 2 (bases 1 to 475)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA

FEATURES
source Location/Qualifiers
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BASE COUNT 99 a 144 c 152 g 80 t

ORIGIN

Query Match 0.1%; Score 50; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15903 GAGCATCATCCAGCGCACACCTGTCGTACTCCACCATGATACAGGAC 15952
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1 GAGCATCATCCAGCGCACACCTGTCGTACTCCACCATGATACAGGAC 50

Db

RESULT 12
AF159036 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis 037 gamma virus DNA
DEFINITION Polymerase (pol) gene, partial cds.
ACCESSION AF159036
VERSION AF159036.1 GI:6671080
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kaposi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
PUBMED 20204465
10738144

REFERENCE 2 (bases 1 to 336)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA

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ETVTLRGRT"

BASE COUNT 75 a 101 c 107 g 53 t

ORIGIN

Query Match 0.1%; Score 48; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15975 CCTGACGCCGAGCAGCTACGAGAGCTTCGCTGAGCGGAGCGGT 16022
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40 CCTGACGCCGAGCAGCTACGAGAGCTTCGCTGAGCGGAGCGGT 87

Db

RESULT 13
AF159037 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis 040 gamma virus DNA
DEFINITION Polymerase (pol) gene, partial cds.
ACCESSION AF159037
VERSION AF159037.1 GI:6671082
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kaposi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
PUBMED 20204465
10738144

REFERENCE 2 (bases 1 to 336)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA

FEATURES
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gene
CDS

Query Match 0.1%; Score 48; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15975 CCTGACGCCGAGCAGCTACGAGAGCTTCGCTGAGCGGAGCGGT 16022
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40 CCTGACGCCGAGCAGCTACGAGAGCTTCGCTGAGCGGAGCGGT 87

Db

RESULT 14
AF159035 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca nemestrina 139 gamma virus DNA
DEFINITION
ACCESSION AF159035
VERSION AF159035.1 GI:6671078
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM
Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
AUTHORS Strand,K.B., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 336)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
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Query Match 0.18; Score 47; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 6.9e-16;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15976 CTGACGGCGGACGACTACGAGCTGCTGCTGCGCGGCGACCGGT 16022.
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Db 41 CTGACGGCGGACGACTACGAGCTGCTGCTGCGCGGCGACCGGT 87
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LOCUS Pseudorabies virus DNA polymerase gene, partial cds.
DEFINITION
ACCESSION L24487
VERSION L24487.1 GI:438894
KEYWORDS DNA polymerase.
SOURCE Pseudorabies virus
ORGANISM Pseudorabies virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE
AUTHORS Bertelme,H., Monahan,S.J., Parris,D.S., Jacquemont,B. and
Epstein,A.L.
TITLE Cloning, sequencing, and functional characterization of the two
subunits of the pseudorabies virus DNA polymerase holoenzyme:
evidence for specificity of interaction
JOURNAL J. Virol. 69 (5), 2811-2818 (1995)

MEDLINE 95222727
PUBMED 7707503
COMMENT Original source text: Pseudorabies virus (Individual_Isolate
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Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1720 TTTCGCCAGCTGTACCGACATCCAGCGCACCACTGTGCT 1765
RESULT 16
AF159038 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis 050 gamma virus DNA
DEFINITION
ACCESSION AF159038
VERSION AF159038.1 GI:6671084
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 336)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
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Location/Qualifiers

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BASE COUNT      76 a      101 c      106 g      53 t
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Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 17
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LOCUS      Mandrillus herpesvirus 2 isolate animal Mnd15 DNA polymerase (pol)
DEFINITION      gene, partial cds.
ACCESSION      AF282937
VERSION      AF282937.1 GI:11611783
KEYWORDS
SOURCE
ORGANISM
  Mandrillus herpesvirus 2
  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
  Gammaherpesvirinae; Rhadinovirus.
REFERENCE
  1 (bases 1 to 475)
  Lacoste,V., Maucletre,P., Dubreuil,G., Lewis,J.,
  Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.
  Simian homologues of human gamma-2 and betaherpesviruses in
  mandrill and drill monkeys
  J. Virol. 74 (24), 11993-11999 (2000)
JOURNAL
  MEDLINE
  PUBMED
  2 (bases 1 to 475)
  Lacoste,V., Maucletre,P., Dubreuil,G., Lewis,J.,
  Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.
  Direct Submission
  Submitted (28-JUN-2000) Departement du SIDA et des Retrovirus,
  Institut Pasteur, 28, rue du Dr. Roux, Paris cedex 15 75724, France
FEATURES
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Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      16270 ATGCTGAGANGTCAAGCTTACGTGAGGCCCTGAC 16307
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Db      368 ATGCTGAGANGTCAAGCTTACGTGAGGCCCTGAC 405

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DEFINITION      gene, partial cds.
ACCESSION      AF282938
VERSION      AF282938.1 GI:11611785
KEYWORDS
SOURCE
ORGANISM
  Mandrillus herpesvirus 2
  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
  Gammaherpesvirinae; Rhadinovirus.
REFERENCE
  1 (bases 1 to 475)
  Lacoste,V., Maucletre,P., Dubreuil,G., Lewis,J.,
  Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.
  Simian homologues of human gamma-2 and betaherpesviruses in
  mandrill and drill monkeys
  J. Virol. 74 (24), 11993-11999 (2000)
JOURNAL
  MEDLINE
  PUBMED
  2 (bases 1 to 475)
  Lacoste,V., Maucletre,P., Dubreuil,G., Lewis,J.,
  Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.
  Direct Submission
  Submitted (28-JUN-2000) Departement du SIDA et des Retrovirus,
  Institut Pasteur, 28, rue du Dr. Roux, Paris cedex 15 75724, France
FEATURES
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BASE COUNT      109 a      149 c      137 g      80 t
ORIGIN
Query Match      0.1%; Score 38; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      368 ATGCTGAGANGTCAAGCTTACGTGAGGCCCTGAC 405

RESULT 19
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LOCUS
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DEFINITION	MANDRILLUS HERPESVIRUS 2 ISOLATE	ANIMAL MND401 DNA POLYMERASE (POL)
ACCESSION	AF282939	
VERSION	AF282939.1	GI:11611787
KEYWORDS		
SOURCE		
ORGANISM	Mandrillus herpesvirus 2	
REFERENCE	Mandrillus herpesvirus 2	
AUTHORS	Vitusas; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.	
TITLE	1 (bases 1 to 475)	
JOURNAL	Lacoste,V., Maucelere,P., Dubreuil,G., Lewis,J., Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.	
PUBLISHED	Simian homologues of human gamma-2 and betaherpesviruses in	
REFERENCE	Mandrill and drill monkeys	
AUTHORS	J. Virol. 74 (24), 11993-11999 (2000)	
TITLE		
JOURNAL		
FEATURES	Location/Qualifiers	
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Query Match	0.1%	Score 38; DB 1; Length 475;
Best Local Similarity	100.0%	Pred. No. 1.4e-10;
Matches	38; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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DB	368 ATGCTGAGATGTCAAAGCTTCTAGCTGGAGGCCCTGCAC	405
RESULT 20		
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DEFINITION	Mandrillus herpesvirus 2, isolate animal mnd402 DNA polymerase (Pol)	
ACCESSION	AF282940	
VERSION	AF282940.1	GI:11611789
KEYWORDS		
SOURCE	Mandrillus herpesvirus 2	
ORGANISM	Mandrillus herpesvirus 2	
REFERENCE	Vitusas; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.	
AUTHORS	1 (bases 1 to 475)	
TITLE	Lacoste,V., Maucelere,P., Dubreuil,G., Lewis,J., Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.	
JOURNAL	Simian homologues of human gamma-2 and betaherpesviruses in	
	Mandrill and drill monkeys	
	J. Virol. 74 (24), 11993-11999 (2000)	

MEDLINE	20542003
PUBMED	11090203
REFERENCE	2 (bases 1 to 475)
AUTHORS	Lacoste,V., Mauciere,P., Dubreuil,G., Lewis,J., Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.
TITLE	Direct Submission
JOURNAL	Submitted (28-JUN-2000) Departement du SIDA et des Retrovirus, Institut Pasteur, 28, rue du Dr. Roux, Paris cedex 15 75724, France
FEATURES	Location/Qualifiers 1..475
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CDS	<1..>475 /gene="Pol" /codon_start=2 /product="DNA polymerase" /protein_id="AAC39063.1" /db_xref="GI:11611790" /translation="SIQAHNLVCSTMIHGRLHLNPTLQDDYETFLLSGGPVHFKKHKRESILGRLLTWLDKRREIRALAKCDPPSKTILDKOQLIKVTCAWVGFTGVASGLPCISIAEIVTLRGRTMLEKSKSYEVALTPDEQTRLRRAVHAGPSARFRVV"
BASE COUNT	109 a 149 c 137 g 80 t
ORIGIN	
Query Match	0.1%; Score 38; DB 1; Length 475;
Best Local Similarity	100.0%; Pred. No. 1,4e-10;
Matches	38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	16270 ATGCTGGAGATGTCAAAGTCTTTACGTGGAGCCCTGCAC 16307
Dn	368 ATGCTGGAGATGTCAAAGTCTTTACGTGGAGCCCTGCAC 405
RESULT 21	
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DEFINITION	Macaca mulatta rhadinovirus 26-95 long unique region L-DNA, complete sequence.
ACCESSION	AF210726
VERSION	AF210726.1 GI:7329990
KEYWORDS	Macaca mulatta rhadinovirus 26-95 Macaca mulatta rhadinovirus 26-95 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
SOURCE	1 (bases 1 to 130733) Alexander,L., Denekamp,L., Knapp,A., Auerbach,M.R., Damanla,B. and Desroliers,R.C.
ORGANISM	The primary sequence of rhesus monkey rhadinovirus isolate 26-95: sequence similarities to Kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 17577
REFERENCE	J Virol. 74 (7), 3388-3398 (2000)
AUTHORS	1 (bases 1 to 130733) Alexander,L., Denekamp,L.M., Knapp,A., Auerbach,M., Czajak,S., Damanla,B. and Desroliers,R.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-DEC-1999) Microbiology, New England Regional Primate Research Center, One Pinehill Dr, Southborough, MA 01772, USA
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 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23879 GTTGGTTTGTGTTACACTTCCTATATATAT 23911
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 Db 115354 GTTGGTTTGTACAGTCCATATATATAT 115322

RESULT 22
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 LOCUS Macaca mulatta rhadinovirus 17577, complete genome.
 ACCESSION AF083501
 VERSION AF083501.3 GI:8714565
 KEYWORDS
 ORGANISM
 Macaca mulatta rhadinovirus 17577
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae; Rhadinovirus.
 1 (bases 1 to 133719)
 Seales,R.P., Bergquam,E.P., Atheljm,M.K. and Wong,S.W.
 Sequence and genomic analysis of a Rhesus macaque rhadinovirus with
 similarity to Kaposi's sarcoma-associated herpesvirus/human
 herpesvirus 8
 J. Virol. 73 (4), 3040-3053 (1999)

JOURNAL MEDLINE
 PUBMED 99174001
 10074154
 REFERENCE
 AUTHORS 2 (bases 1 to 133719)
 TITLE Seales,R.P., Bergquam,E.P., Atheljm,M.K. and Wong,S.W.
 JOURNAL Direct Submission
 Submitted (11-AUG-1998) Division of Pathobiology and Immunology,
 Oregon Health Sciences University/ Oregon Regional Primate Research
 Center, 505 NW 18th Avenue, Beaverton, OR 97006, USA
 3 (bases 1 to 133719)
 Seales,R.P., Bergquam,E.P., Atheljm,M.K. and Wong,S.W.
 Direct Submission
 Submitted (16-JUL-1999) Division of Pathobiology and Immunology,
 Oregon Health Sciences University/ Oregon Regional Primate Research
 Center, 505 NW 18th Avenue, Beaverton, OR 97006, USA
 4 (bases 1 to 133719)
 Seales,R.P., Bergquam,E.P., Atheljm,M.K. and Wong,S.W.
 Direct Submission
 Submitted (26-JUN-2000) Division of Pathobiology and Immunology,
 Oregon Health Sciences University/ Oregon Regional Primate Research
 Center, 505 NW 18th Avenue, Beaverton, OR 97006, USA
 REMARK
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Sequence update by submitter
 On Jun 26, 2000 this sequence version replaced gi:5508840.

FEATURES
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 CDS
 CDS
 CDS

Location/Qualifiers
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 SEIPGKDTNEENGIRKRYOYVEKNNK"
 3676..5613
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 GETALRESPGVYVNTKITTTECLQNGMSTNPQDRRCRCPADLLNGAHHGSD
 NALKRGSNIYECNEGYDILGSLNVRCLIQDTBNVMDNSVEYCELOKIKRPAVHG
 DYLPMQDVNYGDALTEFKCSLYTLVGSTYLLVCTSKRWKNSNFPCLQKICRPAVHG
 GYIDIGLSRHHQOSITVKGSDGVNIVGPELTCTNTMTVPLPCVATVNNPSTPM
 PETMPETPTPYOKINLSTAKTATPNAFVTVTVSPEDDVPYCVKPHREYVAKEN
 DKESYSGASVELICRPFTKQSTVSCVSLGNTGTAPNACRHKCPQDLGCE
 YIVTSGEADKYGTNTTKCNQYGLGSMVNIKMDKLQATVDEPKRPIQDIECK
 PPQITNGKHYHVKDPTQYLDVTVBSCHNDFSLYDDEMTCTISNTNKKFPRRQDITC
 SAPNIAHGRLTGSSSVYKYGQSVTIGCTGFLIGSEISTCKDSSWDPPLPTCVAV
 SMPDTPKPEKTKKPNTPPEAKRPNTPNVGRHTPFPKPPONPPIAPPMKMKRHVVL
 LFAVSASLFLVLAALYCPLK"
 6045..9443
 /note="ORF 6: similar to Kaposi's sarcoma-associated
 herpesvirus ORF 6"
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 /db_xref="GI:4494911"
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 NRPSSGVSISPLVGLTYHEHPEPLTVKAAKYKVDPTTAAVYVYCHRRVYVHNASTL
 FRPVEFGTLELNECEBARALFGTQPIEGRPSTINPLECQRLPKDEMLFVAYTE
 GERERLMRCGLVAVFQYQVOYIAGQKQKVPYUDLDAIPHGRHPRRYHNDVSAVL
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 YDSLVVAELALSGCMFLCPDQACELLYVDSMPIDGSDSPARVNALEIRMSAEQAV
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 KVPASNALDGSSFTPHYHLVYASFSPLLAKLYCYNPFQHHKSSNQONAFNHYVGT
 KANSECTLCNGTATCLNTLRYRLKDRPVAVTTQRRDPVYVYGTATGNDLELIG
 NFASFQDREDDNPADDEHRYTYWQLQVTEKLSAIGITEHDNHNVALITNQSFLR
 VERKIDSIYDGEVMEKFNMSIKNNFNFRHVSVHHIIGFCCNVDNACAVFLNLY
 KSLMTIIOIDICPYCMYIEQDNPAMGILISEMLKMHFORLMTNFKACIDRGLTGE
 LKIVHDMFCDFEDDAGSNGMLAPKQVYKRAMVVPKSIKIKRITIFSTAGSE
 AVOSGVPKPTGRTDYVAVGPKPLNSLHRLALFPDTRKALYLMHKISQTNKTPYAK
 DVPDELAELVSVKTNSTLAFETINLVDPVPSLMSYAIKILGALIKLGGCOGYFAT
 TLHCITPVLQTIIDAEYYPHVLGSAALATPVAVLAELRGRTALTIVQTTARQPAVATGR

CDS

RPVITPVWVKKYKVCVNGNNVHEGNGTFCAGRGVDPNLMPESSPEKTKVSNMTRK
RHVMTPIIDILIRAKAGOTTSTFEASVSKSVQALDEKDNPLKSLTIELRHUG
KGCODLSEEDVOYVLYGDCMLTDEVLFITLDNIADSGVPTIEDAALLIEDQDADDLQ
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9468..11528

/note="ORF 7: similar to Kaposi's sarcoma-associated
herpesvirus ORF 7"

/codon_start=1

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/db_xref="GI:4494912"

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PECHHSTVTFOTFGGGLIDVNMCLINDVELCKRGVPTICIGANEHLSGNRYLT
LSTLNGISPIPHDLYTVSPVOCLREIELVPCOGSSLLAVLADRHDLCKKVRAT
PIHGLFETELSQLGKTKRSDATQHGVSASSDQLEBSLAIODHNTFKKVSIME
LSNLYMAAGOTLGOTGENESQMARLLTHEADHHEHRLITPELTKHVSDDCRPD
PIESFCGGFNISIDDTINALSRDQSVTFPOANTNMRKONELFPTLNSLRGSA
GSOCPAPSEPTTVAATAASDVYKKAQYRKEDQYMKVARDKFRKLTCEQTQSAYL
ANALCMRWGGVATGEASELVNHLRREYALPEAKRSDQILFENSKYTKSLIS
QRLSREHVEITTLQFYGLITGLTRQSDLPFGPAVALAQCFEAGMLPHKMLVSEM
IMPOLOPKMDIDOTFNREYQLPEGLDANVQKSAFCIFELVLSVALYNRWTEKLTIF
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HDDN"

CDS

11515..14004

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herpesvirus ORF 8"

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/protein_id="AAD21335.1"

/db_xref="GI:4494913"

CDS

14122..17166

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herpesvirus ORF 9"

/codon_start=1

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/protein_id="AAD21336.1"

/db_xref="GI:4494914"

CDS

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CLRTPGAGGMIPVTIPPEPPYFENGARGDVLANDBSMTTARDKRPVAPDDOSITP
HAYVETTYADACAEVPSRFQDILIPSGVILKLTGTEGTSVCNANVFOQYFVA
KVPAGINVTHTLQALKNVAGRAAGSTTRVNRKILKTYVAEPVETILSSGML
STSDRLVACGEVSVNDVARRVLDHGTFTGWYSCARAPRLAARDRTLEED
CSMEDLSVQADRSMPPIRIVADIECEGAEFPACEDGDAVIOISCFVTFTEGAP
NPNNILFSGTCDIPIDTDLVEPSEEDMLVSFAMIDEFDLTGYNISNFDPLYL
ITRASOYNLRLNRYTKIKTGSIFEVHRRGGGQPMKSVSKIKIAGIVPDMOYCR
EKLSDYKLDTVARQCLGKKEDEYSTKIDIPPLRSGEGRAKVGSTVMDSVLMDL
LKMFMHVEISEIAKLAKIQARVLTGQOQRVSCLEAARENFLIPVTPGQGG
YQAGAVINPIPGFDEPVLVDFASLVSIIQANLICTIMHGRDHLNHLNPLDY
ETFVLSGPPVHFVKHRESLLGRLLVWLEKRAIRRTLAACDPSLKTLLDKOOLA
IKVMCAVYGTGASGLIPCINAEVYTLTGRTMLEMSKVSVEALITDPRPTELEGR
VTARHGAERVYGDSTLFIACDGYSAENASACDILAIARTITADIPPRKLEAKET
FKCLLTLTKRTIYGLNDKMWKMGVDITIRKTAQFOERKATILDLVLPHEKAA
RLICKRPHVAEGLPAGFKIVEIVNASTYLDLNSVLPTEOLTFSTELSRCVDCV
TTNLPHLAVOKLASCBEELPOVHDRIPIYVVDVDSKSLDAEHPVYVROHQIIPAV
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17261..18511

/note="ORF 10: similar to Kaposi's sarcoma-associated

CDS

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PESLDLHORFAGCIYVRLKEIPFESCVALLIPLDSGGADARAPAGVULDSRP
LITVYNASGRITIRCLFLKPIRIDERAVTYFEGENGARSSEGTPTKATIESLPGGP
LRVSGEASQVTHSPHSVAFPANSVACISLIRLOVRPESDDAARDARTISKRYVFSN
SGVNCVKSASVTHSPSCRTAOMELIYAPGDPNMEIYVGGSPVLPHTGGVAGVYA
DAEKTIOGSSAEVAVOLIFQOGAARGLAFIVTGAPELFFVTPALLISGCTTHL
RLPNNGTPTTIKRTDITVAAPPCPVVLTSSADAPRDLVASPTGALSIINAFTIPVG
FPGVVSACHYVSLDNGVHERMNH"
18520..19749
/note="ORF 11: similar to Kaposi's sarcoma-associated
herpesvirus ORF 11"

Query Match 0.1%; Score 33; DB 1; Length 133719;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23879 GTTGGCTTTGTACAGTTCCTATATAT 23911
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Db 117575 GTTGGCTTTGTACAGTTCCTATATAT 117543

RESULT 23
CRM251574 454 bp DNA linear VRL 11-JAN-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DNA polymerase: pol gene.
Chlorocephus rhadinovirus 2 (Chrv2)
Chlorocephus rhadinovirus 2
Viruses: dsDNA viruses, no RNA stage: Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Greensill J., Sheldon J.A., Renwick N.M., Beer B.E., Norley S.,
Goudsmilt J. and Schulz T.F.
Two distinct gamma-2 herpesviruses in African green monkeys: a
second gamma-2 herpesvirus lineage among old world primates?
J. Virol. 74 (3), 1572-1577 (2000)
20094948
10627572
2 (bases 1 to 454)
REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES

source
1..454
/organism="Chlorocephus rhadinovirus 2"
/viroion
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/isolate="animal L1"
/specific_host="Chlorocephus aethiops"
/db_xref="taxon:109048"

CDS

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1..454
/gene="pol"
<1..>454
/codon_start=2
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/protein_id="CAB61754.1"
/db_xref="GI:6469148"
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INAEVYTLTGRTMLEMSKVAEALTEDEQTRLSRAVTDAPGARFRV"

BASE COUNT 92 a 153 c 137 g 72 t
ORIGIN

Query Match 0.1%; Score 32; DB 1; Length 454;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16192 TACGGTTACCGGGGTGGCCACGGCCTTCT 16223
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 Db 269 TACGGTTACCGGGGTGGCCACGGCCTTCT 300

RESULT 24
 AY237372 523 bp DNA linear VRL 14-APR-2003
 LOCUS Caprine herpesvirus 2 glycoprotein B gene, partial cds.
 DEFINITION AY237372
 ACCESSION AY237372
 VERSION AY237372.1 GI:29826255
 KEYWORDS
 SOURCE Caprine herpesvirus 2
 ORGANISM Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae.

REFERENCE 1 (bases 1 to 523)
 Li, H., Galbreath, K., Flach, E.J., Holmes, E.C., Keller, J. and Crawford, T.B. Phylogenetic Relationships of Selected Ruminant Rhadinoviruses Unpublished
 2 (bases 1 to 523)
 Li, H., Galbreath, K., Keller, J. and Crawford, T.B. Direct Submission
 Submitted (14-FEB-2003) Animal Disease Research Unit, USDA-ARS, 3003 ADRF, Washington State University, Pullman, WA 99164, USA
 Location/Qualifiers
 1..523
 /organism="Caprine herpesvirus 2"
 /mol_type="genomic DNA"
 /db_xref="taxon:135102"
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 /protein_id="AA08173.1"
 /db_xref="GI:29826256"
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 DDOQSVLHNRNRPYKGDHAECHSRPVFKFTNDSHLYKGLGVNNEILLTVALEY
 CHEHTEHYFOGDNMYFKYRHKVTPVDATLDTFTLVNLTIVENIDFOVIELYS
 REEKRMSTVFDELT"

CDS
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 REEKRMSTVFDELT"

BASE COUNT 133 a 151 c 144 g 95 t

ORIGIN

Query Match 0.1%; Score 31; DB 1; Length 523;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12958 CTGAGCAAGATTACCCACGACCGATTATCA 12988
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 Db 29 CTGAGCAAGATTACCCACGACCGATTATCA 59

RESULT 25
 AF159039 395 bp DNA linear VRL 28-APR-2000
 LOCUS Macaque gamma virus strain Macaca nemestrina gamma virus
 DEFINITION AF159039
 ACCESSION AF159039
 VERSION AF159039.1 GI:6671086
 KEYWORDS
 SOURCE Macaque gamma virus
 ORGANISM Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae; Rhadinovirus.

REFERENCE 1 (bases 1 to 395)
 Strand, K., Harper, E., Thormahlen, S., Thoulless, M.E., Tsai, C., Rose, T. and Bosch, M.L.
 Two distinct lineages of macaque gamma herpesviruses related to the Kaposi's sarcoma associated herpesvirus

JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
 MEDLINE 20204465
 PUBMED 10738144
 REFERENCE 2 (bases 1 to 395)
 AUTHORS Strand, K.B. and Bosch, M.L.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box 357238, Seattle, WA 98125, USA
 Location/Qualifiers
 1..395
 /organism="Macaque gamma virus"
 /mol_type="genomic DNA"
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 /db_xref="GI:6671087"
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BASE COUNT 98 a 115 c 114 g 68 t

ORIGIN

Query Match 0.1%; Score 29; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11788 GGCATCTGATGGTGTAAATAAATAT 11816
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 Db 30 GGCATCTGATGGTGTAAATAAATAAT 58

RESULT 26
 AF031811 469 bp DNA linear VRL 27-APR-1998
 LOCUS Bovine herpesvirus 4 DNA dependent DNA polymerase (pol) gene,
 DEFINITION AF031811
 ACCESSION AF031811
 VERSION AF031811.1 GI:2832252
 KEYWORDS
 SOURCE Bovine herpesvirus 4
 ORGANISM Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae.

REFERENCE 1 (bases 1 to 469)
 Rovnak, J., Quackenbush, S.L., Reyes, R.A., Balnes, J.D., Parrish, C.R. and Casey, J.W. Detection of a novel bovine lymphotropic herpesvirus
 J. Virol. 72 (5), 4237-4242 (1998)
 TITLE Detection of a novel bovine lymphotropic herpesvirus
 JOURNAL 98216791
 MEDLINE 9557713
 PUBMED 9557713
 REFERENCE 2 (bases 1 to 469)
 Rovnak, J., Quackenbush, S.L. and Casey, J.W. Direct Submission
 Submitted (29-OCT-1997) Microbiology and Immunology, College of Veterinary Medicine, Cornell Univ., Ithaca, NY 14853
 3 (bases 1 to 469)
 Rovnak, J., Quackenbush, S.L. and Casey, J.W. Direct Submission
 Submitted (04-FEB-1998) Microbiology and Immunology, College of Veterinary Medicine, Cornell Univ., Ithaca, NY 14853
 Sequence update by submitter
 On Feb 5, 1998 this sequence version replaced gi:2660736.
 Location/Qualifiers
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 /organism="Bovine herpesvirus 4"
 /mol_type="genomic DNA"
 /strain="DN 599"

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ORIGIN

Query Match 0.1%; Score 29; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15919 CACACCTGTGCTACTCCACCATGATACA 15947
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16 CACACCTGTGCTACTCCACCATGATACA 44

RESULT 27
AF005477 3638 bp DNA linear VRL 07-JUL-2000
LOCUS
DEFINITION Kaposi's sarcoma-associated herpesvirus glycoprotein B gene,
partial cds; DNA polymerase (pol) gene, complete cds; and ORF
10-like protein gene, partial cds.
ACCESSION AF005477 AF204169
VERSION AF005477.2 GI:8714518
KEYWORDS
SOURCE Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
ORGANISM Human herpesvirus 8
Virusess: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

REFERENCE 1 (bases 2226 to 2701)
AUTHORS Rose,T.M., Strand,K.B., Schultz,E.R., Schaefer,G., Rankin,G.W. Jr.,
Thouless,M.E., Tsai,C.C. and Bosch,M.L.
IDENTIFICATION of two homologs of the Kaposi's sarcoma-associated
herpesvirus (human herpesvirus 8) in retroperitoneal fibromatosis
of different macaque species
J. Virol. 71 (5), 4138-4144 (1997)

JOURNAL 97248469
MEDLINE 9094697
PUBMED
2 (bases 1 to 3638)
AUTHORS Schultz,E.R., Rankin,G.W. Jr., Blanc,M.P., Raden,B.W., Tsai,C.C.
and Rose,T.M.
TITLE Characterization of two divergent lineages of macaque
J. Virol. 74 (10), 4919-4928 (2000)
PUBMED 10775636
3 (bases 2226 to 2701)
AUTHORS Rose,T.M. and Strand,K.B.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1997) Pathobiology, University of Washington, Box
357238, Seattle, WA 98195, USA
4 (bases 1 to 3638)
AUTHORS Rose,T.M.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-2000) Pathobiology, University of Washington, Box
357238, Seattle, WA 98195, USA
REMARK Sequence update by submitter
COMMENT On Jun 26, 2000 this sequence version replaced gi:2245590.
FEATURES
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/db_xref="taxon:37296"

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individual"
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SLERGE"
455..3493
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/note="similar to herpesvirus saimiri ORF 9"
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/protein_id="AAC57974.2"
/db_xref="GI:8714519"
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GVNLTHVLDQALAGFGRASGSGSTPEVRKKILRAYDQOYAVOKITLSSPMKRTLS
DRITTCGCEPVESNVDAIRFVLDHGSETEGNCSPAPRTQARDSTETEPSCSME
DLKFTPERTPEPSTILSFDECKGEKGFPAQDDEMTIIGVLTGVNDKRYTMA
LLGGTCDPLPGVVFEPSEYDMIAFLSMRLQYNEVITGVIANEDLYIIAAT
QVYDFKLDQDFKIKTGVSVEVHQRGSGDGNFMRSSKVSIGSIVIDMYQCREKL
SLSDYKLDIVAKOCLGRKDDISYKDIPLKSGPDRAGKNGCIVDYSVMDLLR
FQTHVEISEIAKLAKIPRRLVTDGQOIRVPSCLLEAATGYLLPVKGVAVSYOG
ATVTSPEPFPDPLVVDPAISLTPSIIQAHNLCTSTLIPDSGLHLPHLSPDYEF
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TCNAVGTGTGASGILPCLNLAETVTLQGRTEMLERKAFEMTTPRLSDIYSVPICDDASFRV
SPDARFVYVGDTSLSFLICGFMNDSDVDFAEELASITNTLFRSPKLEAEKIFEC
LLLTLLKRYGVSLDDKVLKMGVLDIKRTACRFYQEKSSQVLDLILEPSSYKAAKLI
SGAOTDMVYREGLEPEGRVKKIIOVNAHSRELCERSVPVDKLFTTELSRPLADYKTON
LPRLTVYOKLOAROEELPOLHDIRIPYFVAVPAGSLRSELAHEPPIYVQHGLRAVADLY
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3611..>3638
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/protein_id="AAF78829.1"
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/translation="MGTETATFTL"
BASE COUNT 930 a 1037 c 931 g 740 t
ORIGIN

Query Match 0.1%; Score 29; DB 1; Length 3638;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14938 CTGGAGTTTGACTGCAGCTGGAGGACCT 14966
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1259 CTGGAGTTTGACTGCAGCTGGAGGACCT 1287

RESULT 28
AF318573 108873 bp DNA linear VRL 18-MAY-2001
LOCUS
DEFINITION Bovine herpesvirus 4 long unique region, complete sequence.
ACCESSION AF318573 AF271211
VERSION AF318573.1 GI:12802528
KEYWORDS
SOURCE Bovine herpesvirus 4
ORGANISM Bovine herpesvirus 4
Virusess: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.

REFERENCE 1 (bases 1 to 108873)
AUTHORS Zimmermann,W., Broll,H., Ehlers,B., Buhk,H.J., Rosenthal,A. and
Goltz,M.
TITLE Genome sequence of bovine herpesvirus 4, a bovine Rhadinovirus, and
identification of an origin of DNA replication


```

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/protein_id="AAK07928.1"
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LSVYIOQTLNGVKNQCKFSITQERKKILKEPDSLYKFTTASAPENQVLN
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FHEEOOMPPTIMSPDIEGIGGCPACPKDEYDIOISCIPTTCCSPONILLS
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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      15957 CACAACCTGTGCTACTCCACATGATACA 15985

RESULT 29
LOCUS      U93872      133661 bp      DNA      linear      VRL_09-JUL-2001
DEFINITION      Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNA
      replication protein, glycoprotein, DNA replication protein, FLICE
      inhibitory protein and V-cyclin genes, complete cds, and tegument
      protein gene, partial cds.
ACCESSION      U93872
VERSION      U93872.2 GI:14627174
KEYWORDS
SOURCE      Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
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ORGANISM      Human herpesvirus 8
      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
      Gammaherpesvirinae; Rhadinovirus.
      1 (bases 29032 to 30108: 117733 to 118431)
      Zhong,W., Wang,H., Herndler,B. and Ganem,D.
      Restricted expression of Kaposi sarcoma-associated herpesvirus
      (human herpesvirus 8) genes in Kaposi sarcoma
      Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
JOURNAL      96270595
MEDLINE      8692871
PUBMED
REFERENCE      2 (bases 17242 to 17856)

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AUTHORS      Neipel,F., Albrecht,J.C., Ensser,A., Huang,Y.Q., Li,J.J.,
      Friedman-Kien,A.E. and Fleckenstein,B.
TITLE      Human herpesvirus 8 encodes a homolog of interleukin-6
JOURNAL      J. Virol. 71 (1), 839-842 (1997)
MEDLINE      97138401
PUBMED      8985427
REFERENCE      3 (bases 123309 to 124082)
      Li,M., Lee,H., Yoon,D.W., Albrecht,J.C., Fleckenstein,B., Neipel,F.
      and Jung,J.U.
      Kaposi's sarcoma-associated herpesvirus encodes a functional cyclin
      J. Virol. 71 (3), 1984-1991 (1997)
JOURNAL      97184528
MEDLINE
PUBMED      9032330
REFERENCE      4 (bases 122660 to 123226)
      Thome,M., Schneider,P., Hofmann,K., Fickenscher,H., Meisl,E.,
      Neipel,F., Matmann,C., Burns,K., Bodner,J.L., Schotter,M.,
      Scaifdi,C., Krammer,P.H., Peter,M.E. and Tschopp,J.
      Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced
      by death receptors
      Nature 386 (6624), 517-521 (1997)
JOURNAL      97242415
MEDLINE      9087414
PUBMED
REFERENCE      5 (bases 1 to 133661)
      Neipel,F., Albrecht,J.C. and Fleckenstein,B.
      Cell-homologous genes in the Kaposi's sarcoma-associated
      rhadinovirus human herpesvirus 8: determinants of its
      pathogenicity?
      J. Virol. 71 (6), 4187-4192 (1997)
JOURNAL      97296220
MEDLINE      9151804
PUBMED
REFERENCE      6 (bases 1 to 133661)
      Neipel,F., Albrecht,J.C., Ensser,A., Huang,Y.-O., Li,J.J.,
      Friedman-Kien,A.E. and Fleckenstein,B.
      The genome of human herpesvirus 8 cloned from Kaposi's sarcoma
      Unpublished
      7 (bases 1 to 133661)
      Neipel,F., Albrecht,J.-C., Ensser,A., Huang,Y.-O., Li,J.J.,
      Friedman-Kien,A.E. and Fleckenstein,B.
      Direct Submision
      Submitted (17-MAR-1997) Virology, University of Erlangen,
      Schlossgarten 4, Institut for Klinische und Molekulare, Erlangen
      91054, Germany
      8 (bases 1 to 133661)
      Neipel,F., Albrecht,J.-C., Ensser,A., Huang,Y.-O., Li,J.J.,
      Friedman-Kien,A.E. and Fleckenstein,B.
      Direct Submision
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REMARK      Sequence update by submitter
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CDS

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CDS

Oy 14938 CTGAGTGTGACGACGCTGGAGGACCT 14966
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RESULT 30
LOCUS KSU75698 137508 bp DNA linear VRL 03-MAY-1997
DEFINITION Kaposi's sarcoma-associated herpesvirus long unique region, 80
putative ORF's and Kaposin gene, complete cds.
ACCESSION U75698.1 GI:2065526
VERSION
KEYWORDS
SOURCE

ORGANISM

Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
Gammaherpesvirinae: Rhadinovirus.
1 (bases 47193 to 47522: 133099 to 133729)
Chang, Y., Cesarman, E., Pessin, M.S., Lee, F., Culpepper, J.,
Knowles, D.M. and Moore, P.S.
Identification of herpesvirus-like DNA sequences in AIDS-associated
Kaposi's sarcoma
Science 266 (5192), 1865-1869 (1994)

REFERENCE

REFERENCE AUTHORS TITLE
JOURNAL MEDLINE
PUBMED
95090463
7997879

REFERENCE

2 (bases 35021 to 55726)
Moore, P.S., Gao, S.-J., Dominguez, G., Cesarman, E., Lungu, O.,
Knowles, D.M., Garber, R., Pellett, P.E., McGeoch, D.J. and Chang, Y.
Primary characterization of a herpesvirus agent associated with
Kaposi's sarcoma
J Virol 70 (1), 549-558 (1996)

JOURNAL

60699469
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3 (bases 28661 to 29741; 117919 to 118101)

PUBMED


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 Db 12167 CTGAGTTTACCTGACCTGGAGACCT 12195

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 LOCUS Bovine lymphotropic herpesvirus DNA dependent DNA polymerase (Pol)
 DEFINITION gene, partial cds.
 ACCESSION AF031808
 VERSION AF031808.1 GI:2832250
 KEYWORDS .
 SOURCE Bovine lymphotropic herpesvirus
 ORGANISM Bovine lymphotropic herpesvirus
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; unclassified
 Herpesviridae.
 1 (bases 1 to 480)
 Authors Rovnak,J., Quackenbush,S.L., Reyes,R.A., Baines,J.D., Parrish,C.R.
 and Casey,J.W.
 Title Detection of a novel bovine lymphotropic herpesvirus
 JOURNAL J Virol. 72 (5), 4237-4242 (1998)
 MEDLINE 96216791
 PUBMED 9557713
 2 (bases 1 to 480)
 Authors Rovnak,J., Quackenbush,S.L. and Casey,J.W.
 Title Unpublished (1998)
 JOURNAL Unpublished (1998)
 3 (bases 1 to 480)
 Authors Rovnak,J., Quackenbush,S.L. and Casey,J.W.
 Title Direct Submission
 JOURNAL Submitted (29-OCT-1997) Microbiology and Immunology, College of
 Veterinary Medicine, Cornell Univ., Ithaca, NY 14853
 4 (bases 1 to 480)
 Authors Rovnak,J., Quackenbush,S.L. and Casey,J.W.
 Title Direct Submission
 JOURNAL Submitted (04-FEB-1998) Microbiology and Immunology, College of
 Veterinary Medicine, Cornell Univ., Ithaca, NY 14853
 REMARK Sequence update by submitter
 COMMENT On Feb 5, 1998 this sequence version replaced gi:2660730.
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 DEFINITION cds.
 ACCESSION AF327830
 VERSION AF327830.1 GI:13517547
 KEYWORDS .
 SOURCE Bovine lymphotropic herpesvirus
 ORGANISM Bovine lymphotropic herpesvirus
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; unclassified
 Herpesviridae.
 1 (bases 1 to 1295)
 Authors Chmielewicz,B., Goltz,M. and Ehlers,B.
 Title Detection and multigenic characterization of a novel
 JOURNAL gammaherpesvirus in goats
 MEDLINE 21212029
 PUBMED 11311431
 2 (bases 1 to 1295)
 Authors Chmielewicz,B., Goltz,M. and Ehlers,B.
 Title Direct Submission
 JOURNAL Submitted (12-DEC-2000) P24 Xenotransplantation, Robert
 Koch-Institut, Nordufer 20, Berlin, 13353, Germany
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 QY 15919 CACAACTGTGTACTCCACCATGATA 15945
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 DB 603 CACAACCTGTGTACTCCACCATGATA 629
 RESULT 33
 LOCUS AF005478 475 bp DNA linear VRL 26-JUN-2000
 DEFINITION Retroperitoneal fibromatosis-associated herpesvirus DNA polymerase
 (pol) gene, partial cds.
 ACCESSION AF005478
 VERSION AF005478.1 GI:2245592
 KEYWORDS
 SOURCE Retroperitoneal fibromatosis-associated herpesvirus
 ORGANISM Retroperitoneal fibromatosis-associated herpesvirus
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae; Rhadinovirus.
 REFERENCE 1 (bases 1 to 475)
 Rose, T.M., Strand, K.B., Schultz, E.R., Schaefer, G., Rankin, G.W. Jr.,
 Thoulmes, M.E., Tsai, C.C., and Bosch, M.L.
 Identification of two homologs of the Kaposi's sarcoma-associated
 herpesvirus (human herpesvirus 8) in retroperitoneal fibromatosis
 of different macaque species
 J. Virol. 71 (5), 4138-4144 (1997)
 MEDLINE 97248469
 PUBMED 9094697
 REFERENCE 2 (bases 1 to 475)
 Rose, T.M. and Strand, K.B.
 Direct Submission
 JOURNAL Submitted (28-MAY-1997) Pathobiology, University of Washington, Box
 357238, Seattle, WA 98195, USA
 FEATURES
 source
 1. 475
 /organism="Retroperitoneal fibromatosis-associated
 herpesvirus"
 /mol_type="genomic DNA"
 /isolate="Mme78114"
 /specific_host="Macaca nemestrina"
 /db_xref="taxon:111469"
 /note="Isolated from a retroperitoneal fibromatosis lesion
 of a Macaca nemestrina"
 <1..>475
 /gene="pol"
 <1..>475
 /gene="pol"
 /codon_start=2
 /product="DNA polymerase"
 /protein_id="AAC57975.1"
 /db_xref="GI:2245593"
 /translation="SIMOAHNLCSYLTITGSAALHGHPELPDDYETPHLSGCTVAFVK
 KHVESLISKLTLLAKRKREIKRLNASCPTPTRTITDKQOLIKVCNMYGFTG
 ASGILPCININIEYTLQGRKMLFESQAFVEGISPTALDLQRPLEASPEARFYI"
 BASE COUNT 129 a 145 c 120 g 81 t
 ORIGIN
 Query Match 0.1%; Score 26; DB 1; Length 475;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16150 GATAAACACAGCTGGCATCAAGGT 16175
 ||||||||||||||||||||||||||||||||
 DB 248 GATAAACACAGCTGGCATCAAGGT 273
 RESULT 34
 AF204166

LOCUS AF204166 3554 bp DNA linear VRL 04-JUL-2000
 DEFINITION Retroperitoneal fibromatosis-associated herpesvirus glycoprotein B
 gene, partial cds; DNA polymerase gene, complete cds; and ORF
 10-like protein gene, partial cds.
 ACCESSION AF204166
 VERSION AF204166.1 GI:8925891
 KEYWORDS
 SOURCE Retroperitoneal fibromatosis-associated herpesvirus
 ORGANISM Retroperitoneal fibromatosis-associated herpesvirus
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae; Rhadinovirus.
 REFERENCE 1 (bases 1 to 3554)
 Schultz, E.R., Rankin, G.W. Jr., Blanc, M.P., Raden, B.W., Tsai, C.C.
 and Rose, T.M.
 Characterization of two divergent lineages of macaque
 rhadinoviruses related to Kaposi's sarcoma-associated herpesvirus
 J. Virol. 74 (10), 4919-4928 (2000)
 MEDLINE 20240083
 PUBMED 10775636
 REFERENCE 2 (bases 1 to 3554)
 Rose, T.M.
 Direct Submission
 JOURNAL Submitted (12-NOV-1999) Pathobiology, School of Public Health and
 Community Medicine, University of Washington, Seattle, WA 98195,
 USA
 FEATURES
 source
 1. 3554
 /organism="Retroperitoneal fibromatosis-associated
 herpesvirus"
 /mol_type="genomic DNA"
 /isolate="Mme442N"
 /specific_host="Macaca nemestrina"
 /db_xref="taxon:111469"
 <1..334
 /codon_start=2
 /product="glycoprotein B"
 /protein_id="AAF81661.1"
 /db_xref="GI:8925892"
 /translation="WIVIVGIVILIEMLNRTNMAQAPYKMIYPIEDRHGGGCT
 VDKDEIKRILGLHQLHOEROKERKRETPSMFORANEIRORIRKQROETE
 LEAEASV"
 373..3414
 /note="similar to Kaposi's sarcoma-associated herpesvirus
 ORF 9"
 /codon_start=1
 /product="DNA polymerase"
 /protein_id="AAF81662.1"
 /db_xref="GI:8925893"
 /translation="MDPFPFLDRTHRNPRANARAPSPNPANPALQICRLIPAC
 RETGLPGVVPDTPPPPTYYRGGPRGDIYLNKBRASMTTRRASGVPTGEPAPLPHY
 YDIEVETTYARCGDVPFRFOTDIIIPSGVILKLGRTVDGTCVNFROKCYTTRA
 PPGVNLHVLQOOSLQSTVGRAPCAFTTELVKKILRYVDIEEYEVRYVILSSPMMA
 LSDLRLTAGCEVFESNDALIRFVLDGRFTFFGWACARARQADARDAWTEFFDS
 WEDELRLDHTMPRYRILSFEDICMGEEGPRATRDVDVLIQSCVFHGDGEAPYT
 RMLSLGCDPLEMTLEIFPEPSEYDMLTAFTTMRDQDVDTITGYNLANPLPYITR
 ATQYNDPLKNTYKIKTGSMEFEVIEPRAGSGGFIARSOSKYSISIVIPDYQVRDL
 SLSDYKLDYTAHCLSKQKDDISTYRDIPPRPSGAGAKIGRCVDSVYVMDLRA
 FQTHVEIAELKRLAPARVLTGQOIRVPSCLLEASRGVYLPVNGTGGYGG
 AATVSPISPEFVDVLVDFEASLPSIMQANLCYSTLITGSAALHGHPELPDDYET
 HLGSGVHFKVKKHRESLSKLLFTMLAKREIKRLNASCPTPTRTITDKQOLIKVCN
 YGFTGASGILPCININIEYTLQGRKMLFESQAFVEGISPTALDLQRPLEASPEARFYI
 SPEARFYITGDTSLFVCCVGSNYSVSFADDLAITTYTLKPAIKLEAKIFQC
 LLLTKRYGVLTDEVLNMGVDLIRKTYACRFVQETSRLELLRDPVAKAAKLI
 SHQPADWYREGDEGLVKIITLINHSRRLHGDVVEKLTFTTELGPRACEYKTN
 LPHLSVYRKLDLRQEEELQIDRIPIYFIRAPGKSLDLAEHPEYVARHGIQVAVDLY
 FDKAVHGAINLQCLFHNDAATVAALYNFLDPPRMPFSR"
 3528..>3554
 /note="similar to Kaposi's sarcoma-associated herpesvirus
 ORF 10"
 /codon_start=1
 /product="ORF 10-like protein"
 /protein_id="AAF81663.1"
 /db_xref="GI:8925894"

BASE COUNT 865 a 1078 c 935 g 676 t
ORIGIN

Query Match 0.1%; Score 26; DB 1; Length 3554;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16150 GATTAACACAGCGGCATCAAGCT 16175
Db 2392 GATTAACACAGCGTGGCATCAAGCT 2417

RESULT 35
AF250880 475 bp DNA linear VRL 12-OCT-2000
LOCUS Pan troglodytes rhadinovirus 1a isolate PancamDja DNA polymerase
DEFINITION (pol) gene, partial cds.
ACCESSION AF250880
VERSION AF250880.1 GI:10798913
KEYWORDS
SOURCE Pan troglodytes rhadinovirus 1a
ORGANISM Pan troglodytes rhadinovirus 1a
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Lacoste,Y., Maucelere,P., Dubreuil,G., Lewis,J.,
Georges-Courbot,M.C. and Gessain,A.
TITLE KSHV-like herpesviruses in chimps and gorillas
JOURNAL Nature 407 (6801), 151-152 (2000)
MEDLINE 20454683
PUBMED 11001045
REFERENCE 2 (bases 1 to 475)
AUTHORS Lacoste,Y., Dubreuil,G., Maucelere,P., Lewis,J.,
Georges-Courbot,M.C. and Gessain,A.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Unité d'Oncologie Virale-Departement du
SIDA et des Retrovirus, Institut Pasteur, 28, rue du Dr. Roux,
Paris cedex 15 75724, France
FEATURES
source Location/Qualifiers
1..475
/organism="Pan troglodytes rhadinovirus 1a"
/mol_type="genomic DNA"
/isolate="PancamDja"
/specific_host="Pan troglodytes troglodytes"
/db_xref="taxon:138896"
/country="Cameroon"
/note="PanrhV1a"
/gene="pol"
/gene="pol"
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AAG3140.1"
/db_xref="GI:10798914"
/translation="SITQAHNLCTSLIPGDSLHLPHLSPPDYETFLSGPVHFK
KHRESLARLTWLAKKREIKRTLASCHDPTKTLDQGLIKVTCNAVGETGV
ASGLPLNTAETVTLGRKMLRSQAFVEAISPRLVGLRKFINVSTDRKRYT"

BASE COUNT 130 a 143 c 107 g 95 t
ORIGIN

Query Match 0.1%; Score 23; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15904 AGCATCATCCAGCGCACACACT 15926
Db 2 AGCATCATCCAGCGCACACACT 24

RESULT 36
AF327831

LOCUS AF327831 1297 bp DNA linear VRL 03-APR-2001
DEFINITION Ovine herpesvirus 2 DNA polymerase (DPOU) gene, partial cds.
ACCESSION AF327831
VERSION AF327831.1 GI:13517549
KEYWORDS
SOURCE Ovine herpesvirus 2
ORGANISM Ovine herpesvirus 2
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Chmielewicz,B., Goltz,M. and Ehlers,B.
TITLE Detection and multigenic characterization of a novel
JOURNAL gammaherpesvirus in goats
MEDLINE 21212029
PUBMED 11311431
REFERENCE 2 (bases 1 to 1297)
AUTHORS Chmielewicz,B., Goltz,M. and Ehlers,B.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2000) P24 Xenotransplantation, Robert
Koch-Institut, Nordufer 20, Berlin, 13353, Germany
FEATURES
source Location/Qualifiers
1..1297
/organism="Ovine herpesvirus 2"
/mol_type="genomic DNA"
/db_xref="taxon:10398"
/note="Isolated from infected organ material"
/gene="DPOU"
/gene="DPOU"
/gene="DPOU"
/gene="DPOU"
/codon_start=2
/product="DNA polymerase"
/protein_id="AAK28844.1"
/db_xref="GI:13517550"
/translation="SRVQLPPEYSKRTNSLFYVYKPEQGNFRAHSHKYLSCVVI
DMVHICREKLSISNYKLVNTYAKECMGKADVTYKDPILFRGSSHRAKIGLYCVD
AVLVNLQHMTHIEITETIAKINIPPRVITDGOQIRVACILAAOEGYILPMP
TAGATSGOGATVINPISGFYNPVLVDFASVPSIIQAHNLCTSLIPENLSNP
DLPNDYETFLSGPVHFKHKSLSLASLKTWLAKRATKEKECCODELRAI
LDKQDLAIKTCNSVYGFYVASMELCLMAETVTLQGRMLEKTKQFVENDVQSL
QQICPTQTLKIHAGHPPTFVVGVDPSLFINCEGFDMDVLEFSORLASHSTSLF
SAPKILSESEVFOCLLLTKRKYGLISNNKILMKGVDLV"

BASE COUNT 337 a 372 c 314 g 274 t
ORIGIN

Query Match 0.1%; Score 23; DB 1; Length 1297;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15919 CACAACCTGCTACTCCACCAT 15941
Db 602 CACAACCTGCTACTCCACCAT 624

RESULT 37
AF275657 1339 bp DNA linear VRL 01-JAN-2002
LOCUS Badger herpesvirus DNA polymerase gene, partial cds.
DEFINITION Badger herpesvirus DNA polymerase gene, partial cds.
ACCESSION AF275657
VERSION AF275657.1 GI:18027277
KEYWORDS
SOURCE Badger herpesvirus
ORGANISM Badger herpesvirus
Virus; dsDNA viruses, no RNA stage; Herpesviridae; unclassified
Herpesviridae.
REFERENCE 1 (bases 1 to 1339)
AUTHORS King,D.P. and Banks,M.
TITLE Characterization of a herpesvirus isolated from the Eurasian badger
JOURNAL (Meles meles)
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 1339)
King,D.P. and Banks,M.

TITLE Direct Submission
JOURNAL Submitted (05-JUN-2000) Virology, Veterinary Laboratories Agency,
Woodham Lane, Addlestone, Surrey KT15 3NB, UK
FEATURES
source
1. 1339
/organism="Badger herpesvirus"
/vion
/mol_type="genomic DNA"
/specific_host="Eurasian badger (Meles meles)"
/db_xref="taxon:132610"
/note="Isolated from badger lung"
CDS
1. 1339
/codon_start=2
/product="DNA polymerase"
/protein_id="AAL55728.1"
/db_xref="GI:18027278"
/translation="LGENGFNATRDDEMILOISVLMKGTGTPPKLLFNIGTCDP
IPDTEVECEPSEIDMLYLFTMLRDNIETIGYNNANDPFIIDRAOVNPNLKD
FTRINSSMEFVHTPONSAGFMAVSKIKISGFCIDMYNCKEKLSTNKLNTVA
KOCISGOKEDVSKDIPHLFRGPRGAKLGYCYKDSIEIVLQLEKFTHEISEIA
KIAKIPTRRVLTGQOIRVSCLLVADQNYILPOKRGSDSDYGAGVADIPGEFY
NPIIVVFPASLYPTIIQANNLCYSTMLPHEKLIHYNISPHDYQTEFNSSGPFHVK
HKOVSLATLIDAMLSKRAIKTKTQSVDPMLRTIIDKOALIKVTCNAAVYGFVGS
SGILPCKIAETITTEGRMRLEKSKNFENITPVELERLIHKPINCAVYANRV"

BASE COUNT 441 a 242 c 259 g 397 t

ORIGIN

Query Match 0.1%; Score 23; DB 1; Length 1339;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16162 CTGGCCATCAAGTCACATGTAA 16184
DB 1127 CTGGCCATCAAGTCACATGTAA 1149
|||||
|||||

RESULT 38
AF376034 6165 bp DNA linear VRL 25-JUN-2002
LOCUS Badger herpesvirus envelope glycoprotein B (gb) and DNA polymerase
DEFINITION (pol) genes, complete cds.
ACCESSION AF376034
VERSION AF376034.1 GI:21552713
KEYWORDS
SOURCE Badger herpesvirus
ORGANISM Badger herpesvirus
Viruses; dsDNA viruses, no RNA stage; Herpesviridae; unclassified
Herpesviridae.
1 (bases 1 to 6165)
Banks, M., King, D.P., Danielis, C., Starg, D.A. and Gavler-Widen, D.
Partial characterization of a novel gammaherpesvirus isolated from
a European badger (Meles meles)
J. Gen. Virol. 83 (Pt 6), 1325-1330 (2002)
22024835
12029147
2 (bases 1 to 6165)
King, D.P. and Banks, M.
Direct Submission
Submitted (03-MAY-2001) Virology, Veterinary Laboratories Agency,
Woodham Lane, Addlestone, Surrey KT15 3NB, UK
FEATURES
source
1. 6165
/organism="Badger herpesvirus"
/mol_type="genomic DNA"
/specific_host="Meles meles"
/db_xref="taxon:132610"
69. .2623
/gene="gb"
69. .2516
/gene="gb"
/codon_start=1
/product="envelope glycoprotein B"
/protein_id="AAM62281.1"

/db_xref="GI:21552714"
/translation="MNKVLNVIYVVCFFHHINNTPVKSGSTPPDGKYNLTNLSLN
ISTIEVMPFVSCASTVGEIFRRPVDOHCDDDEHHEGLAIVIKNLIPMFIRK
YKRLVSTIVYGLDYALTNOFTNSPPQYEVNLIJROFCFNAIOVTEGTFNNV
TDRDYNKTKVMLOPYDGLTGNIMRYASOKLYVGMAGVAFRTTIVLVCLEMMAK
SVHPVEFTTASGDFVEMSPFLDNNMRSKSPRESLVNLIITNTHTVSYDRAFSM
KIRFVNTGDHYISMARESENSTCKFCGKWPFTALIQTKOTNSHFILANETPAFV
PLEPDESNTSHCLMEETINQIOSLSTINTKNTGNSVOTKITGNLITAMQPLIP
IELSLALNANDSOQAQNTNNSVRRKRRLSPSSNSLATAQLOFAYDNLASIKVL
HELSEAWCREEQORAAQOMPELSKINPTSVMSAIVGKPVASRFLGDIIVTECVIDQA
KYDLHOSMPPGPDMVNCYSRPVTEFKSGTGVFGOLGPRNEILLSTNVLVETCKDQA
VHYFOSGHOMHKFENVYHHNSTIDINHFSTLNFALNFTIENIDFEVEVEXSKREK
LANVIDESMREPNYTYQRLSGISKELNTEYNNRDALIRPQNIODIGNCSVV
NVAAGFTLFGSITVGLINFIRPTGMLTILITLGAVALVFMNRRTMRMEADITKI
LVPHIDQSAQDEPVQPIQOOLKILAMHNPQOEBHAKLIEEKSNKSGSSLANI
ATKFLNRKRGSALTKTS"
2618. .2623
/gene="gb"
/note="putative"
2875. .6050
/gene="pol"
2875. .5865
/gene="pol"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAM62282.1"
/db_xref="GI:21552715"
/translation="MAGNFENYLPNPKFIKTQESCVENLEETRLIPLCFKTPHQP
GVPTTHRPPTPEFNGKEELVFPQGRKSIYKHSNPPVDKTRRELFTHVVDIETTY
HSOQPNVPEDIHPSGTVALKILGRTEDNVSQVNVFOQYEVYVADTIGAMHIOOTL
RQOTGYSIVIMKKKILREYQGCNRYKVSTSKNDINTIIDKORAGCELEFENNQ
AVKRFVINDSGTFCGYHCKLAHPRLNRRDSMTDDEPSCMKOULFDEBRIDMPPNOY
LSEFIECEGENGFNATRDDEMILOISVLMKGTGTPPKLLFNIGTCDPDTVEF
BCPSEIDMLYLFTMLRDNIETIGYNNANDPFIIDRAOVNPNLKDPTRIKNS
SMFEEVHTPONSAGFMAVSKIKISGFCIDMYNCKEKLSTNKLNTVAKOCIGGO
KEDVSKDIPHLFRGPRGAKLGYCYKDSIEIVLQLEKFTHEISEIAKIAIPT
RRVLTGQOIRVSCLLVADQNYILPOKRGSDSDYGAGVADIPGEFYNPIIVVFPAS
DPAISYPTIIQANNLCYSTMLPHEKLIHYNISPHDYQTEFNSSGPFHVKKROVSL
ATLIDAMLSKRAIKTKTQSVDPMLRTIIDKOALIKVTCNAAVYGFVGSGLIPLCL
KIAETIYEGRRMLESKNFENITPVELERLIHKPINCAVYANRVIGTDSLEIE
COGAYTISEVSGFQDLAKITTEALFEPEIKLEAEKIPQCLIIISKRYIGLISKGL
MKGVDLIRKTSCKFIQNTSKVNLNLDHTEVEKLAACNLSKQINSVSEGLPLFK
VIDIINDSKYKTKLENTVPIDETFTTETSKPAEYKSTPLPIVYHKIISNEEPPQ
IHDRIPYVFPASPNATIKSDMAEDPAFQOQHNPILAVLDYFDKVKRGAANILQCFGN
SDKRAVSVLYNLDLPFTVNAVHR"
6045. .6050
/gene="pol"
/note="putative"

BASE COUNT 2045 a 1164 c 1150 g 1806 t

ORIGIN

Query Match 0.1%; Score 23; DB 1; Length 6165;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16162 CTGGCCATCAAGTCACATGTAA 16184
DB 4849 CTGGCCATCAAGTCACATGTAA 4871
|||||
|||||

RESULT 39
EHVU20824
LOCUS EHVU20824 184427 bp DNA linear VRL 02-FEB-1996
DEFINITION Equine herpesvirus 2, complete genome.
ACCESSION U20824
VERSION U20824.1 GI:6951172
KEYWORDS
SOURCE
ORGANISM
EQUINE herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
1 (bases 1 to 184427)
Telford, E.A., Watson, M.S., Aird, H.C., Perry, J. and Davison, A.J.

TITLE The DNA sequence of equine herpesvirus 2
JOURNAL J. Mol. Biol. 249 (3), 520-528 (1995)
MEDLINE 95302501
PUBMED 7783207
REFERENCE 2 (bases 1 to 184427)
AUTHORS Telford, E.A.R.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1995) Elizabeth A.R. Telford, Institute of Virology, MRC Virology Unit, University of Glasgow, Church Street, Glasgow G11 5JR, United Kingdom
FEATURES Location/Qualifiers
source 1..184427
/organism="Equine herpesvirus 2"
/mol_type="genomic DNA"
/strain="86/67"
/db_xref="taxon:133899"
1..17553
repeat_region
/rpc_type-direct
9248..10399
CDS
/feature="ORF E1"
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/product="G protein-coupled receptor"
/protein_id="AAC13788.1"
/db_xref="GI:695173"
/translation="MATTSATSTVNTSLATMTNTNFTSLTSVTTIASLVPSTNNS
EDYDDLDVDVEESAPCYSDTTLAAOVPAALYLFLFGLGNIILVILVIRMK
IKNTLMNLNLAIISDLFLTLTPFMHIGWYHDMTFGISLCKILRGVCMISYOV
RCIILLTYDRYLAAYVAYATLRFRTYTCGYVCVCMPLAGLSLPEFFPHODNG
RYQCDYRPEMSTNWRRAHAKVIMLSLIDPLIAVCYVIRLRLRPSKRTKA
IRLIFVIMAYFVFWTPYNIIVLLTFEHTLNLQCALSSNLDMLILTKYVAATHCC
INPVYAFGEKFRHLHFHTLYVAIYLCKYIFLSDGDEGEGPTR"
10494..10499
polyA_signal
/feature="ORF E1"
10660..10665
repeat_region
/feature="ORF E1"
12533..13114
14197..14541
CDS
/feature="ORF E2: product has hydrophobic N-terminus"
/codon_start=1
/protein_id="AAC13789.1"
/db_xref="GI:695174"
/translation="MILGLVLSLASTASTAIAQAMPVITGHEGRPLSVRCHVAK
NPSKPTMLMLKTIEGSAEGTIVPFKGPVYTKSSCGSTGVFTSDSLHMDAGRYA
CAVSENDKDEKSCSDYHTATNTNIVLETRRRSLGQLPTAGPSTGOTSGP
LSSQSESVAVYKRGVYKYGSSLSHVECOFGAGTAGINISAVLFFKVGEGAYAST
ISTSSLTITDLSPIVIEGTQAKWCGYNATKEDSGEYMCMTGMDFPGEDEGDEDESG
VDFKITVTEGEDEDEDYLYTSSEKK"
19761..19766
polyA_signal
/feature="ORF E2"
19784..19789
polyA_signal
/feature="ORF E2"
20320..20844
CDS
/feature="ORF E3: product has N- and C- hydrophobic domains
and 6 N-linked glycosylation sites"
/codon_start=1
/protein_id="AAC13790.1"
/db_xref="GI:695175"
/translation="MATEYQFACALVYLCCGYAGTPPTSKSLTIYNSQNTTPYSIE
NQSSLYXNGSWFIRIEFNCSSGYLEQGMPTTCLFMPKNGITWNGPPSCVKLNTT
TLMPSTSTPTPTGTFFPDPONTHTHTVTRRPINILRFGYTPMAITLVIL
LVWVINCMMGPMF"
21360..25319
CDS
/feature="ORF 03"
/codon_start=1
/product="tegument protein"
/protein_id="AAC13791.1"
/db_xref="GI:695176"
/translation="MDSTKSSFRKARAGRATVYFVPTWQHGPGCGPVSSAFSL
VNEVGVFLDYGCAGTGGATGARAADPCVAFAPMEITRTVIGRAGVASELP
AGIGSYTSGDAGAGPCTLSRDVAPMOMALBLELRGQOOLRPLVGAGACAGCP
GGEATPTPKILAAVFEHTLWSLHSHKOHAYMCLNQLSSPASFCRTGYLGFTPLG
DGERPDLKFARVPVAPALAHPRADALAKLPEMREHDSVLTGTIRGAIRKIRPENG

polyA_signal

LGVLORLVAPTSKEVIDRDFSSNGKPDYFGVYOVGISTGASELDLTSBAGTFGW
GNVLISLGVNCSGDEPFALQJELSHMLAQRCSGAPTLTGFRVWDGSAAPGMPA
SRPSTGTGRASITISPKACLSPVRRGGASVPMLGDFEOPRORAGAVSHSGRLA
STIAVOPFINVAGRAVLTSCOSQVEMMAKIAACGMGLTKYTTSLPREAVSEL
SHFSPGMASMRNSITLSKLTANEAQVILTYVNTPRNRITILEGKRTGCRSLGLH
ARAKITLVLDSDSPDCCOGPRYLCKFKMKPRYALPIDWCGTASTRPTASRPVNS
SDAGSPDAREVLILIRHPTVCCKNYIKYHVDRCGASGVAAQCCGPIDLVADSM
VYVEPSAGPPSMPEWMTETPOVDDCFILHIDGVSGVCSALGKKSVPFVPEAGAK
MAIASVLSIALAPRIARDYVNTSLAMPKKGAGVEFTLLTRCRCEAGVGCN
VNSCASSRRAGGDDPEGADIKSFYASFAYPQAFMKLTFPDILKARAVITLPLASP
GKHARASYQOVRQKKTKYGSFVNISGATLGLARVYLHRAKRLAVSHDGDGLM
AALAEAMAGMRSLOVEPVRLDGPMDGLTSETPEVALVEPLJSSASAVELRSTYI
LCRYVGTGHTKCEKRMFJTRDQVLECEQEEVGEAMSHSVRMERGPCCNRHAG
EGPYREREAFLATYPTFLINRPNKRRVAVLLPGCPPLAALDALRSRGTALVS
HDLALVLTDEVCGLTFLVAGVNTSPDTSALTVLASHRNGVIRDFILSDKDTSLG
VGSMACTILFDGDMASVPALOSRDYRCVAVASCKEESRLNFINOSNPVAVPRLTG
SILPCMAOHTLGFAGAPSPCEDRLVLAQSQAASMTGSDVAGAPMAVPTETLPV
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TESFKERLRCOLVWVESQIQSVRGEACAFVPLPDGLFAKSPCLREMLRYFYHAGV
SLTLEAHYTSLAQALRVDRVDGLIGALRGVFDHDKLPKRYECEPEPATGIRGSD
GATLYDVATVELAVSGSLFLEVPDEGALLSYFDMKPIFECEGPEPEQVEALTOGA
KQAVHYSOLFSGNSVLYLARIOKASNSFGGNGENYFPMGHACLAAPROKNG
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LYGTANTPWCELCRGSPASCANTLTLYLRLRFPVAVSVRDPVAVGAVANDL
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SELYKFEIDGIVDGEVAREFINSVMNNVYESIKSHIHIOYVQVCMWOPCPVFL
NLXYRCLVWODICLPTCMYEOENPARGVSGEMLKMHYOTLMPKMTKNCIDKVL
TGEYKVVYAKDOCPDPODSARGEVSCQVRSRLMMAPRMKIKNRTIEENS
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PVPVNPRESVTELANYVEQNSRLHGETSIDVPEPNFYAKAVRLNALFRACGQTO
FYATTIHLCTPKIQTVPABEYPHALCARVAVGEYLGAARELTPTVQCTSDNICE
VGKCRIVTLPVLVKNKYTGVTGNSQIFOCANLGYFGRVCDKMLIPDAGSFKKQGVST
SMKRRIWMTPLSDHLRLRSVGOAAVAFLEIEGVRVROOILSDGNDPHVIRDVLOLV
KSLGECRSVSEYDLEYWGOYIIPAGVSEBRLQSLSDIGOMSEMAISLYGEEEDP
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VSDDPYIGVFNELRHLDGADARAAGACAGGRESERGRVYDADDEDEDEPPDGGDA
GGGAALRVLTSSLSVLAGHTIIEEDGGLAEISNLYVSSAADRCGVCGTARATSS
HMAKFAHEARMHRSRAWLGRGAPSHFPALHPSPLSLFCGGVAGNSIDDTIAALOKD
CSATFLKKSNTQTLIOOQNELVYRLNLYNGRGREGGAKGEALIDARVLPDGGAS
CPDRVLESDARVRDLTKLRLDGLRLTDCIETGRVLSLTLSDVAGSALYASAA
RLVNHLEFRROVYGVGMADLTAGGEAAFPNSKYIKALALNMRHLDISVYVHFRL
TGPLSTQNSHSPVDPNVVALAYCAAGAMPOKQIYITPMIPGKSKSDIOCNFSP
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Query Match	0.14; Score 23; DB 1; Length 184427;
Best Local Similarity	100.08; Pred. No. 0.2;
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	15445 CCATAGACATGTACAGGTGTG 15467
Db	36394 CCATAGACATGTACAGGTGTG 36416
RESULT 40	
LOCUS	AY037858 171096 bp DNA circular VRL-19-NOV-2002
DEFINITION	Cercopithecine herpesvirus 15 strain LC18664, complete genome.
ACCESSION	AY037858 AF148640 AF159308 AF227125 AF159309 AF159310 AF227123 AF227124 045963 093160 093909
VERSION	AY037858.1 GI:18025465
KEYWORDS	Cercopithecine herpesvirus 15 Cercopithecine herpesvirus 15 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
SOURCE	
ORGANISM	
REFERENCE	1 (bases 1 to 171096) Franken,M., Devergne,O., Rosenzweig,M., Annis,B., Kieff,E. and Wang,F.
AUTHORS	Comparative analysis identifies conserved tumor necrosis factor receptor-associated factor 3 binding sites in the human and simian Epstein-Barr virus oncogene LMP1
TITLE	JOURNAL J. Virol. 70 (11), 7819-7826 (1996)
JOURNAL	MDLINE 97048062
REFERENCE	8892903 2 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Strong selective pressure for evolution of an Epstein-Barr virus LMP2B homologue in the rhesus lymphocryptovirus
AUTHORS	J. Virol. 73 (10), 8867-8872 (1999)
JOURNAL	MDLINE 99412410
PUBMED	10482645
REFERENCE	3 (bases 1 to 171096) Jiang,H., Cho,Y.G. and Wang,F. Structural, functional, and genetic comparisons of Epstein-Barr virus nuclear antigen 3A, 3B, and 3C homologues encoded by the rhesus lymphocryptovirus
AUTHORS	J. Virol. 74 (13), 5921-5932 (2000)
JOURNAL	MDLINE 20304984
PUBMED	10846073
REFERENCE	4 (bases 1 to 171096) Rao,P., Jiang,H. and Wang,F. Cloning of the rhesus lymphocryptovirus viral capsid antigen and Epstein-Barr virus-encoded small RNA homologues and use in diagnosis of acute and persistent infections
AUTHORS	J. Clin. Microbiol. 38 (9), 3219-3225 (2000)
JOURNAL	MDLINE 20440633
PUBMED	10970361
REFERENCE	5 (bases 1 to 171096) Rivallier,P., Jiang,H., Cho,Y.G., Quink,C. and Wang,F. Complete nucleotide sequence of the rhesus lymphocryptovirus: genetic validation for an Epstein-Barr virus animal model
AUTHORS	J. Virol. 76 (1), 421-426 (2002)
JOURNAL	MDLINE 21602573
PUBMED	11739708
REFERENCE	6 (bases 1 to 171096) Wang,F., Franken,M. and Annis,B. Direct Submission
AUTHORS	Submitted (11-JAN-1996) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
JOURNAL	MDLINE 11739708
PUBMED	11739708
REFERENCE	7 (bases 1 to 171096) Moghaddam,A., Koch,J., Annis,B. and Wang,F. Direct Submission
AUTHORS	Submitted (12-MAR-1997) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
JOURNAL	MDLINE 11739708
PUBMED	11739708
REFERENCE	8 (bases 1 to 171096) Moghaddam,A., Annis,B. and Wang,F. Direct Submission
AUTHORS	Submitted (17-MAR-1997) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
JOURNAL	MDLINE 11739708
PUBMED	11739708
REFERENCE	9 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Direct Submission
AUTHORS	Submitted (04-MAY-1999) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
JOURNAL	MDLINE 11739708
PUBMED	11739708
REFERENCE	10 (bases 1 to 171096) Jiang,H. and Wang,F. Direct Submission
AUTHORS	Submitted (16-JUN-1999) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
JOURNAL	MDLINE 11739708
PUBMED	11739708
REFERENCE	11 (bases 1 to 171096) Rao,P.V., Jiang,H. and Wang,F. Direct Submission
AUTHORS	Submitted (21-JAN-2000) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
JOURNAL	MDLINE 11739708
PUBMED	11739708
REFERENCE	12 (bases 1 to 171096) Rivallier,P., Jiang,H., Cho,Y.-G., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	13 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	14 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	15 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	16 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	17 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	18 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	19 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	20 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	21 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	22 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	23 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	24 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	25 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	26 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	27 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	28 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	29 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	30 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	31 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	32 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	33 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	34 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	35 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	36 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	37 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	38 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526.
JOURNAL	MDLINE 97048062
PUBMED	11739708
REFERENCE	39 (bases 1 to 171096) Rivallier,P., Quink,C. and Wang,F. Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
AUTHORS	Sequence updated by submitter On or before Dec 31, 2001 this sequence version replaced g1:9651728, g1:96


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QY 14555 CCAGCGTGTCGTGACGTGTT 14576
Db 151918 CCAGCGTGTCGTGACGTGTT 151897

RESULT 41
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LOCUS
DEFINITION
Unidentified herpesvirus natural-host Pan troglodytes DNA
ACCESSION
AF292063
VERSION
AF292063.1 GI:13345036
KEYWORDS
SOURCE
ORGANISM
unidentified herpesvirus
viruses: dsDNA viruses, no RNA stage; Herpesviridae; unclassified
Herpesviridae.
1 (bases 1 to 949)
AUTHORS
Worley,M.B.
TITLE
A herpesvirus of the slow loris related to the HHV6/HHV7 group of
betaherpesviruses
JOURNAL
REFERENCE
2 (bases 1 to 949)
Worley,M.B.
Direct Submission
Submitted (02-AUG-2000) Research, San Diego Zoo, P.O. Box 120551,
San Diego, CA 92112, USA
FEATURES
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BASE COUNT 172 a 281 c 331 g 165 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15919 CACAACCTGTGCTACTCCACC 15939
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17 CACAACCTGTGCTACTCCACC 37

Db

RESULT 42
AF283477 3623 bp DNA linear VRL 26-MAR-2001
LOCUS Caprine herpesvirus 2 glycoprotein B (gB) and DNA polymerase (DPOL)
DEFINITION genes, partial cds.
ACCESSION AF283477 AF327829
VERSION AF283477.2 GI:13447464
KEYWORDS
SOURCE
ORGANISM Caprine herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
REFERENCE
AUTHORS Chmielewicz, B., Goltz, M. and Ehlers, B.
TITLE Detection and multigenic characterization of a novel
gammaherpesvirus in goats
JOURNAL Virus Res. 75 (1), 87-94 (2001)
MEDLINE 21212029
PUBMED 11311431
REFERENCE
AUTHORS Chmielewicz, B., Goltz, M. and Ehlers, B.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-2000) P24, Robert Koch-Institut, Nordufer 20,
Berlin 13353, Germany
3 (bases 1 to 3623)
REFERENCE
AUTHORS Chmielewicz, B., Goltz, M. and Ehlers, B.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-2000) P24, Robert Koch-Institut, Nordufer 20,
Berlin 13353, Germany
REMARK
COMMENT Sequence update by submitter
FEATURES
On Mar 26, 2001 this sequence version replaced gi:10121846.
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BASE COUNT 827 a 1085 c 997 g 714 t

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Db 2974 CACAACCTGTGCTACTCCACC 2994

RESULT 43
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LOCUS Walleye dermal sarcoma virus complete genome.
DEFINITION AF033822
ACCESSION AF033822
VERSION AF033822.1 GI:2801519
KEYWORDS
SOURCE
ORGANISM Walleye dermal sarcoma virus
Viruses; Retroid viruses; Retroviridae; Epsilonretrovirus.
REFERENCE
AUTHORS Petropoulos, C.J.
TITLE Appendix 2: Retroviral taxonomy, protein structure, sequences, and
genetic maps
JOURNAL (in) Coffin, J. M. (Ed.):
RETROVIRUSES: 757;
Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York,
NY, USA (1997)
2 (bases 1 to 12708)
REFERENCE
AUTHORS Chappay, C.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1997) NIH, NLM, Rockville Pike, Bethesda, MD
20894, USA
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[illegible]

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Db	9560 TATTAGTTTATATTTTTTTT 9580							
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LOCUS								
DEFINITION	Walleye dermal sarcoma virus gag polyprotein (GAG), envelope glycoprotein (ENV), ORF-A, ORF-B, and ORF-C genes, complete cds.							
ACCESSION	L41838							
VERSION	L41838.1 GI:786142							
KEYWORDS	envelope polyprotein; gag polyprotein; oncogenic; retrovirus.							
SOURCE	Walleye dermal sarcoma virus							
ORGANISM	Walleye; dermal sarcoma virus							
REFERENCE	Viruses; Retroviridae; Epsilonretrovirus.							
AUTHORS	Holtschuh D.L., Martineau D., Fodor S.K., Vogt V.M., Bowser P.R. and							

Page 61

TITLE Casey, J.W.
Nucleotide sequence and protein analysis of a complex piscine
retrovirus, walleye dermal sarcoma virus
JOURNAL J. Virol. 69 (9), 5320-5331 (1995)
MEDLINE 95363939
PUBMED 7636975

FEATURES
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DLKVDGVTLSOHTTVPSSNITIKKGTSVQOPIRNPYTGEGMLTAOVNRPRL
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DMERTNLRDLTEETPVLTEETEPSPTE"
BASE COUNT 4196 a 2806 c 2456 g 3250 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33762 TATTAGTTTATATTTT 33782
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Db 10000 TATTAGTTTATATTTT 10020

RESULT 45
AF005370
LOCUS AF005370 130608 bp DNA linear VRL 19-OCT-2001
DEFINITION Alcelaphine herpesvirus 1 L-DNA, complete sequence.
ACCESSION AF005370
VERSION AF005370.1 GI:2337967
KEYWORDS
SOURCE Alcelaphine herpesvirus 1 (wildbeest herpesvirus)
ORGANISM Alcelaphine herpesvirus 1
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
1 (bases 1 to 130608)
Ensser, A., Pflanz, R., and Fleckenstein, B.
Primary structure of the alcelaphine herpesvirus 1 genome
J. Virol. 71 (9), 6517-6525 (1997)
MEDLINE 97404659
PUBMED 9261371
2 (bases 1 to 130608)
Ensser, A., Pflanz, R., and Fleckenstein, B.
Direct Submission
Submitted (27-MAY-1997) Institut fuer klinische und Molekulare
Virologie, Friedrich-Alexander-Universitaet Erlangen-Nuernberg,
Schlossgarten 4, Erlangen 91054, Germany
Location/Qualifiers
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polya_signal

CDS

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Query Match

0.1%; Score 21; DB 1; Length 130608;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11042 CCTGATACGGCGCCCTGAC 11062

Db 16290 CCTGATACGGCGCCCTGAC 16310

Search completed: September 26, 2003, 12:28:56
Job time : 1258 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 02:54:04 ; Search time 396 Seconds

(without alignments)
11960.308 Million cell updates/sec

Title: us-09-831-000-1
Perfect score: 14020
Sequence: 1 gcgaccgaagtcactaac.....cggcaccgcgcgacatct 14020

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 189188 seqs, 168911627 residues

Word size : 0

Total number of hits satisfying chosen parameters: 378376

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : gb_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	14020	100.0	133719	1 AF083501 Macaca mu
2	7651	54.6	130733	1 AF210726 Macaca mu
3	172	1.2	130733	1 AF210726 Macaca mu
4	20	0.1	2007	1 CHV1GC 249225 Caprine her
5	20	0.1	5077	1 KSU82242 082242 Kaposi's sa
6	20	0.1	6671	1 AY189899 Pseudorab
7	20	0.1	8481	1 KSU40384 040394 Kaposi's sa
8	20	0.1	28559	1 AF148805 093872 Kaposi's sa
9	20	0.1	133661	1 U93872 075698 Kaposi's sa
10	20	0.1	137508	1 KSU75698 20824 Equine herp
11	20	0.1	184427	1 EHVU20824 20824 Equine herp
12	19	0.1	165	1 AH002374S1 K06699 Middelburg
13	19	0.1	824	1 AF251159 AF251159 Human her
14	19	0.1	947	1 AF251158 AF251158 Human her
15	19	0.1	1213	1 HSL1S81 V00460 Fragment fr
16	19	0.1	1303	1 HSL1S81 V00460 Fragment fr
17	19	0.1	1303	1 HSL1S81 J02223 HSV-1 (stra
18	19	0.1	1346	1 HSL1CP345B M33700 Herpes simp
19	19	0.1	1367	1 HSL1CP345C M33701 Herpes simp
20	19	0.1	1367	1 HSL1CP345A M33699 Herpes simp
21	19	0.1	1166	1 HSL1CP345A M33699 Herpes simp
22	19	0.1	1794	1 HSL1CP345A M33699 Herpes simp
23	19	0.1	2038	1 AF015716 AF015716 Alfalfa m
24	19	0.1	2038	1 AF015717 AF015717 Alfalfa m
25	19	0.1	2121	1 BHV4GH Z79653 Bovine herp
26	19	0.1	3008	1 AF359760 AF359760 Buffalo h
27	19	0.1	3113	1 AF078726 AF078726 Bovine he
28	19	0.1	5175	1 CP6VTC47 X79773 Cydia pomon
29	19	0.1	7919	1 HPV10 Z74465 Human papil
30	19	0.1	30000	1 BHV130KB Z48053 Bovine herp
31	19	0.1	35450	1 SV1344259 AJ344259 Sulloloda
32	19	0.1	106873	1 AB096160 AB096160 Cercopit
33	19	0.1	108873	1 AF318573 AF318573 Bovine he

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	35	19	0.1	144575	1 HD1293568	AJ293568 Yaba-1ike
	36	19	0.1	152261	1 HE1CG	X14112 Human herpe
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	38	19	0.1	156789	1 AF533768	AF533768 Cercopit
	39	19	0.1	232392	1 AF250284	AF250284 Amsacta m
	40	18	0.1	780	1 HSEIE1	M30497 Equine herp
	41	18	0.1	824	1 AF251159	AF251159 Human her
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	44	18	0.1	1175	1 AF347327	AF347327 HIV-1 iso
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ALIGNMENTS

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ACCESSION	AF083501.3	GI:8714565			
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KEYWORDS					
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ORGANISM					
REFERENCE					
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CDS

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CDS

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6045..9443

CDS

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RHVMATPIIDRLIKRAGQITSTFEAESVRSYVALLEDKDNPLKSVILELIRLHG
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9468..11528

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herpesvirus orf 7"

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herpesvirus orf 8"

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ADLDDVQVNTVYVDSITLPGSIVGEINIKRPFGGMMLVLAIVAVLVAFLAPL
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14122..17166

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/note="orf 9: similar to kaposi's sarcoma-associated
herpesvirus orf 9"

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KVPAGINVTYHILQOALKNTAGRAACGDSITRVNRLIKLTYVAVHPVEITLSSGML
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17261..18511

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herpesvirus orf 10"

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18520..19749

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/note="orf 11: similar to kaposi's sarcoma-associated
herpesvirus orf 11"

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Db	121860	CCTGAAGCTAAACACCGGGCGAABACCGGCTTGGCGACGGCGTTGGABATTCCTCAACACGATG	121919
Qy	121920	ACGGACTAGAACCTCTGACCCCTATGAGCGACCCCTTGGGATGAGACCCGACCTCGATTCGGTG	121979
Db	121920	ACGGACTAGAACCTCTGACCCCTATGAGCGACCCCTTGGGATGAGACCCGACCTCGATTCGGTG	121979
Qy	121980	GCCGTTTGCGTCCGATCCGTGCCCTTGTTCGACACCCCGCAGCTTGGCGCTTGAT	122039
Db	121980	GCCGTTTGCGTCCGATCCGTGCCCTTGTTCGACACCCCGCAGCTTGGCGCTTGAT	122039
Qy	122040	GTTGTTGGACGGGGGGCGGGGTGGGGGGGTGGGGGGGGCGGTGGCACGGCCCTGGCCG	122099
Db	122040	GTTGTTGGACGGGGGGCGGGGTGGGGGGGTGGGGGGGGCGGTGGCACGGCCCTGGCCG	122099
Qy	122100	GCGCTCCGGCCCTGTTCTCTAGTGGCGCGCGCTCTCTCCGAATGTGCCCTTCGACGAACTT	122159
Db	122100	GCGCTCCGGCCCTGTTCTCTAGTGGCGCGCGCTCTCTCCGAATGTGCCCTTCGACGAACTT	122159
Qy	122160	CGCAACCCGTTGTCGCCGATACTATGCGGAAAGATGTGCGCGCTGCCCCACATGTTCCGG	122219
Db	122160	CGCAACCCGTTGTCGCCGATACTATGCGGAAAGATGTGCGCGCTGCCCCACATGTTCCGG	122219
Qy	122220	GTTTACTGCGTAAAAAAAGCAGATTAAGTATGATGTGCCCTTCCACGACCCCGCAGCCA	122279
Db	122220	GTTTACTGCGTAAAAAAAGCAGATTAAGTATGATGTGCCCTTCCACGACCCCGCAGCCA	122279
Qy	122280	CCTGAGCGCGCGCACGAGAACCTATGTTTAGTGGATTGCGATTATGTCCGTAGGTGG	122339
Db	122280	CCTGAGCGCGCGCACGAGAACCTATGTTTAGTGGATTGCGATTATGTCCGTAGGTGG	122339
Qy	122340	CGGGGTATTTTATCTCGCGCGGACGCAATFACCGCTTATGTTGGGGCGCACGGCGCTTAA	122399
Db	122340	CGGGGTATTTTATCTCGCGCGGACGCAATFACCGCTTATGTTGGGGCGCACGGCGCTTAA	122399
Qy	122400	CCGACGCGAGCACCGCACGGCGGTTTAACTTTCCTACTATTAACGTTTAACTTAAATCCG	122459
Db	122400	CCGACGCGAGCACCGCACGGCGGTTTAACTTTCCTACTATTAACGTTTAACTTAAATCCG	122459
Qy	122460	TGGCGGATTTTGGGGGCGAGTGTGAAGTACAGCGCGCGCGCGCCCTTACTCTGTCCG	122519
Db	122460	TGGCGGATTTTGGGGGCGAGTGTGAAGTACAGCGCGCGCGCGCCCTTACTCTGTCCG	122519
Qy	122520	CGGCGAACCGCGGAAAGTCTGTTCGCGCGCGACGCGCGGGCGCTGCCGAAACCAACG	122579
Db	122520	CGGCGAACCGCGGAAAGTCTGTTCGCGCGCGACGCGCGGGCGCTGCCGAAACCAACG	122579
Qy	122580	CGCTTGAATTTTCGCGGGCGGCTTGGGTCTCAGTGAATTCACACAGATGGCGATGTGAT	122639
Db	122580	CGCTTGAATTTTCGCGGGCGGCTTGGGTCTCAGTGAATTCACACAGATGGCGATGTGAT	122639
Qy	122640	TGGGCGTGTGTCAACGTCATTTGTTTAAACCGCTTAAATCTGGAATTCCTTGTCCGCGG	122699
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Qy	122700	CCGGTGAACCCCGGACCTTAAGCCTTATAGTGTGTGACAGCATCTGAAACTCGAAGCT	122759
Db	122700	CCGGTGAACCCCGGACCTTAAGCCTTATAGTGTGTGACAGCATCTGAAACTCGAAGCT	122759
Qy	122760	GGCCATTAATAACCCAGTATGGCGTTGGGTGTGCGGGGCAACCTTTTAAAAAGATTTA	122819
Db	122760	GGCCATTAATAACCCAGTATGGCGTTGGGTGTGCGGGGCAACCTTTTAAAAAGATTTA	122819
Qy	122820	TTGGCGCGGGGTTTAAAGACCAACACGACCGCTGGCTTTCATTAATGTCCGGAGAGAT	122879
Db	122820	TTGGCGCGGGGTTTAAAGACCAACACGACCGCTGGCTTTCATTAATGTCCGGAGAGAT	122879
Qy	122880	TACATTAACGCTGCTGTGTGGGAGCGTTGCAACGCTTGGGTGGCGCTTTCAAACGACATA	122939
Db	122880	TACATTAACGCTGCTGTGTGGGAGCGTTGCAACGCTTGGGTGGCGCTTTCAAACGACATA	122939

Db	122880	TCACATTAAAGCGCTGCTGTCGGACGACCCCTTCCACCGGTTGCGTGGCGCTTTCACAAACGACACTA	122933
QY	122940	TGCGGGGGGTCCTCCGTCGACCTCAACGCGGTCCTCGGGGGTCGCTTAAAGACACCCACAGA	122999
Db	122940	TGCGGGGGGTCCTCCGTCGACCTCAACGCGGTCCTCGGGGGTCGCTTAAAGACACCCACAGA	122999
QY	123000	CGTTCCTATCGTTACCTGGCCAAAACAGGAATCGCCTAGTCCGCTTAAACGTGGCCACATA	123059
Db	123000	CGTTCCTATCGTTACCTGGCCAAAACAGGAATCGCCTAGTCCGCTTAAACGTGGCCACATA	123059
QY	123060	TAGTTCGCCAAGGGGACAGGTGCTTCAGCCCCCGTTCGCCGGTAGGGTTGACATTCGCCGA	123119
Db	123060	TAGTTCGCCAAGGGGACAGGTGCTTCAGCCCCCGTTCGCCGGTAGGGTTGACATTCGCCGA	123119
QY	123120	ACACAAGTTGAGACCAACAGCACCCTGAAGTTTATATGCGACCCCTGAGAGAGAGAGGGGTG	123179
Db	123120	ACACAAGTTGAGACCAACAGCACCCTGAAGTTTATATGCGACCCCTGAGAGAGAGAGGGGTG	123179
QY	123180	CTACCTGTGTATCTTTTAAACGGCTTTGAGGTGGAAAGCTGTGCGAACCCTGCTTGAC	123239
Db	123180	CTACCTGTGTATCTTTTAAACGGCTTTGAGGTGGAAAGCTGTGCGAACCCTGCTTGAC	123239
QY	123240	GGTTACAGTCCCCGTCGTCACATGTCGTCACGTTTAAACCCCGAGTAAACCCGACAGCT	123299
Db	123240	GGTTACAGTCCCCGTCGTCACATGTCGTCACGTTTAAACCCCGAGTAAACCCGACAGCT	123299
QY	123300	CGTCTGTGGGGCGGAGGCGAGTCCCGACACCGTCGGTCAACTGAGACCGGCGTGC	123359
Db	123300	CGTCTGTGGGGCGGAGGCGAGTCCCGACACCGTCGGTCAACTGAGACCGGCGTGC	123359
QY	123360	GCTGTGACAGCAACCTGAAGTGTTCCTCCCGGCCCAACGAGAACACCTCGTGTGGGTG	123419
Db	123360	GCTGTGACAGCAACCTGAAGTGTTCCTCCCGGCCCAACGAGAACACCTCGTGTGGGTG	123419
QY	123420	CTGCACACTTAACGTCGTGGTGGACCCCGAAGACCTTGAAGAACGACAGTGCCTGTCACCTCA	123479
Db	123420	CTGCACACTTAACGTCGTGGTGGACCCCGAAGACCTTGAAGAACGACAGTGCCTGTCACCTCA	123479
QY	123480	TATAGGCGGTTTGGCCGCGGCGGCGCCCTGGAACCCCGTGTGGATCCCTCGGAAG	123539
Db	123480	TATAGGCGGTTTGGCCGCGGCGGCGCCCTGGAACCCCGTGTGGATCCCTCGGAAG	123539
QY	123540	GACGAGCCACATCGTGTGGTGGTGTGGACACGGCGCGCTTAAAGCATTTTAAAC	123599
Db	123540	GACGAGCCACATCGTGTGGTGGTGTGGACACGGCGCGCTTAAAGCATTTTAAAC	123599
QY	123600	GGGTGTTTTGTATAGGTATATGTGAGCGCGCGTGTCCCGCTCTAGTGTGTGTT	123659
Db	123600	GGGTGTTTTGTATAGGTATATGTGAGCGCGCGTGTCCCGCTCTAGTGTGTGTGTT	123659
QY	123660	CCCCAGTGAAGTCTCCCATGACAAATTAAGTGGCTTTTAAAGGTGGGTCT	123719
Db	123660	CCCCAGTGAAGTCTCCCATGACAAATTAAGTGGCTTTTAAAGGTGGGTCT	123719
QY	123720	TGTGGAGAGCTCTCGTGTAACTGATACACCGGGGTGTGCGCAGAGAAACCGCTCC	123779
Db	123720	TGTGGAGAGCTCTCGTGTAACTGATACACCGGGGTGTGCGCAGAGAAACCGCTCC	123779
QY	123780	CTTTATGTCCGCTCGCCCTCCACAGCGAAAGTGAAGTGTCTCTGGGGCTTTGGCG	123839
Db	123780	CTTTATGTCCGCTCGCCCTCCACAGCGAAAGTGAAGTGTCTCTGGGGCTTTGGCG	123839
QY	123840	TTGAAGAGTGGGGGATGTGGCCGTAGGGGGTGTGCAAAAGCTACACCGGTTCTGTT	123899
Db	123840	TTGAAGAGTGGGGGATGTGGCCGTAGGGGGTGTGCAAAAGCTACACCGGTTCTGTT	123899
QY	123900	TTTTTCTTTTGTCAAGACAAACATGAGCGCTTGAACAAATTAACCTTAACCTGCTGATG	123959
Db	123900	TTTTTCTTTTGTCAAGACAAACATGAGCGCTTGAACAAATTAACCTTAACCTGCTGATG	123959
QY	123960	GATTTTCTGTCTAACTATTCGAATGTGACAGTAACTTATGACAGCAATATGTCTTAACCC	124019
Db	123960	GATTTTCTGTCTAACTATTCGAATGTGACAGTAACTTATGACAGCAATATGTCTTAACCC	124019

QY	124020	TTAGACACGGAATCCACGCGTGTGCCTGACGCGTGTTCCTCACACCTATTATGCG	124079
Db	124020	TTAGACACGGAATCCACGCGTGTGTGGCGAGCGTGTTCCTCACACCTATATGCG	124079
QY	124080	ATTATATCGTTTTTATTTTATTTTGGCAATTAACGCGTTTGGGAAGCGTGTGCTATATAT	124139
Db	124080	ATTATATCGTTTTTATTTTATTTTGGCAATTAACGCGTTTGGGAAGCGCGTGTGCTATATAT	124139
QY	124140	TTTTTAAATTTAAAGCGCTGCCCAACTCTGTGGATGTACTATGGCTGGTGTGTGT	124199
Db	124140	TTTTTAAATTTAAAGCGCTGCCCAACTCTGTGGATGTACTATGGCTGGTGTGTGT	124199
QY	124200	AACCTCCGTGTTCTGTGGCGCTGTTTTTGTTCAGCTGGCTGTACTGCGGCCACAG	124259
Db	124200	AACCTCCGTGTTCTGTGGCGCTGTTTTTGTTCAGCTGGCTGTACTGCGGCCACAG	124259
QY	124260	ATGCTCAGCTCCGGCAGCGGCAAGGAGGAAATCTTTTCTTACCTGTACACGTCCTTT	124319
Db	124260	ATGCTCAGCTCCGGCAGCGGCAAGGAGGAAATCTTTTCTTACCTGTACACGTCCTTT	124319
QY	124320	GCGCTGTACATTGTGTGTGTATACAGCCTTATCAGGTGCTGTAACTGTGTTTTCCCG	124379
Db	124320	GCGCTGTACATTGTGTGTGTATACAGCCTTATCAGGTGCTGTAACTGTGTTTTCCCG	124379
QY	124380	CGCCCGTGGGTCAACGACGCGGCGCTTCCTGCTGCTGTGTGTCTTTAATCGTG	124439
Db	124380	CGCCCGTGGGTCAACGACGCGGCGCTTCCTGCTGCTGTGTGTCTTTAATCGTG	124439
QY	124440	GCGCTGGGCGCTGTCTGCGCAACGCGGACCTCTATAGAGGCGCCTGTGCAACCGAGAC	124499
Db	124440	GCGCTGGGCGCTGTCTGCGCAACGCGGACCTCTATAGAGGCGCCTGTGCAACCGAGAC	124499
QY	124500	AGCGAGTGGATATGCTTACGAAGATGCCGGGGAAGATACCGTCAACTGGAAGCTGAGAATC	124559
Db	124500	AGCGAGTGGATATGCTTACGAAGATGCCGGGGAAGATACCGTCAACTGGAAGCTGAGAATC	124559
QY	124560	AGAACCCACGCGCGATCTGCGGGTTTTTGTTCGCTTTGGCGTATGTGCTCTTTTAC	124619
Db	124560	AGAACCCACGCGCGATCTGCGGGTTTTTGTTCGCTTTGGCGTATGTGCTCTTTTAC	124619
QY	124620	GGACTTACGTTGATGTATGTTTAAAGACAGAGCTGCCAGAAAGGAGCGCTTAGGGG	124679
Db	124620	GGACTTACGTTGATGTATGTTTAAAGACAGAGCTGCCAGAAAGGAGCGCTTAGGGG	124679
QY	124680	GTAATTGTGACGCGTGTGTGCTGTTTTTAAATTTTGGCTGCCCTATCACTGTGCAAC	124739
Db	124680	GTAATTGTGACGCGTGTGTGCTGTTTTTAAATTTTGGCTGCCCTATCACTGTGCAAC	124739
QY	124740	TTTTTTGACACCCCTGTGAGGACCGGTTTTTCTGGCGGAAGGTGTACTCAAGGACGTG	124799
Db	124740	TTTTTTGACACCCCTGTGAGGACCGGTTTTTCTGGCGGAAGGTGTACTCAAGGACGTG	124799
QY	124800	ATCACGCGGCGCATGCATATATGTGCCCTGTACAGAGCATGTATGCGCGTTGCGGCCA	124859
Db	124800	ATCACGCGGCGCATGCATATATGTGCCCTGTACAGAGCATGTATGCGCGTTGCGGCCA	124859
QY	124860	GTCGTGTATTCGTGCTTGGGCTCTGTTTTAGAGAGAAGGTTAAGGATACCTGTGCTGTG	124919
Db	124860	GTCGTGTATTCGTGCTTGGGCTCTGTTTTAGAGAGAAGGTTAAGGATACCTGTGCTGTG	124919
QY	124920	TTTACGTGTTCCTCAGCTCAGGTATTTATGAGACATCAGCGGACACTTGGTTGGATT	124979
Db	124920	TTTACGTGTTCCTCAGCTCAGGTATTTATGAGACATCAGCGGACACTTGGTTGGATT	124979
QY	124980	GTTTGTGTACATTTATTTCAATTTGTGTACATTTATTTTCAATTTAAAGCATGTGACCTG	125039
Db	124980	GTTTGTGTACATTTATTTCAATTTGTGTACATTTATTTTCAATTTAAAGCATGTGACCTG	125039
QY	125040	CAGACCTTACCTGACGTTTACTGTCTGTTTATGACACAGAGAAAGGAGCTGGAAG	125099
Db	125040	CAGACCTTACCTGACGTTTACTGTCTGTTTATGACACAGAGAAAGGAGCTGGAAG	125099

QY	125100	GCCACCGCCACAGGGGAAACTGTCAATGTCCCGAAGCTGGGGCGGCACGTACGCCCACTCG	125159
Db	125100	GCCACGCGCCACAGGGGAAACTGTCAATGTCCCGAAGCTGGGGCGGCACGTACGCCCACTCG	125159
QY	125160	CAGGGGTGGAACGTACAGCGCGGGGTGCACAGGAGGCCAGGGGGCGCCGTCCGGTGC	125219
Db	125160	CAGGGGTGGAACGTACAGCGCGGGGTGCACAGGAGGCCAGGGGGCGCCGTCCGGTGC	125219
QY	125220	GTGAAGGGGGCCACGGCGCGAGTGTGGCAGACGGGGTTGCGTGGGTAGTGCCTCGCGAATATC	125279
Db	125220	GTGAATGGGGCCACGGCGCGAGTGTGGCAGACGGGGTTGCGTGGGTAGTGCCTCGCGAATATC	125279
QY	125280	CTCGGGTCGGCGTGTGCCGTGTGTGATGTTCAAGGCGATCGCTGTCTGTGGATTGAGATGG	125339
Db	125280	CTCGGGTCGGCGTGTGCCGTGTGTGATGTTCAAGGCGATCGCTGTCTGTGGATTGAGATGG	125339
QY	125340	TACTCCATGSGCTCGCGGGGTATCTACGCCAGGTACCGGCGGTGGGCCCAACCTGGG	125399
Db	125340	TACTCCATGSGCTCGCGGGGTATCTACGCCAGGTACCGGCGGTGGGCCCAACCTGGG	125399
QY	125400	AGGACGAGGCGCCCGAAGAACCTTAAACATGATGCTATGTGTGGGTGCGGGGATGTGAGAG	125459
Db	125400	AGGACGAGGCGCCCGAAGAACCTTAAACATGATGCTATGTGTGGGTGCGGGGATGTGAGAG	125459
QY	125460	TTTATCCAGAGGCACTGTGTGTTCCCTGTATGGCTTCTCTCCAGGTGATGTCCACTGG	125519
Db	125460	TTTATCCAGAGGCACTGTGTGTTCCCTGTATGGCTTCTCTCCAGGTGATGTCCACTGG	125519
QY	125520	TCGGGGGTTTGGGTCCGGGCGTGTCTGTAAGGGGTCTCTATAAGAACCGAGCGCCCC	125579
Db	125520	TCGGGGGTTTGGGTCCGGGCGTGTCTGTAAGGGGTCTCTATAAGAACCGAGCGCCCC	125579
QY	125580	AGGACCTGGAAACCCAAACCTCCCGGAGCATATGAAATATGTATCCGCTCGCGCGAAGAG	125639
Db	125580	AGGACCTGGAAACCCAAACCTCCCGGAGCATATGAAATATGTATCCGCTCGCGCGAAGAG	125639
QY	125640	GCCATTAAGGCCCCCATATGACCCACAGGGTGTTGAGAAGAACCCATGATTCGCGATCGGGCC	125699
Db	125640	GCCATTAAGGCCCCCATATGACCCACAGGGTGTTGAGAAGAACCCATGATTCGCGATCGGGCC	125699
QY	125700	CCGACGTACGTCCTTCGATGCGCCAGGTTTCCACCATGATGTCAGACCGGGAATCCCGG	125759
Db	125700	CCGACGTACGTCCTTCGATGCGCCAGGTTTCCACCATGATGTCAGACCGGGAATCCCGG	125759
QY	125760	AGGATGTTCCCTCTAAGGTGCTGTGGAGAGCGGCGCGCGATCGMAACCCGACGTTG	125819
Db	125760	AGGATGTTCCCTCTAAGGTGCTGTGGAGAGCGGCGCGCGATCGMAACCCGACGTTG	125819
QY	125820	GTGAAGCGGCGCATCAGCGCCCTGTGGGAACCGGGGACCGGGGGTGTGACCAAGCGGCGACT	125879
Db	125820	GTGAAGCGGCGCATCAGCGCCCTGTGGGAACCGGGGACCGGGGGTGTGACCAAGCGGCGACT	125879
QY	125880	GCTGGCGGCTCTGACGGCGTTGCMAACAGAGTCAAGTTCGCTGTTTGCMAACCTCGGCG	125939
Db	125880	GCTGGCGGCTCTGACGGCGTTGCMAACAGAGTCAAGTTCGCTGTTTGCMAACCTCGGCG	125939
QY	125940	AGGTGGCCCAAGTGTGTGTGGTTCACCGGTATCTTCTGTGAAGTTCTTCGGCGGCG	125999
Db	125940	AGGTGGCCCAAGTGTGTGTGGTTCACCGGTATCTTCTGTGAAGTTCTTCGGCGGCG	125999
QY	126000	GTGAAGCTGGGCGCCCATGATACCACTTTGTGTCGAATAACGAGGTCCAGTTTGGCGCC	126059
Db	126000	GTGAAGCTGGGCGCCCATGATACCACTTTGTGTCGAATAACGAGGTCCAGTTTGGCGCC	126059
QY	126060	ACCGAAGTGAAGGCTGTGTGAATAGACTTCATCGTTGTGTGTGAAGATGACAGATTCCTTTC	126119
Db	126060	ACCGAAGTGAAGGCTGTGTGAATAGACTTCATCGTTGTGTGTGAAGATGACAGATTCCTTTC	126119
QY	126120	GACAGACCTCTGTGACCCACGTCGCGCACACGGTGGCCCCGGCAGTCAAAAGTTTGGCAC	126179
Db	126120	GACAGACCTCTGTGACCCACGTCGCGCACACGGTGGCCCCGGCAGTCAAAAGTTTGGCAC	126179
QY	126180	GECTGGGCGCACTGTGTGACGTGTGGGGCTGGATTTCMAAGATGACGCCCGGGGTTTGG	126239

Db	126180	GCCTGGCGACCTCTGTGACGTGCTGGGGCTGGATTTCGAAGATGACGCCCGGGGTTTCG	126239
Qy	126240	GACACGACCCACTGACAGGGGGTTTCTCTGACGGGATGGGAATCTGTAGCCCTCGGTTA	126299
Db	126240	GACACGACCCACTGACAGGGGGTTTCTCTGACGGGATGGGAATCTGTAGCCCTCGGTTA	126299
Qy	126300	CCGGCCAGGGCCATCTGATATAGCGGTAAACCACTGCTCCGTGCTGACGCTGTGGCCG	126339
Db	126300	CCGGCCAGGGCCATCTGATATAGCGGTAAACCACTGCTCCGTGCTGACGCTGTGGCCG	126339
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Db	117729	ACAGCGCGCAGCGGCGCGCCACACGAGGAGGCGGCGCGCGGCTGCGCGGCTTACAGA	117788	

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D	120007	GCCTGTAAAAAAGCGAGATTAAAGTATGTCCTTTCCACGACCGCAGCCACTGAGC	120066
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D	120187	GAGACCGCGACGGGGTTTTAGTTGCTTACTATTAAGTTTAGTTAAATCCGTGGCGGA	120246
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O	122527	CCGCGAAAGTCTGTCCGCGCGGACGCGCGCGCGCTGCGCAACACCGCCCTTGA	122586
D	120307	CCGCGAAAGTCTGTCCGCGCGGACGCGCGCGCGCTGCGCAACACCGCCCTTGA	120366
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D	120427	GGTGTCAACGTCATTGTTAAACCGGTAATCTTGAAATCTTGTCCGCGCGCGGTGA	120486
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D	120487	GGCGGGGGCCCTTAAGCTTATAGTGTGTGACAGGATCCTGAATCGAAAGCTGGCCATA	120546
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D	120607	CGGGTGTTAAGCACCAACACCGACCGCTGTTTCAATATATGCGGAGAAATTACTTA	120666
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DEFINITION	Macaca mulatta rhadinovirus 26-95 long unique region 1-DNA,		
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VERSION	AF210726.1	GI:7329990	
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SOURCE	Macaca mulatta rhadinovirus 26-95		
ORGANISM	Macaca mulatta rhadinovirus 26-95		
REFERENCE	1 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L., Knapp, A., Auerbach, M. R., Damania, B. and Destroiers, R. C.		
TITLE	The primary sequence of rhesus monkey rhadinovirus isolate 26-95: sequence similarities to Kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 17577		
JOURNAL	J. Virol. 74 (7), 3388-3398 (2000)		
MEDLINE	20173730		
PUBMED	10708456		
REFERENCE	2 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L. M., Knapp, A., Auerbach, M., Czajak, S., Damania, B. and Destroiers, R. C.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-DEC-1999) Microbiology, New England Regional Primate Research Center, One Pinehill Dr, Southborough, MA 01772, USA		
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 709 CCGGGCCCGGGCCGCTCG 690
RESULT 5 5077 bp DNA linear VRL 28-AUG-2000
KSU82242
LOCUS
DEFINITION Kaposi's sarcoma-associated herpesvirus chemokine receptor homolog
gene, complete cds and large viron protein gene, partial cds.
ACCESSION U82242
VERSION
KEYWORDS
SOURCE
ORGANISM Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
Human herpesvirus 8
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 5077)
AUTHORS Guo,H.G., Browning,P., Nicholas,J., Hayward,G.S., Tschachler,E.,
Jiang,Y.W., Sadowska,M., Raffeld,M., Colombini,S., Gallo,R.C. and
Reltz,M.S.
TITLE Characterization of a chemokine receptor-related gene in human
herpesvirus 8 and its expression in Kaposi's sarcoma
JOURNAL Virology 228 (2), 371-378 (1997)
MEDLINE 97223350
PUBMED 9123844
REFERENCE 2 (bases 1 to 5077)
AUTHORS Guo,H.G., Browning,P., Nicholas,J., Hayward,G.S., Tschachler,E.,
Jiang,Y.W., Sadowska,M., Raffeld,M., Colombini,S., Gallo,R.C. and
Reltz,M.S.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-1996) Inst. of Human Virology, University of
Maryland, Baltimore, 725 W. Lombard St., Baltimore, MD 21201, USA
REFERENCE 3 (bases 1 to 5077)
AUTHORS Guo,H.G., Browning,P., Nicholas,J., Hayward,G.S., Tschachler,E.,
Jiang,Y.W., Sadowska,M., Raffeld,M., Colombini,S., Gallo,R.C. and
Reltz,M.S.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2000) Inst. of Human Virology, University of
Maryland, Baltimore, 725 W. Lombard St., Baltimore, MD 21201, USA
REMARK Sequence update by submitter
COMMENT On Aug 28, 2000 this sequence version replaced gi:1930013.
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Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6 6671 bp DNA linear VRL 16-FEB-2003
AY189899
LOCUS
DEFINITION Pseudorabies virus strain Ea UL15 (UL15), UL17 (UL17), UL16 (UL16),
and UL14 (UL14) genes, complete cds; and UL13 (UL13) gene, partial
cds.
ACCESSION AY189899
VERSION AY189899.1 GI:28395421
KEYWORDS
SOURCE
ORGANISM Pseudorabies virus
Pseudorabies virus
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE 1 (bases 1 to 6671)
AUTHORS Xiao,S.B., Zhang,H., Fang,L.R., Niu,C.S., Ma,X.R. and Chen,H.C.
TITLE Sequences analysis and identification of splice site of
1 UL15, UL16 and UL17
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6671)
AUTHORS Xiao,S.B., Zhang,H., Fang,L.R., Niu,C.S., Ma,X.R. and Chen,H.C.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Lab of Animal Virology, College of Animal
Science and Veterinary Medicine, Huazhong Agricultural University,
Wuhan, Hubei 430070, P.R. China
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Best local similarity 100.0%: Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3695 CCGCGCGCGCGGTGAGCCGC 3714
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LOCUS
DEFINITION
KSU40394
Kaposi's sarcoma-associated herpes-like virus linear vrl 14-JAN-1999
homolog, G-protein coupled receptor homolog, and ORF 73 unknown
protein genes, complete cds.
U40394 U24269 U24275
U40394.1 GI:4154094
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
1 (bases 1 to 8481)
Chang, Y., Cesarman, E., Pessin, M.S., Lee, F., Culpepper, J.,
Knowles, D.M. and Moore, P.S.
Identification of herpesvirus-like DNA sequences in AIDS-associated
Kaposi's sarcoma
Science 266 (5192), 1865-1869 (1994)
JOURNAL
MEDLINE
PUBMED
7997879
2 (bases 1 to 8481)
Cesarman, E., Nador, R.G., Bai, F., Chang, J., Moore, P.S. and
Knowles, D.M.
Sequence and expression analysis of a region of Kaposi's
sarcoma-associated herpesvirus containing homologs of G
protein-coupled receptors and cyclins
Unpublished
3 (bases 1 to 8481)
Cesarman, E. and Knowles, D.M.
Direct Submission
Submitted (08-NOV-1995) Ethel Cesarman, Pathology, New York
Hospital/Cornell University Medical Center, 525 East 68th Street,
New York, NY 10021, USA
On or before Jan 14, 1999 this sequence version replaced
gi:1628494, gi:1621028.
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 Number Q01035"

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DEFINITION	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds;		
			VRL 02-AUG-1999

ACCESSION	AF148805
VERSION	AF148805.1
KEYWORDS	GI:5669888
SOURCE	Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8)

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
Human herpesvirus 8 viruses; dsDNA viruses; no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.	1 (bases 1 to 28559)	Glenn, M., Rainbow, L., Aured, F., Davison, A. and Schulz, T.F.	Identification of a spliced gene from Kaposi's sarcoma-associated herpesvirus encoding a protein with similarities to latent membrane proteins 1 and 2A of Epstein-Barr virus	J. Virol. 73 (8), 6953-6963 (1999)	99329221	10400794	2 (bases 1 to 28559)	Glenn, M.A., Rainbow, L., Aured, F., Davison, A.J. and Schulz, T.F.	Direct Submission Submitted (15-APR-1999) MRC Virology Unit, Church Street, Glasgow G11 5UR, UK	Location/Qualifiers I. .28559	

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Matches 20;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
LOCUS	U93872	133661 bp	DNA linear VRL 09-JUL-2001
DEFINITION	Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNA replication protein, glycoprotein, DNA replication protein, FLICE inhibitory protein and v-cyclin genes, complete cds, and tegument protein gene, partial cds.		
ACCESSION	U93872		
VERSION	U93872.2	GI:14627174	
KEYWORDS	Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8)		
SOURCE	Human herpesvirus 8		
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.		
REFERENCE	1 (bases 29032 to 30108; 117733 to 118431)		
AUTHORS	Zhong, W., Wang, H., Herndler, B., and Ganem, D.		
TITLE	Restricted expression of Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genes in Kaposi sarcoma		

CDS	GSTDNLSYTGQAFYADKLRGGINOVLEELISAKRREOVRLNLMYELSKINPTSVMTA LYGRVSKAEVNDIAIVTECINVDQSSVNIHKSJRTNSKDVACAPLATEFLWSSNL FTGQLGARNEIILLNNNOVETCKDCEHFTVCNTRVYKATVRLNTNLTIVHTF IALNLSFIONIDFAIEIYSSAEKRLASVSDLETFMEFVYVYTHRLAGLEDMDNTI DMKRFVRLDSIEIVADIGSGITGVANVASVGLTGVTFNFIHPHGMIMTI IVIAIILIIIFMLSRRTNIAQAPVKMIYPPDDRARPGGGAPTEEEKIKILLGNHQLD OEEROKKADDLKSTPSVFGQRANGLRQRLKRYTKLTLGSDISPETGE" 11344..14382 /note="ORF 09, DNA polymerase homolog" /codon_start=1 /protein_id="AAB62593.1" /db_xref="GI:2246468" /translation="MDPEPRVDPDPRGPRATVROPSPSPVPSERVCRLLPAC QTPRGVAVDTTPPTPTFQGRKGEVFAETESIMTKRGQARNAPMSHLITVHD IVETVYADRCEDVPSFDIDIPSGVTLKILGRILASGVAVFRQRCYFYLAPQ GVNLHVLQALQAGFASCSGFSTEPYRKILRAYDQOAVAKITLSSSPMSTIS DLRTCCGEVESVNDARIREFLDHGFSTFGMCSNPAPRTQARSDTELEFPCSM DLKFIPTETMPPTLISFDIECGEGKFPNADDEMIIOISGLVHTGVNDKPYTRM LLGIGTDDPLPGVEVPEPSPYDMLAFLSLRDNVEFTIGYNIANDPYITARAT OYDFKLODFKITGTSVFEVHPRGSGDGNFRSOSKVAISGIVLDMIOVCERKL SLSDYKLDITVAKQLGRQKDISYKDIPLERKSGPDGAKVNCVIDSVLMDLLR FQTHVEISEIKAKIKRVLITDGOQIRVFSCLLEAATGYILPYKGVAVGQOG ATVISPSPGFDDPVLVDFASLYPSIIQANLCYSTLIPDSHLHPLSPDYETF VLGGPVHFKVKKRESILAKLTVMILAKREIKRTLASCTDPAIKTILDKOOLAIV TCNAVGTGVSAGIILPCINLAETVTLQGRMERSQAFVAISPERIAGLRPIDV SPDARFYIYDTSLSITCCGFMDSVSDAEELATITVTLRSPKLEAEITFK LLILTKRYVGLSDDKVLMKGVLDLIRKTACRFQKSSVQLDLIRPPVAAKALI SGQATDWYRREGLEGEVKIIOVLNASHRELCERSVDKLTFTTELSRPADRYTON LPHLVQYOKLQARQELPQIHRIPIYVDFVDSGLRSLSLAHPREVXQHGIRVAVDLY FDKLVAVANIIQCLFQNNMSAVAMLYNFIIDIVTPTP" 14500..15756 /note="ORF 10, herpesvirus salmaiti ORF 10 homolog, conserved in other gamma-herpesviruses" /codon_start=1 /protein_id="AAB62594.1" /db_xref="GI:2246469" /translation="MGTETAPRILGDWEITVSNCFCTCSLTCGLYRSSGDYFRLRIP	
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Db	132104 CCGGCGAGGCCATCTCGAT 132123	
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DEFINITION	Kaposi's sarcoma-associated herpesvirus long unique region, 80	
ACCESSION	U75698	
VERSION	U75698.1 GI:2065526	
KEYWORDS		
SOURCE	Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -	
ORGANISM	Human herpesvirus 8	
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.	
AUTHORS	1 (bases 47193 to 47522; 133099 to 133729) Chang, Y., Cesarman, E., Pessin, M. S., Lee, F., Culpepper, J., Knowles, D. M., and Moore, P. S.	
TITLE	Identification of herpesvirus-like DNA sequences in AIDS-associated Kaposi's sarcoma	
JOURNAL	Science 266 (5192), 1865-1869 (1994)	
MEDLINE	95090463	
PUBMED	7997879	
REFERENCE	2 (bases 35021 to 55726) Moore, P. S., Gao, S. J., Dominguez, G., Cesarman, E., Lungu, O., Knowles, D. M., Garber, R., Pellett, P. E., McGeoch, D. J. and Chang, Y.	
AUTHORS	Primary characterization of a herpesvirus agent associated with Kaposi's sarcoma	
TITLE		
CDS		
JOURNAL	J. Virol. 70 (1), 549-558 (1996)	
MEDLINE	96099469	
PUBMED	8523568	
REFERENCE	3 (bases 28661 to 29741; 117919 to 118101) Zhong, W., Wang, H., Herndler, B. and Ganem, D.	
AUTHORS	Restricted expression of Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genes in Kaposi sarcoma	
TITLE		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)	
MEDLINE	96270595	
PUBMED	8692871	
REFERENCE	4 (bases 122794 to 123567; 123809 to 127297; 129372 to 130400; 130551 to 134441) Cesarman, E., Nador, R. G., Bai, F., Bohenzky, R. A., Russo, J. J., Moore, P. S., Chang, Y. and Knowles, D. M.	
AUTHORS	Kaposi's sarcoma-associated herpesvirus contains G protein-coupled receptor and cyclin D homologs which are expressed in Kaposi's sarcoma and malignant lymphoma	
TITLE		
JOURNAL	J. Virol. 70 (11), 8218-8223 (1996)	
MEDLINE	97048116	
PUBMED	8892957	
REFERENCE	5 (bases 1 to 137508) Moore, P. S., Boshoff, C., Weiss, R. A. and Chang, Y.	
AUTHORS	Molecular mimicry of human cytokine and cytokine response pathway genes by KSHV	
TITLE		
JOURNAL	Science 274 (5293), 1739-1744 (1996)	
MEDLINE	97094384	
PUBMED	8939871	
REFERENCE	6 (bases 1 to 137508) Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M., Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and Moore, P. S.	
AUTHORS	Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8)	
TITLE		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14862-14867 (1996)	
MEDLINE	97121480	
PUBMED	8962146	
REFERENCE	7 (bases 1 to 137508) Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M., Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and Moore, P. S.	
AUTHORS	Direct Submission	
TITLE	Submitted (17-OCT-1996) Dept of Pathology/Genome Center/Division of Epidemiology, Columbia University, 650 West 168th Street, New York, NY 10032, USA	
REFERENCE	8 (bases 1 to 137508) Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M., Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and Moore, P. S.	
AUTHORS	Direct Submission	
TITLE	Submitted (02-MAY-1997) Dept of Pathology/Genome Center/Division of Epidemiology, Columbia University, 650 West 168th Street, New York, NY 10032, USA	
REMARK	Sequence update by submitter	
COMMENT	On May 3, 1997 this sequence version replaced gi:1718251.	
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Db 65128 CTCCTGGGGCCATGACGCC 65147

RESULT 12
AH002374S1/c 165 bp RNA linear VRL 11-APR-2003
LOCUS AH002374S1 165 bp RNA linear VRL 11-APR-2003
DEFINITION Middleburg virus nonstructural polyprotein gene, partial cds.
ACCESSION K00699
VERSION K00699.1 GI:331523
KEYWORDS
SEGMENT 1 of 2
SOURCE Middleburg virus
ORGANISM Middleburg virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
Alphavirus.
1 (sites)
REFERENCE Ou, J.H., Trent, D.W. and Strauss, J.H.
TITLES The 3'-non-coding regions of alphavirus RNAs contain repeating
sequences
JOURNAL J. Mol. Biol. 156 (4), 719-730 (1982)
MEDLINE 83010261
PUBMED 6288962

REFERENCE
AUTHORS Ou, J.H., Strauss, E.G. and Strauss, J.H.
TITLES The 5'-terminal sequences of the genomic RNAs of several
alphaviruses
JOURNAL J. Mol. Biol. 168 (1), 1-15 (1983)
MEDLINE 83268700
PUBMED 6308269

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OY 131128 TGACCTGCTCTGCTCGAT 131146
Db 155 TGACCTGCTCTGCTCGAT 137

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LOCUS AF251159 824 bp DNA linear VRL 12-DEC-2000
DEFINITION Human herpesvirus 1 mutant gamma1 34.5 gene, complete sequence.
ACCESSION AF251159
VERSION AF251159.1 GI:11640715
KEYWORDS
SOURCE Human herpesvirus 1
ORGANISM Human herpesvirus 1
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 824)
REFERENCE Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLES A gamma1 34.5 null mutant of herpes simplex virus type 1 strain +GC
is neurovirulent
JOURNAL Unpublished
REFERENCE Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLES 2 (bases 1 to 824)
JOURNAL Direct Submission
TITLES Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR
72205, USA

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Db 60 CCGCGCCGCCGCCGCC 78

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DEFINITION Human herpesvirus 1 gamma1 34.5 gene, complete cds.
ACCESSION AF251158
VERSION AF251158.1 GI:11640713
KEYWORDS
SOURCE Human herpesvirus 1
ORGANISM Human herpesvirus 1
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 947)
REFERENCE Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLES A gamma1 34.5 null mutant of herpes simplex virus type 1 strain +GC
is neurovirulent
JOURNAL Unpublished
REFERENCE Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLES 2 (bases 1 to 947)
JOURNAL Direct Submission
TITLES Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR

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Best Local Similarity	100.0%; Pred. No. 8.9;				
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
OY	132498 CCGCGCGCCCGCGGCC 132516				
Db	183 CCGCCGCCCGCGGCC 201				
RESULT 15					
LOCUS	HS1LS81 1213 bp DNA linear VRL 02-AUG-1993				
DEFINITION	HSV-1 (strain USA-8) L-S inversion region.				
ACCESSION	K01836				
VERSION	K01836.1 GI:330170				
KEYWORDS	repeat region; terminal inverted repeat.				
SEGMENT	1 of 2				
SOURCE	1 of 2				
ORGANISM	Human herpesvirus 1				
	Human herpesvirus 1				
	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.				
TITLE	1 (bases 1 to 1213)				
REFERENCE	Davison A.J. and Wikkie N.M. Nucleotide sequences of the joint between the L and S segments of herpes simplex virus types 1 and 2 J. Gen. Virol. 55 (Pt 2), 315-331 (1981)				
JOURNAL	82032334				
MEDLINE	6270266				
PUBMED					
COMMENT	Original source text: Herpes simplex virus type 1 strain USA-8 DNA. This sequence contains a single b'a'c' sequence. See comment for other HSV-1 L-S inversion region entries.				
FEATURES	location/Qualifiers				
source	1..1213				
	/organism="Human herpesvirus 1"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:10298"				
	<1..330				
	/note="b' repeat"				
repeat_region	311..327				
	/note="DRI repeat"				
repeat_region	331..744				
	/note="a' repeat"				
repeat_region	408..495				
	/note="reiteration Ia (8 copies)"				
repeat_region	495..639				
	/note="reiteration Ib (6 copies)"				
repeat_region	726..742				
	/note="DRI repeat"				
repeat_region	745..>1213				
	/note="c' repeat"				
repeat_region	974..>1213				
	/note="reiteration II (15 copies)"				
BASE COUNT	138 a 569 c 352 g 154 t				

ORIGIN	1 bp upstream of HinfI site.
Query Match	0.1%; Score 19; DB 1; Length 1213;
Best Local Similarity	100.0%; Pred. No. 9;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	132498 CCGCGCGCCCGCGCGCC 132516
DB	186 CCGCGCGCCCGCGCGCC 168
RESULT 16	
HEHPSV/c	
LOCUS	HEHPSV 1303 bp DNA linear VRL 03-NOV-1992
DEFINITION	Fragment from the Herpes b'a'c' region (L-S component junction).
ACCESSION	V00460 J02223
VERSION	V00460.1 GI:59814
KEYWORDS	repetitive sequence; terminal repeat.
SOURCE	Human herpesvirus 1
ORGANISM	Human herpesvirus 1
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.
AUTHORS	1 (bases 1 to 1303)
TITLE	Mocarski, E.S. and Roizman, B.
JOURNAL	Site-specific inversion sequence of the herpes simplex virus
MEDLINE	genome: domain and structural features
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 78 (11), 7047-7051 (1981)
FEATURES	6273905
SOURCE	Location/Qualifiers
	1..1303
	/organism="Human herpesvirus 1"
	/mol_type="genomic DNA"
	/db_xref="taxon:10298"
BASE COUNT	146 a 711 c 290 g 156 t
ORIGIN	
Query Match	0.1%; Score 19; DB 1; Length 1303;
Best Local Similarity	100.0%; Pred. No. 9;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	132498 CCGCGCGCCCGCGCGCC 132516
DB	61 CCGCGCGCCCGCGCGCC 43
RESULT 17	
HSLSFA/c	
LOCUS	HSLSFA 1303 bp DNA linear VRL 02-AUG-1993
DEFINITION	HSV-1 (strain F+) L-S inversion region.
ACCESSION	J02223
VERSION	J02223.1 GI:330173
KEYWORDS	repeat region; terminal inverted repeat.
SOURCE	Human herpesvirus 1
ORGANISM	Human herpesvirus 1
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.
AUTHORS	1 (bases 1 to 1303)
TITLE	Mocarski, E.S. and Roizman, B.
JOURNAL	Site-specific inversion sequence of the herpes simplex virus
MEDLINE	genome: domain and structural features
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 78 (11), 7047-7051 (1981)
REFERENCE	6273905
AUTHORS	2 (bases 185 to 685)
TITLE	Mocarski, E.S. and Roizman, B.
JOURNAL	Structure and role of the herpes simplex virus DNA termini in
MEDLINE	inversion, circularization and generation of virion DNA
PUBMED	Cell 31 (1), 89-97 (1982)
COMMENT	83129341
	6297756
	Original source text: HSV-1 (strain F+) DNA, clones PB115 and
	PB104.

The herpes simplex viral genome consists of a long and a short unique segment (UL and US) each of which is flanked by regions of repetitive sequence. The repeated sequence flanking the UL segment lies with opposite orientation at each end and is labeled ab at one end and b'a' at the other. The repeated sequence flanking the US segment also lies in opposite orientations and is labeled a'c' at one end and ca at the other end. Thus the complete genome can be represented by: ab-UL-b'a'a'c'-US-ca. The region represented by a'b'a'c' is called the L-S region. The two segments UL and US can recombine in many ways. A population of virions is found to have equal concentrations of four different species of DNA molecules differing only in the orientations of the UL and US segments with respect to one another. Because of this the L-S region has also been called the inversion region. The four species of DNA can be represented by

ab-UL-b'a'a'c'-US-ca
ab-UL-b'a'a'c'-SU-ca
ab-LU-b'a'a'c'-US-ca
ab-LU-b'a'a'c'-SU-ca

Due to the frequency with which the UL and US segments recombine the L-S or -b'a'a'c'- region is very polymorphic, with varying numbers of copies of a' being present; and varying numbers of shorter repetitive sequences (called 'retention' sequences) within a' being present.

Compared with EMBL id = nehpsv, dated 08-VUL-1982.

FEATURES	Location/Qualifiers
source	1. .1303

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repeat_region      <1. .184 /note="b" repeat"
repeat_region      185. .685 /note="a repeat"
repeat_region      185. .204 /note="DR1 repeat"
repeat_region      205. .268 /note="ub region [2]"
repeat_region      269. .497 /note="reiteration Ia (DR2 in [2] (19 copies) [2]"
repeat_region      497. .608 /note="reiteration Ib (DR4 in [2] (3 copies) [2]"
repeat_region      608. .665 /note="uc region [2]"
repeat_region      666. .685 /note="DR1 repeat"
repeat_region      686. .>1303 /note="c' repeat"
repeat_region      914. .1217 /note="reiteration II (19 copies) [2]"

BASE COUNT      145 a      711 c      250 g      157 t
ORIGIN      1 bp upstream of BstBII site.

```

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Query Match      0.1%; Score 19; DB 1; Length 1303;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
```

	RESULT 18
HS1ICP345B	
LOCUS	1346 bp DNA linear VRL_02-AUG-1993
DEFINITION	Herpes simplex virus type 1 infected-cell protein (ICP34.5) gene,
ACCESSION	complete cds.
VERSION	M3700
KEYWORDS	M3700.1 GI:330116
SOURCE	Infected-cell protein 34.5; neurovirulence factor.
ORGANISM	Human herpesvirus 1
	Human herpesvirus 1
	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
1	(bases 1 to 1346)	Chou, J. and Roizman, B.	The herpes simplex virus 1 gene for ICP34.5, which maps in inverted repeats, is conserved in several limited-passage isolates but not in strain 17syn+	J. Virol. 64 (3), 1014-1020 (1990)	90156694	2154589
Original source text: Herpes simplex virus type 1 (strain MGH-10)						

Draft entry and computer-readable sequence for [1] kindly submitted by J. Chou, 13-APR-1990.

```
FEATURES
    source      Location/Qualifiers
                1..1346
                /organism="Human herpesvirus 1"
                /mol_type="genomic DNA"
                /db_xref="taxon:10298"
    CDS         134..871
```

```

/note="infected-cell protein 34.5"
/codon_start=1
/protein_id="AAA579.1"
/db_xref="GI:330117"
/translation="MARRRRNRHRRPPRRPGGAPVTAQSYTSPINSEPVYRSR
AAGGPPSPCSLLKQWLHPESASDDDDDDDDWSPPEPEEARPTAAAPRSPSP
GAGGGGANGSHPSRPFLRLPLRLATAEHLALRLRAGGEAPAPPAIPATP
ATPTPTPTPTPTPARVRESPHVRVHLLVYVMSAARLARGSWAREADRRRVVAA
EAYVGPGLGEARALARGAGPNSV"
BASE COUNT      161 a      576 c      437 g      172 t
ORIGIN

```

BASE COUNT	161	a	576	c	437	g	172	t
ORIGIN								
Query Match	0.1%; Score 19; DB 1; Length 1346;							
Best Local Similarity	100.0%; Pred. No. 9;							
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
QY	132498	CCGCCGCCCGGCCGCC	132516					
Db	166	CCGCCGCCCGGCCGCC	184					

RESULT 19					
LOCUS	HS1ICP345C				
DEFINITION	Herpes simplex virus type 1 infected-cell protein (ICP34.5aa) gene,				
ACCESSION	M33701				
VERSION	M33701.1	GI:330118			
KEYWORDS	Infected-cell protein 34.5; neurovirulence factor.				
SOURCE	Human herpesvirus 1				
ORGANISM	Human herpesvirus 1				
REFERENCE	Alphaherpesvirinae: Simplexvirus.				
AUTHORS	1 (bases 1 to 1367)				
TITLE	Chou,u. and Koltman,B.				
	The herpes simplex virus 1 gene for ICP34.5, which maps in inverted repeats, is conserved in several limited-passage isolates but not in strain 178yn+				
JOURNAL	J. Virol.	64 (3),	1014-1020	(1990)	
MEDLINE	90156694				
PUBMED	2154589				
COMMENT	Original source text: Herpes simplex virus type 1 (strain CVG-2)				
	DNA.				

Draft entry and computer-readable sequence for [1] kindly submitted by J.Chou, 13-APR-1990.

FEATURES	SOURCE	location/Qualifiers
		1..1367
		/organism="human herpesvirus 1"
		/mol_type="genomic DNA"
		/db_xref="taxon:10298"
CDS		134..892
		/note="Infected-cell protein 34.5"
		/codon_start=1
		/protein_id="AAA45792.1"

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/note="infected-cell protein 34.5"
/codon_start=1
/protein_id="AA045792.1"

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[illegible]

VERSION	K01835.1	GI:330169
SOURCE	repeat_region; terminal inverted repeat.	
ORGANISM	Human herpesvirus 1 Human herpesvirus 1 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus. 1 (bases 1 to 1766)	
REFERENCE	Davison,A.J. and Malikle,N.M.	
AUTHORS	Nucleotide sequences of the joint between the L and S segments of herpes simplex virus types 1 and 2	
JOURNAL	J. Gen. Virol. 55 (Pt 2), 315-331 (1981)	
MEDLINE	82032334	
PUBMED	6270266	
COMMENT	Original source text: Herpes simplex virus type 1 strain 17 DNA, clone K1. See comment in other HSV-1 L-S inversion region entries. This sequence contains a single b'a'c' sequence.	
FEATURES	Location/Qualifiers	
source	1..1766	/organism="Human herpesvirus 1"
	/mol_type="genomic DNA"	
	/db_xref="taxon:10298"	
	<1..328	/note="b' repeat"
repeat_region	311..331	/note="DR1 repeat"
	329..728	/note="a' repeat"
repeat_region	408..631	/note="reiteration I (18.5 copies)"
	710..730	/note="DR1 repeat"
repeat_region	729..>1766	/note="c'repeat"
	928..959	/note="reiteration IIA (2 copies)"
repeat_region	960..1066	/note="reiteration IIB (6.7 copies)"
	1167..1489	/note="reiteration III (19 copies)"
repeat_region	/note="(1527..>1766) complement(1527..>1766) /product="Vmw immediate Early 175 mRNA"	
mRNA	167 a 935 c 436 g 228 t	
BASE COUNT	1 bp upstream of HinfI site.	
ORIGIN	0.1%; Score 19; DB 1; Length 1766; Best Local Similarity 100.0%; Pred. No. 9.1; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	132498 CCGCCGCCCGCCGCGCCC 132516	
Db	186 CCGCCGCCCGCCGCGCCC 168	
RESULT 22	HSIIICPL 1794 bp DNA linear VRL 02-AUG-1993	
LOCUS	Herpes simplex virus type 1 (a region x, infected cell protein gene, complete cds.	
DEFINITION	MI2240.1 GI:330122	
ACCESSION	Infected cell protein. Human herpesvirus 1 Human herpesvirus 1 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus. 1 (bases 1 to 1794) Chou,J. and Roizman,B. The terminal a sequence of the herpes simplex virus genome contains the promoter of a gene located in the repeat sequences of the L component	
VERSION	MI2240.1	
KEYWORDS	Human herpesvirus 1	
SOURCE	Human herpesvirus 1	
ORGANISM	Human herpesvirus 1	
REFERENCE	Alphaherpesvirinae; Simplexvirus.	
AUTHORS	Chou,J. and Roizman,B.	
TITLE	The terminal a sequence of the herpes simplex virus genome contains the promoter of a gene located in the repeat sequences of the L component	
JOURNAL	J. Virol. 57 (2), 629-637 (1986)	
MEDLINE	86115412	

PUBMED 3003394
COMMENT Original source text: Herpes simplex virus type 1 (HSV1, strain F)
DNA, passed in Vero cells, clones PRB13196, 3197, 3198].
Draft entry and computer-readable sequence for [1] kindly provided
by F.J.Jenkins, 03-JUN-1988.

FEATURES
source
1. 1794
/organism="Human herpesvirus 1"
/mol_type="genomic DNA"
/db_xref="taxon:10298"
65..>1228
/note="ICP mRNA (alt.)"
80..>1228
/note="ICP mRNA (alt.)"
145..1221
/note="Infected cell protein"
/codon_start=1
/protein_id="AA45794.1"
/db_xref="GI:330123"
/translation="MLACQTLPPRHALLGPPRRHAGPPRRPPTGAVPTAOPV
TSTPNSPAPVRSAPAAPPPPPGPPSCSLRLQMLHVESASDDDDDDDDPSP
PEPAPPGAPPAAPRRSPRPGCGGCAAPSPSPRPRLRLRLVTEHLAR
LRDARAGGAGAPATPATPATPATPATPATPATPARRSPTVVRHL
VWASARLRAAARPGASGPTGLSGAGWRPSSSGRAMPGRALPGAPARRTS
NVTPEAWSSAEELRTKPLSRDDGRSRAVIRMEPARPGRGPPSEGGTGSAGRGRC
PANQPPSLRGPPMAGPAHFVW"
1794..>1794
/product="alpha-0 mRNA"
BASE COUNT 222 a 728 c 603 g 241 t
ORIGIN SmaI site.

Query Match 0.1%; Score 19; DB 1; Length 1794;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132498 CCGCGCGCCCGCGCCG 132516
Db 219 CCGCGCGCCCGCGCCG 237

RESULT 23
AF015716 2038 bp RNA linear VRL 13-JAN-1999
LOCUS Alfaifa mosaic virus VRU movement protein (P3) and coat protein
DEFINITION genes, complete cds.
ACCESSION AF015716
VERSION AF015716.1 GI:2654871
KEYWORDS Alfaifa mosaic virus
SOURCE Alfaifa mosaic virus
ORGANISM Alfaifa mosaic virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage: Bromoviridae;
Alfamovirus.

REFERENCE 1 (bases 1 to 2038)
AUTHORS Thole,V., Miglino,R. and Bol,J.F.
TITLE Amino acids of alfaifa mosaic virus coat protein that direct
formation of unusually long virus particles
J. Gen. Virol. 79 (Pt 12), 3139-3143 (1998)

JOURNAL MEDLINE 98094642
PUBMED 9880033
REFERENCE 2 (bases 1 to 2038)
AUTHORS Thole,V. and Bol,J.F.
TITLE Direct Submission
Submitted (23-JUL-1997) Institute of Plant Molecular Sciences,
Gortaeus Laboratories, Leiden University, Einsteinweg 55, Leiden
2333 CC, The Netherlands

FEATURES
source
1. 2038
/organism="Alfaifa mosaic virus"
/mol_type="genomic RNA"
/strain="VRU"
/db_xref="taxon:12321"
242..1144
/gene="P3"

gene

CDS
242..1144
/gene="P3"
/codon_start=1
/product="movement protein"
/protein_id="AAD04692.1"
/db_xref="GI:2654872"
/translation="MENTKTNASGSGISSSSSFVSVAEBMLADEVSKNMSNLTCP
NOLKCTQVLVNSGAAPVVLSVSKERKSTLNMLPKIGRMVYHHSAIYLVNPTL
KSSSGSTTLKLFNEATGELVDVTDHDATACLEPAGYPSIIAKDAKGDHDKLVH
AVASTNANSVGVLYPIWDELRSKQILEGAPRLPRLPTEPPVLDLNAKGLTPV
LDRTILGVSGSKGPNVYLEPRKAVGAKATVTPESGVPNTIVKGIAPTVINDGS
PKGLGVKGFYTESFIKDELTPH"
1194..1859
/codon_start=1
/product="coat protein"
/protein_id="AAD04693.1"
/db_xref="GI:2654873"
/translation="MSSSOKKAGKAGKPKYRSQNTAALRKAOLPKPPALKVPVAKPT
NTILPQTGCWQSLIGTPLSLSSNSGIGARLYEFLKDFAPARILEEDLIRMFESTIP
SHAGSFCLTDDVTEDGRAVAHGNPMQEPHGAFHANEKGFELVTAAPAHAGMON
FKSYVAVALCLDFDALPEGRNPSYRENEVVERKAPFRAGPLRSLLITVGLFPDADDL
DRQ"

BASE COUNT 550 a 441 c 456 g 591 t
ORIGIN

Query Match 0.1%; Score 19; DB 1; Length 2038;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121169 GTGCATCTGTCGCCAAT 121187
Db 358 GTGCATCTGTCGCCAAT 376

RESULT 24
AF015717 2038 bp RNA linear VRL 13-JAN-1999
LOCUS Alfaifa mosaic virus 15/64 movement protein (P3) and coat protein
DEFINITION genes, complete cds.
ACCESSION AF015717
VERSION AF015717.1 GI:2654874
KEYWORDS Alfaifa mosaic virus
SOURCE Alfaifa mosaic virus
ORGANISM Alfaifa mosaic virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage: Bromoviridae;
Alfamovirus.

REFERENCE 1 (bases 1 to 2038)
AUTHORS Thole,V., Miglino,R. and Bol,J.F.
TITLE Amino acids of alfaifa mosaic virus coat protein that direct
formation of unusually long virus particles
J. Gen. Virol. 79 (Pt 12), 3139-3143 (1998)

JOURNAL MEDLINE 98094642
PUBMED 9880033
REFERENCE 2 (bases 1 to 2038)
AUTHORS Thole,V. and Bol,J.F.
TITLE Direct Submission
Submitted (23-JUL-1997) Institute of Plant Molecular Sciences,
Gortaeus Laboratories, Leiden University, Einsteinweg 55, Leiden
2333 CC, The Netherlands

FEATURES
source
1. 2038
/organism="Alfaifa mosaic virus"
/mol_type="genomic RNA"
/strain="15/64"
/db_xref="taxon:12321"
242..1144
/gene="P3"
/codon_start=1
/product="movement protein"
/protein_id="AAD04694.1"
/db_xref="GI:2654875"

gene

/translation="MENTKNASGSGISSSSFSYSAEMHLLADEVRNMSSTLIG
NOKICTOLVUSNCAAPVYLSVSKRSKSLRMPLPTGQRYVHSAIYLLIMPNIL
KSSSGITLKFENATGELVVDHDTQACIFAGRPRLSLADAKGHDKLIVH
AVASTNANSAGVLPIMEDELSKQILBERGADFLKPIIAETEPYDILNKGKLTDFV
LDRTNLGVSGRDPNPVLEBRAPKATKATKEFFIEGIGIPNTIYVNGITPTVRIDAGS
PKGCVPGKGFYSEFIRKDELLPDH"
1194.1859
CDS
/codon_start=1
/product="coat protein"
/protein_id="AAD04695.1"
/db_xref="GI:2654876"
/translation="MSSQKRRGKAGKPTKRSQNYALARKAOLPKPALVPAKPT
NTILPQGCVMQSLGTPSLSSNGIGARPLXSLKDPVARELLEDILFNVESITP
SHAGSFCLTDYTTEDGRAYAHGNPMQEPFGAFHANKEGEELVFTAPTHAGQMNQ
FKHSAVALCLDFDALPEGSKNPSYRNFENWVERKAFPRAPGRLSLITVKKLEDDADL
DRQ"
BASE COUNT 544 a 445 c 458 g 591 t
ORIGIN
Query Match 0.1%; Score 19; DB 1; Length 2038;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 121169 GTGATCCTGGGTCCCAAT 121187
|||||
Db 358 GTGATCCTGGGTCCCAAT 376
RESULT 25
LOCUS BHV4H 2121 bp DNA linear VRL 12-SEP-1997
DEFINITION Bovine herpesvirus type 4 glycoprotein H gene.
ACCESSION Z79633
VERSION Z79633.1 GI:1515108
KEYWORDS glycoprotein H.
SOURCE Bovine herpesvirus 4
ORGANISM Bovine herpesvirus 4
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
REFERENCE 1 (bases 1 to 2121)
AUTHORS Lomonte,P., Fillee,P., Lyaku,J.R., Bublolt,M., Pastoret,P.P. and
Thiry,E.
TITLE Analysis of the biochemical properties of, and complex formation
between, glycoproteins H and L of the gamma2 herpesvirus bovine
herpesvirus 4
JOURNAL J. Gen. Virol. 78 (Pt 8), 2015-2023 (1997)
MEDLINE 97410287
PUBMED 9267002
REFERENCE 2 (bases 1 to 2121)
AUTHORS Lomonte,P.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-1996) Patrick Lomonte, Virology, University of
Liege, Faculty of Veterinary Medicine, Bd De Colonster, Liege,
4000, BELGIUM
FEATURES
Source Location/Qualifiers
1. 2121
/organism="Bovine herpesvirus 4"
/mol_type="genomic DNA"
/strain="V. TEST"
/db_xref="taxon:10385"
/tissue_type="kidney"
1..>2121
/codon_start=1
/product="glycoprotein H"
/protein_id="CAB01909.1"
/db_xref="GI:1515109"
/db_xref="SPTREMBL:096635"
/translation="MKLFIPLFLSLCHSYCAVRGDSLEENKNTLTHPDGK
YVIMVTRLDVSPQIVQOMDEANVEENLDTYNTKTTGILKPLQIKRLNHNHHC
QGSQTRVDNISQIHAIQDAYLGNFIEOSRLFDNPREKNVTFGSDHFFPKDY
ATITWGNERPISGVTSPFSYVTMANKGQIKDOTTILFGESFGLPAKGVANPNVE
VAKYNLMVYLASKNCGSANLNFLELFINVKONPAEFIDIOSDFMAINSFG
CNTDSMDERKILLFPRVYVSHFKITRTLQKKYVYVMSGISITDLDDLIRMSKCPA

SGVINSGSISTIAIDQINTFPKSEGNRYADTIPNTILSRGEYNTEDVRYV
KRTLEDMTMEFSYFTLSGTQRTILFKIWRLLNFTHDNHNKSLITTYILLSSMC
TNVEIGLMDYERSRHPIDIHETFPCEKSLRFDPSYDKLQSNAPKLESTTKYNTGT
EGFLVHLNDFHKNRKYQPEIKCHQAKIQONIIAIIPLTNTVYVLSDDKLENYLVE
ITFEVLKSGMFLSVLRPDCRFPEDHGVLSLIPVYVNSNPLGCPFCFDSAVIYDES
IGLESMTYINNTYOKNLEFLVSPPEFDDNHLVHMLMNNGTVEIINGARRKYYSI
ILFTIKNFGFTLMITFELKMLSYVI"
BASE COUNT 697 a 322 c 388 g 714 t
ORIGIN
Query Match 0.1%; Score 19; DB 1; Length 2121;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129813 TGAATAAGAGCGCGTA 129831
|||||
Db 2006 TGAATAAGAGCGCGTA 2024
RESULT 26
LOCUS AF359760/c 3008 bp DNA linear VRL 05-JUN-2002
DEFINITION Buffalo herpesvirus 1 glycoprotein B gene, complete cds.
ACCESSION AF359760
VERSION AF359760.1 GI:19481399
KEYWORDS
SOURCE Buffalo herpesvirus 1
ORGANISM Buffalo herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE 1 (bases 1 to 3008)
AUTHORS Ros,C. and Belak,S.
TITLE Characterization of the glycoprotein B gene from ruminant
alphaherpesviruses
JOURNAL Virus Genes 24 (2), 99-105 (2002)
MEDLINE 22012763
PUBMED 12018712
REFERENCE 2 (bases 1 to 3008)
AUTHORS Ros,C.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2001) Chemistry and Biochemistry, University of
Bern and ZIB Bioplasma AG, Bern, Freiestrasse 3, Bern 3012,
Switzerland
FEATURES
Source Location/Qualifiers
1. 3008
/organism="Buffalo herpesvirus 1"
/mol_type="genomic DNA"
/strain="B6"
/db_xref="taxon:171005"
270..3008
/codon_start=1
/product="glycoprotein B"
/protein_id="AAL88794.1"
/db_xref="GI:19481400"
/translation="MAARGAEPAAAGGDRGRRGORRHLPGRVIALALRGPAAGGG
ARALAAALLMAAALLAARAAPRTGGDPDNGTVRALARLAQAAGESRRVYCP
PPSGATVRLAPARCPYEELGRNTBEGIATVIENTAPYFKAYITTKYIVTTTRA
GSTAAITNOYTDNRVPGVGLTDLVVKWMLSKAEILPGRVAAFDNRDWEAP
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Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 130092 GAAATGATAAACCTATA 130110
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Db 3712 GAAATGATAAACCTATA 3730
RESULT 29
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LOCUS Human papillomavirus type 10 genomic DNA.
DEFINITION X74465.1 GI:396901
ACCESSION E1 gene; E2 gene; E4 gene; E6 gene; E7 gene; early protein; L1
VERSION Human papillomavirus type 10
KEYWORDS Human papillomavirus type 10
SOURCE Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
ORGANISM Papillomavirus.
REFERENCE 1 (bases 1 to 7919)
AUTHORS Delius, H. and Hofmann, B.
TITLE Primer-directed sequencing of human papillomavirus types
JOURNAL Curr. Top. Microbiol. Immunol. 186, 13-31 (1994)
MEDLINE 94265501
PubMed 8205838
REFERENCE 2 (bases 1 to 7919)
AUTHORS Delius, H.
TITLE Direct Submision
JOURNAL Submitted (06-AUG-1993) H. Delius, Deutsches
Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506, W
6900 Heidelberg, FRG
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BASE COUNT 2169 a 1651 c 1981 g 2118 t

ORIGIN

Query Match 0.18; Score 19; DB 1; Length 7919;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 131993 TATATTTTAAATTTGCT 132011
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Db 7490 TATATTTTAAATTTGCT 7508

RESULT 30
BHV130KB/c 30000 bp DNA linear VRL 14-AUG-1996
LOCUS Bovine herpesvirus type 1 (Cooper) DNA (30 kb).
DEFINITION 248053.1 GI:971311
ACCESSION 248053.1 GI:971311
VERSION
KEYWORDS capsid protein; deoxyribonuclease; helicase/primase complex;
integral membrane protein; major capsid protein; myristylated
vireon protein; origin-binding protein; serine/threonine protein
kinase; viral packaging; vireon glycoprotein H (gH); vireon
glycoprotein M (gM); vireon protein.
SOURCE Bovine herpesvirus 1
ORGANISM Bovine herpesvirus 1
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicelloviruses.
REFERENCE 1 (bases 1 to 30000)
AUTHORS Vlack,C., Benes,V., Lu,Z., Kutish,G.F., Paces,V., Rock,D.,
Letchworth,G.J. and Schwyzer,M.
TITLE Nucleotide sequence analysis of a 30-kb region of the bovine
herpesvirus 1 genome which exhibits a colinear gene arrangement
with the UL21 to UL4 genes of herpes simplex virus
JOURNAL virology 210 (1), 100-108 (1995)
MEDLINE 95313343
PUBMED 7793062
REFERENCE 2 (bases 1 to 30000)
AUTHORS Schwyzer,M.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1995) Martin Schwyzer, Institute of Virology,
Faculty of Veterinary Medicine, University of Zurich,
Winterthurerstr. 266a, Zurich, CH-8057, Switzerland
FEATURES
source
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complement(8143. .8148)
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Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 30000;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 122895 GCTGGCGACGCTTGCCACG 122913
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DB 18572 GCTGGCGACGCTTGCCACG 18554
RESULT 31
SV1344259/c 35450 bp DNA linear VRL 18-MAR-2002
LOCUS Sulfolobus virus SIRV-2 genomic DNA.
DEFINITION AJ344259
ACCESSION AJ344259
VERSION AJ344259.1 GI:17221347
KEYWORDS
orf 109; ORF102; ORF103a; orf103b; ORF103c; ORF105a; ORF105b;
ORF107b; ORF108; orf110; ORF111; ORF112; ORF114; ORF116; ORF119a;
ORF119b; ORF119c; ORF121; ORF131a; ORF131b; ORF134; orf154; ORF156;
ORF158a; ORF158b; ORF176; ORF207; ORF249; ORF269; orf309; ORF310;
ORF335; ORF356; ORF399; ORF436; ORF488; ORF55; ORF564; ORF56b;
ORF59b; ORF62a; ORF64; ORF69; ORF73; orf76; ORF83a; ORF83b; ORF84a;
ORF84c; ORF90; ORF91; ORF94; ORF95; ORF98.
SOURCE
ORGANISM Sulfolobus virus SIRV-2
Sulfolobus virus SIRV-2
Virus; dsDNA viruses, no RNA stage; Rudiviridae; Rudivirus.
REFERENCE
AUTHORS 1
Peng, X., Blum, H., She, O., Mallok, S., Brugger, K., Garrett, R.A.,
Zillig, W. and Prangishvili, D.
TITLE Sequences and replication of genomes of the archaeal rudiviruses
SIRV1 and SIRV2: relationships to the archaeal lipotrichivirus SIVV
and some eukaryal viruses
JOURNAL Virology 291 (2), 226-234 (2001)
MEDLINE 21874820
PUBMED 11878892
REFERENCE 2 (bases 1 to 35450)
AUTHORS Peng, X.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2001) Peng X., Department of Biological
Chemistry, University of Copenhagen, Soelvgade 83H, 1307
Copenhagen, DENMARK
FEATURES
source
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1584. .1943
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Query Match 0.1%; Score 19; DB 1; Length 35450;
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LOCUS AF318573 108873 bp DNA linear VRL 18-MAY-2001
DEFINITION Bovine herpesvirus 4 long unique region, complete sequence.
ACCESSION AF318573 AF271211
VERSION AF318573.1 GI:12802528
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 108873)
Zimmermann,W., Broll,H., Ehlers,B., Buhk,H.J., Rosenthal,A. and
Golitz,M.
JOURNAL J. Virol. 75 (3), 1186-1194 (2001)
MEDLINE 20583805
PUBMED 11152491
REFERENCE 2 (bases 1 to 108873)
Zimmermann,W., Broll,H., Ehlers,B., Buhk,H.-J., Rosenthal,A. and
Golitz,M.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2000) Project P24, Robert Koch-Institut, Nordufer
20, Berlin D-10555, Germany
FEATURES
source
misc-feature
CDS
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicelloviruses.
 1 (bases 99702 to 103033)
 Wirth U.V., Fraefel,C., Vogt,B., Vlicek,C., Paces,V. and Schwyzer,M.
 Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1 are 3' coterminal and encode a putative zinc finger transactivator protein
 J. Virol. 66 (5), 2763-2772 (1992)
 JOURNAL MEDLINE 92219360
 PUBMED 1313901
 2 (bases 103034 to 111027, 127191 to 135300)
 Schwyzer,M., Vlicek,C., Menekse,O., Fraefel,C. and Paces,V.
 Promoter, spliced leader, and coding sequence for BICP4, the largest of the immediate-early proteins of bovine herpesvirus 1
 Virology 197 (1), 349-357 (1993)
 JOURNAL MEDLINE 94025583
 PUBMED 8212570
 3 (bases 111028 to 114234, 123984 to 127190)
 Schwyzer,M., Wirth,U.V., Vogt,B. and Fraefel,C.
 BICP22 of bovine herpesvirus 1 is encoded by a spliced 1.7 kb RNA which exhibits immediate early and late transcription kinetics
 J. Gen. Virol. 75 (Pt 7), 1703-1711 (1994)
 JOURNAL MEDLINE 94292919
 PUBMED 8021599
 4 (bases 66900 to 96900)
 Vlicek,C., Benes,V., Lu,Z., Kutish,G.F., Paces,V., Rock,D., Letchworth,G.J. and Schwyzer,M.
 Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus 1 genome which exhibits a collinear gene arrangement with the UL21 to UL4 genes of herpes simplex virus
 Virology 210 (1), 100-108 (1995)
 JOURNAL MEDLINE 95313343
 PUBMED 7793062
 5 (bases 1 to 31444)
 Schwyzer,M., Styger,D., Vogt,B., Lowery,D.E., Simard,C., Labotsiere,S., Mista,V., Vlicek,C. and Paces,V.
 Gene contents in a 31-kb segment at the left genome end of bovine herpesvirus-1
 Vet. Microbiol. 53 (1-2), 67-77 (1996)
 JOURNAL MEDLINE 97164286
 PUBMED 9010999
 Accession# 254206
 6 (bases 1 to 135301)
 Schwyzer,M., Paces,V., Letchworth,G.J., Mista,V., Buhk,H.J., Lowery,D.E., Simard,C., Bello,L.J., Thiry,E. and Vlicek,C.
 Complete DNA sequence of bovine herpesvirus 1
 Unpublished
 7 (bases 30801 to 67800)
 Schwyzer,M., Vlicek,C., Lowery,D.E., Bello,L.J., Meyer,G. and Mista,V.
 Gene contents in a 37-kb segment centered in the UL part of the bovine herpesvirus 1 genome: the last gap
 Unpublished
 Accession# 278205
 8 (bases 96901 to 99695)
 Letchworth,G.J. and Kutish,G.F.
 DNA sequence of the BHV-1 UL1 to UL3.5 genes
 Unpublished
 9 (bases 114235 to 122983)
 Goletz,M., Buhk,H.J., Broll,H., Lewin,M., Mankertz,A., Boerner,B., Borchers,K. and Weigelt,M.
 Nucleotide sequence of the HindIII O and K fragments located in the US region of the bovine herpesvirus 1 genome
 Unpublished
 Accession# 298199
 10 (bases 121402 to 123983)
 Schwyzer,M.
 Glycoprotein E and US9 genes of BHV1
 Unpublished
 JOURNAL MEDLINE 11 (bases 1 to 135301)
 Schwyzer,M.
 Direct Submission
 Submitted (08-SEP-1997) Institute of virology, Faculty of

FEATURES
 source Veterinary Medicine, University of Zurich, Winterthurerstrasse 266A, Zurich CH-8057, Switzerland
 Location/Qualifiers
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CDS
Query Match 0.1%; Score 19; DB 1; Length 135301;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 122895 GCTGGCAGCGCTTGCACG 122913
DB 85472 GCTGGCAGCGCTTGCACG 85454

RESULT 35
LOCUS YD1293568
DEFINITION Yaba-like disease virus (YADV), complete genome.
ACCESSION AJ2933568
VERSION AJ2933568.1 GI:1205159
YD1293568 144575 bp DNA linear VRL 30-MAY-2001
DEFINITION Yaba-like disease virus (YADV), complete genome.
ACCESSION AJ2933568
VERSION AJ2933568.1 GI:1205159
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106L gene; 107L gene; 108L gene; 109L gene; 10L gene; 113R gene;
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122R gene; 123R gene; 124R gene; 125R gene; 126R gene; 127R gene;
128L gene; 129R gene; 12L gene; 130L gene; 131R gene; 132R gene;
133L gene; 134R gene; 135R gene; 136R gene; 137R gene; 138R gene;
139R gene; 13L gene; 140R gene; 141R gene; 142R gene; 143R gene;
144R gene; 145R gene; 146R gene; 147R gene; 148R gene; 149R gene;
14L gene; 150R gene; 151R gene; 15L gene; 16L gene; 17L gene; 18L

REFERENCE
AUTHORS
JOURNAL
TITLE
Lee H.J., Essani K. and Smith G.L.
The genome sequence of Yaba-like disease virus, a yatapoxvirus
submitted (13-JUL-2000) Lee H.J., Sir William Dunn School of
Pathology, University of Oxford, South Parks road, Oxford, OX1 3RE,
UNITED KINGDOM
2
3 (bases 1 to 144575)
Lee H.J.
Direct Submission
Submitted (13-JUL-2000) Lee H.J., Sir William Dunn School of
Pathology, University of Oxford, South Parks road, Oxford, OX1 3RE,
UNITED KINGDOM
1. 144575
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/db_xref="taxon:132475"
complement(755. .1756)
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source
gene

SOURCE
ORGANISM
Yatapoxvirus.
Yabovirus.
Yabovirus: dsDNA viruses, no RNA stage: Poxviridae: Chordopoxvirinae;
Yatapoxvirus.
1
Lee H.J.
Theis (2000) Sir William Dunn School of Pathology, University of
Oxford, Oxford, UNITED KINGDOM
2
Lee H.J., Essani K. and Smith G.L.
The genome sequence of Yaba-like disease virus, a yatapoxvirus
submitted (13-JUL-2000) Lee H.J., Sir William Dunn School of
Pathology, University of Oxford, South Parks road, Oxford, OX1 3RE,
UNITED KINGDOM
2
3 (bases 1 to 144575)
Lee H.J.
Direct Submission
Submitted (13-JUL-2000) Lee H.J., Sir William Dunn School of
Pathology, University of Oxford, South Parks road, Oxford, OX1 3RE,
UNITED KINGDOM
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gene; 33L gene; 34L gene; 35L gene; 36R gene; 37R gene; 38R gene;
39L gene; 3L gene; 40R gene; 41L gene; 42L gene; 43L gene; 44L
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50L gene; 51L gene; 52R gene; 53L gene; 54R gene; 55R gene; 56R
gene; 57L gene; 58R gene; 59R gene; 5L gene; 60R gene; 61R gene;
62L gene; 63R gene; 64R gene; 65R gene; 66R gene; 67R gene; 68R
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74L gene; 75L gene; 76R gene; 77R gene; 78R gene; 79R gene; 7L
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protein; CD47-like protein; DNA helicase; DNA polymerase; DNA
polymerase processivity factor; DNA topoisomerase I; DNA-binding
phosphoprotein; DNA-binding protein; DNA-binding virion core
protein; DNA/RNA-binding protein; virio; dsRNA-binding protein an;
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anti-interfero; extracellular virus membran; extracellular virus
membrane protein; glutaredoxin 2; host range protein; interferon
alpha/beta receptor; interleukin-18 binding protein; intermediate
gene transcription facto; late gene transcription elongation factor; late
transcription factor-2; late transcription elongation factor; late
transcription factor; mda-7-like or interleukin-10-11k;
membrane-associated virion protein; monoglyceride lipase; mRNA
capping enzyme large subunit; mRNA capping enzyme small subunit;
Mull protein; myristylprotein; negative regulator of gene
expression; nucleoside triphosphat; poly(A) polymerase catalytic
subunit; poly(A) polymerase regulatory subunit; protease;
ribonucleotide reductase small subunit; RNA and DNA helicase; RNA
polymerase associated transcriptio; RNA polymerase elongation
factor; RNA polymerase subunit rpol13; RNA polymerase subunit
rpol147; RNA polymerase subunit rpol18; RNA polymerase subunit rpol19;
RNA polymerase subunit rpol22; RNA polymerase subunit rpol30; RNA
polymerase subunit rpol35; RNA polymerase subunit rpol7; role in
virus DNA packaging; secreted OX-2-like protein; secreted protein;
serine protease; serine protease inhibitor; serine/threonine
protein kinase; soluble MHC-I-like protein; ssDNA-binding
phosphoprotein; thymidine kinase; topoisomerase II; transmembrane
myristylprotein; transmembrane protein; tyrosine/serine
phosphatase; uracil DNA glycosylase; virion core structural protein
p44; virion membrane protein; virion protein; virion structural
core protein; virion structural protein; virion surface protein;
virulence factor; virion growth factor.
Yaba-like disease virus
Yaba-like disease virus
Yabovirus: dsDNA viruses, no RNA stage: Poxviridae: Chordopoxvirinae;
Yatapoxvirus.

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 Db 7826 AAAATTAAAAATTAATA 7844

RESULT 36
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 ACCESSION X14112 D00317 D00317 D10879 S40593
 VERSION X14112.1 GI:1944536
 KEYWORDS capsid associated tegument protein; capsid protein; complete genome; deoxyribonuclease; deoxyuridine triphosphatase; DNA polymerase; envelope protein; herpes simplex virus; host shut-off factor; immediate early protein; integral membrane protein; IRS; LAT; latency associated transcript; major capsid protein; membrane associated phosphoprotein; minor capsid protein; myristylated tegument protein; neurovirulence factor; neurovirulence factor (ICP34.5); protease; protein kinase; ribonucleotide reductase large subunit; ribonucleotide reductase small subunit; RL1 gene; RL2 gene; RSL gene; subunit of replicative DNA polymerase; tegument protein; tegument/envelope protein; thymidine kinase; TRL; TRS; UL; UL1 gene; UL10 gene; UL11 gene; UL12 gene; UL13 gene; UL14 gene; UL15 gene; UL16 gene; UL17 gene; UL18 gene; UL19 gene; UL2 gene; UL20 gene; UL21 gene; UL22 gene; UL23 gene; UL24 gene; UL25 gene; UL26 gene; UL26.5 gene; UL27 gene; UL28 gene; UL29 gene; UL3 gene; UL30 gene; UL31 gene; UL32 gene; UL33 gene; UL34 gene; UL35 gene; UL36 gene; UL37 gene; UL38 gene; UL39 gene; UL4 gene; UL40 gene;

UL41 gene; UL42 gene; UL43 gene; UL44 gene; UL45 gene; UL46 gene; UL47 gene; UL48 gene; UL49 gene; UL49A gene; UL5 gene; UL50 gene; UL51 gene; UL52 gene; UL53 gene; UL54 gene; UL55 gene; UL56 gene; UL6 gene; UL7 gene; UL8 gene; UL9 gene; urc1L-DNA glycosylase; US; US1 gene; US10 gene; US11 gene; US12 gene; US2 gene; US3 gene; US4 gene; US5 gene; US6 gene; US7 gene; US8 gene; US8A gene; US9 gene; very large tegument protein; viron glycoprotein B; viron glycoprotein C; viron glycoprotein D; viron glycoprotein E; viron glycoprotein G; viron glycoprotein H; viron glycoprotein I; viron glycoprotein J; viron glycoprotein K; viron glycoprotein L; viron glycoprotein M; viron protein; viron protein UL47.

SOURCE
ORGANISM Human herpesvirus 1
Virus: dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.
1 (bases 132605 to 145883)
McGeoch,D.J., Dolan,A., Donald,S. and Rixon,F.J.
Sequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1
J. Mol. Biol. 181 (1), 1-13 (1985)
2984429

REFERENCE
AUTHORS McGeoch,D.J., Dolan,A., Donald,S. and Brauer,D.H.
TITLE Complete DNA sequence of the short repeat region in the genome of herpes simplex virus type 1
JOURNAL Nucleic Acids Res. 14 (4), 1727-1745 (1986)
MEDLINE 86148504
PUBMED 3005980

REFERENCE
AUTHORS McGeoch,D.J., Dalrymple,M.A., Davison,A.J., Dolan,A., Frame,M.C., McAb,D., Perry,L.J., Scott,J.E. and Taylor,P.
TITLE The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1
J. Gen. Virol. 69 (Pt 7), 1531-1574 (1988)
88274327
2839594

JOURNAL
MEDLINE 88274327
PUBMED 2839594
TITLE 4 (bases 113322 to 126373)
Perry,L.J. and McGeoch,D.J.
The DNA sequences of the long repeat region and adjoining parts of the long unique region in the genome of herpes simplex virus type 1
J. Gen. Virol. 69 (Pt 11), 2831-2846 (1988)
89036163

JOURNAL
MEDLINE 89036163
PUBMED 2846760
TITLE 5
Dolan,A., McKie,E., Maclean,A.R. and McGeoch,D.J.
Status of the ICP34.5 gene in herpes simplex virus type 1 strain 17
J. Gen. Virol. 73 (Pt 4), 971-973 (1992)
92341080

JOURNAL
MEDLINE 92341080
PUBMED 1321882
TITLE 6
McGeoch,D.J.
Direct Submission
Submitted (17-JAN-1989) McGeoch D.J., MRC Virology Institute, Institute of Virology, Church Street, Glasgow G11 5JR, GB
Revised by [7]
7 (bases 1 to 152201)
Dolan,A.
Direct Submission
Submitted (16-APR-1997) Dolan A., MRC Virology Institute, Institute of Virology, Church Street, Glasgow G11 5JR, GB
On or before Apr 24, 2003 this sequence version replaced gi:221721, gi:221712, gi:251863, gi:59499.
See also x06461 and x02138.
Residues 1 - 8661 and 148674 - 152260 of TR-L and TR-S, resp. have not been sequenced but are derived from IR-L and IR-S sequences.

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LTR
exon


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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 38
AF533768/c AF533768 156789 bp DNA linear VRL 19-MAY-2003
DEFINITION Cercopithecine herpesvirus 1 strain E2490, complete genome.
ACCESSION AF533768
VERSION AF533768.1 GI:30844242
KEYWORDS
SOURCE Cercopithecine herpesvirus 1 (monkey B virus)
ORGANISM Cercopithecine herpesvirus 1
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 156789)
Pereelygina,L., Zhu,L., Zurkuhlen,H., Mills,R., Borodovsky,M. and
Hilliard,J.K.
Complete sequence and comparative analysis of the genome of herpes
B virus (cercopithecine herpesvirus 1) from a rhesus monkey
J. Virol. 77 (11), 6167-6177 (2003)

TITLE
JOURNAL
MEDLINE 22628476
PUBMED 12743273
2 (bases 1 to 156789)
Pereelygina,L., Zhu,L., Zurkuhlen,H. and Hilliard,J.
AUTHORS Direct Submission
TITLE Submitted (31-JUL-2002) Department of Biology, Georgia State
JOURNAL University, 24 Peachtree Center Ave, Atlanta, GA 30303, USA
FEATURES
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Query Match 0.1%; Score 19; DB 1; Length 156789;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122053 GGGGCGCGGCGGCGGCGC 122071
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Db 63159 GGGGCGCGGCGGCGGCGC 63141

RESULT 39
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LOCUS AF250284 Amsacta moorei entomopoxvirus, complete genome.
DEFINITION AF250284
ACCESSION AF250284
VERSION AF250284.1 GI:9944523
KEYWORDS
SOURCE
ORGANISM
Amsacta moorei entomopoxvirus
Amsacta moorei entomopoxvirus
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
1 (bases 1 to 232392)
Bawden,A.L., Glassberg,K.J., Digdags,J., Shaw,R., Farmerie,W. and
Moyer,R.W.
Complete genomic sequence of the Amsacta moorei entomopoxvirus:
analysis and comparison with other poxviruses
Virology 274 (1), 120-139 (2000)
20396580
PUBMED 10936094
REFERENCE
2 (bases 1 to 232392)
Bawden,A.L., Glassberg,K.J., Digdags,J., Shaw,R., Farmerie,W. and
Moyer,R.W.
Submitted (28-MAR-2000) Molecular Genetics and Microbiology,
University of Florida, P.O. Box 100266, Gainesville, FL 32610, USA
JOURNAL
TITLES
FEATURES
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       220583 AAAATAAAAAATAATGT 220565

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LOCUS      HSEIE1
DEFINITION Equine herpesvirus type 1 immediate-early protein (IE) gene, 5'
flank.
ACCESSION M30497
VERSION M30497.1 GI:330906
KEYWORDS immediate-early protein.
SEGMENT 1 of 2
SOURCE Equine herpesvirus 1
ORGANISM Equine herpesvirus 1
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE 1 (bases 1 to 780)
AUTHORS Hartley R.N., Colle C.F., Grundy F.J. and O'Callaghan D.J.
TITLE Mapping the termini and intron of the spliced immediate-early
transcript of equine herpesvirus 1
JOURNAL J. Virol. 63 (12), 5101-5110 (1989)
MEDLINE 90064773
PUBMED 2555546
COMMENT Original
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      123181 TACCTGTATCTTTAAC 123198
Db      550 TACCTGTATCTTTAAC 567
DEFINITION
AF347327      1175 bp      RNA      linear      VRL 12-JUN-2002
LOCUS      HIV-1 isolate 981681 from Germany pol protein (pol) gene, partial
cds.
AF347327
AF347327.1      GI:13604763
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
1 (bases 1 to 1175)
Human immunodeficiency virus 1 (HIV-1)
Human immunodeficiency virus 1
Viruses; Retroviruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 1175)
Beerenwinkel,N., Schmidt,B., Walter,H., Kaiser,R., Lengauer,T.,
Hofmann,D., Korn,K. and Selbig,J.
Diversity and complexity of HIV-1 drug resistance: a bioinformatics
approach to predicting phenotype from genotype
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8271-8276 (2002)
JOURNAL
MEDLINE
PUBMED
12056123
12060770
2 (bases 1 to 1175)
Schmidt,B., Walter,H., Moschik,G., Patz,C., Weweln,M.,
Schwengel,E. and Korn,K.
Recovery of HIV-1 pol gene sequences by direct sequencing of
amplification products derived from plasma samples
Unpublished
3 (bases 1 to 1175)
Schmidt,B., Walter,H., Moschik,G., Patz,C., Weweln,M.,
Schwengel,E. and Korn,K.
Direct Submission
Submitted (08-FEB-2001) German National Reference Center for
Retroviruses, Institute of Clinical and Molecular Virology,
Schlossgarten 4, Erlangen 91054, Germany
location/Qualifiers
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DB	641	ACTTTGCAGTTCCTTAG	658		
RESULT 45					
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LOCUS	HS1ICP345B		1346 bp	DNA	linear
DEFINITION	Herpes simplex virus type 1 infected-cell protein (ICP34.5) gene,				
ACCESSION	M33700				
VERSION	M33700.1		GI:330116		
KEYWORDS	Infected-cell protein 34.5; neurovirulence factor.				
SOURCE	Human herpesvirus 1				
ORGANISM	Human herpesvirus 1				
REFERENCE	Alphaherpesvirinae; Simplexvirus.				
AUTHORS	1 (bases 1 to 1346)				
TITLE	Chou, J. and Roizman, B.				
JOURNAL	The herpes simplex virus 1 gene for ICP34.5, which maps in inverted				
MEDLINE	repeats, is conserved in several limited-passages isolates but not				
PUBMED	in strain 17syn+				
COMMENT	J. Virol. 64 (3), 1014-1020 (1990)				
	Original source text: Herpes simplex virus type 1 (strain MGH-10)				
	DNA.				
	Draft entry and computer-readable sequence for [1] kindly submitted				
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Search completed: September 30, 2003, 03:36:52
Job time : 429 secs

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Db	49020	CGAGGATTTATGTTTGTGGCTTGAGATATGGCCACCAGCGTCGTACACTTCTTAAT	49079
QY	49080	CGTTTTTAAACAGGAATGCATATGTTGCGACACCCGGGTACGTCGCGTTTGGTGGG	49139
Db	49080	CGTTTTTAAACAGGAATGCATATGTTGCGACACCCGGGTACGTCGCGTTTGGTGGG	49139
QY	49140	TATACACGCGACACACTGCGCATTCGCGCTTTTGGACCGCGGTAACTAAGCAAAATG	49199
Db	49140	TATACACGCGACACACTGCGCATTCGCGCTTTTGGACCGCGGTAACTAAGCAAAATG	49199
QY	49200	CGATGTCACCTAACCTTTTAAATGTTATGATCGTAATCATGAACCAAAAGAAATTGGGC	49259
Db	49200	CGATGTCACCTAACCTTTTAAATGTTATGATCGTAATCATGAACCAAAAGAAATTGGGC	49259
QY	49260	CGTGCCTTACCGTGTACATGAATGAGATATTTCTAGATTTTGTGCCACGGAACTGTGC	49319
Db	49260	CGTGCCTTACCGTGTACATGAATGAGATATTTCTAGATTTTGTGCCACGGAACTGTGC	49319
QY	49320	CCATTAAGGAGCGTGCCTGTGATGGCGGACCTGTGTTAATTCGTTTGGTATACCTTTCTA	49379
Db	49320	CCATTAAGGAGCGTGCCTGTGATGGCGGACCTGTGTTAATTCGTTTGGTATACCTTTCTA	49379
QY	49380	ATGGCGCGAGAGGCTTCCGATTCGCGGCGGCTTGAACCCCATCCGCGGAGAAACGCTGC	49439
Db	49380	ATGGCGCGAGAGGCTTCCGATTCGCGGCGGCTTGAACCCCATCCGCGGAGAAACGCTGC	49439
QY	49440	CCGGGCTAAACAAACAGAAATTTATACACTTCGCAAAAGTGCCTCAAGAGGACAGATAC	49499
Db	49440	CCGGGCTAAACAAACAGAAATTTATACACTTCGCAAAAGTGCCTCAAGAGGACAGATAC	49499
QY	49500	CAGATGCCATTAAGGGGAAAGAGTTCCACCAATAATTCGTTTTTGTGTTTACGGAG	49559
Db	49500	CAGATGCCATTAAGGGGAAAGAGTTCCACCAATAATTCGTTTTTGTGTTTACGGAG	49559
QY	49560	GGGGGTTTGGCACTGTTCTCTGTGATTTTATAGTCTGCTGTCCGCACTGCACA	49619
Db	49560	GGGGGTTTGGCACTGTTCTCTGTGATTTTATAGTCTGCTGTCCGCACTGCACA	49619
QY	49620	CAGTTCCGTCCTGCGCAGAAATCGTTGGGCTTTTACACAGTGGCATTAAGACACGTGA	49679
Db	49620	CAGTTCCGTCCTGCGCAGAAATCGTTGGGCTTTTACACAGTGGCATTAAGACACGTGA	49679
QY	49680	AAATTTGTACGGGGGCCCAAGTACAGTTAAACCCGATATGCGGATACAGCCACCTGACT	49739
Db	49680	AAATTTGTACGGGGGCCCAAGTACAGTTAAACCCGATATGCGGATACAGCCACCTGACT	49739
QY	49740	CGCAAGGAGNCCTACCTGCTGGCCCTGCTTATCTGTCGGGGCGACGGCGGGCGG	49799
Db	49740	CGCAAGGAGNCCTACCTGCTGGCCCTGCTTATCTGTCGGGGCGACGGCGGGCGG	49799
QY	49800	ATGTCCTGGTTTACCGGACAGTTAACTTTTGGGCGCTGCTTGTGACCCCAAGCCTCC	49859
Db	49800	ATGTCCTGGTTTACCGGACAGTTAACTTTTGGGCGCTGCTTGTGACCCCAAGCCTCC	49859
QY	49860	CCAAAGTACCAAGCTGCGTTTAAAGAAACCACCGCCGATACCGATAGAGAGCGCA	49919
Db	49860	CCAAAGTACCAAGCTGCGTTTAAAGAAACCACCGCCGATACCGATAGAGAGCGCA	49919
QY	49920	TGTCGGGGCGTACAGGGCGGAAAGGACCGAGGTGCAACCACTTCGTAACGCTGGCCCTCA	49979
Db	49920	TGTCGGGGCGTACAGGGCGGAAAGGACCGAGGTGCAACCACTTCGTAACGCTGGCCCTCA	49979
QY	49980	TTTCGCCGTCCGGAATTTAAGCCAGTACGCGGTATGCTATACGGGCTCCAGAACTTAAAGCA	50039
Db	49980	TTTCGCCGTCCGGAATTTAAGCCAGTACGCGGTATGCTATACGGGCTCCAGAACTTAAAGCA	50039
QY	50040	TCGTGTTAGCTTCTTATTGAGCAGTCCGACACATACAGGAATCTGGCGCGCTCCGG	50099
Db	50040	TCGTGTTAGCTTCTTATTGAGCAGTCCGACACATACAGGAATCTGGCGCGCTCCGG	50099
QY	50100	GCTCGGGTACAGATGCTTCGCTTTCCTTATGTTCAAGTTCTTGCGCGGAAACA	50159
Db	50100	GCTCGGGTACAGATGCTTCGCTTTCCTTATGTTCAAGTTCTTGCGCGGAAACA	50159
QY	50160	CCTGATATAGCGTGGCATGACCTTCGGAGAAACGGCATTTGGCGACGTGTTTGGTGGG	50219
Db	50160	CCTGATATAGCGTGGCATGACCTTCGGAGAAACGGCATTTGGCGACGTGTTTGGTGGG	50219
QY	50220	CACGTAAACCAAGTGAACGTTTTCACACCGACGAGAAAGCGTATATATGGCCACAC	50279
Db	50220	CACGTAAACCAAGTGAACGTTTTCACACCGACGAGAAAGCGTATATATGGCCACAC	50279
QY	50280	GATCCATGTTTTCCCGTGAACGAGCGGGATTAACAAAAGCGTGTCTGCTTAAACGT	50339
Db	50280	GATCCATGTTTTCCCGTGAACGAGCGGGATTAACAAAAGCGTGTCTGCTTAAACGT	50339
QY	50340	CTGTAAACAGTGTGCTCGGTGTTTCAAAATAAACCAAGGTGTGCTTAAACGTGGCAATTA	50399
Db	50340	CTGTAAACAGTGTGCTCGGTGTTTCAAAATAAACCAAGGTGTGCTTAAACGTGGCAATTA	50399
QY	50400	CTGGTGTGCTTTTCCGGGTGCTTGTATAGACGGGATTAATAACGTGTGCATGTATTA	50459
Db	50400	CTGGTGTGCTTTTCCGGGTGCTTGTATAGACGGGATTAATAACGTGTGCATGTATTA	50459
QY	50460	TTGTTTGTGAAGAGGCTCAAGGACAAACCCGGGACAGTAACTCCATTTAAATAATGA	50519
Db	50460	TTGTTTGTGAAGAGGCTCAAGGACAAACCCGGGACAGTAACTCCATTTAAATAATGA	50519
QY	50520	CGACAGGTTGGCTAAAAACCTGCGCGAGTTCGTGATTAAGGGGCACTTAGGAAACCTTC	50579
Db	50520	CGACAGGTTGGCTAAAAACCTGCGCGAGTTCGTGATTAAGGGGCACTTAGGAAACCTTC	50579
QY	50580	GTCGGTCCGTTGGGCGGATTTGATTCATGATCTGCTTGGGCTTTGGCATTTGGAC	50639
Db	50580	GTCGGTCCGTTGGGCGGATTTGATTCATGATCTGCTTGGGCTTTGGCATTTGGAC	50639
QY	50640	CCGACAAACATGTTTGTAAAGTAGTTTGTGATTTCTCGGTTTAAACCGGGCAACGTAAC	50699
Db	50640	CCGACAAACATGTTTGTAAAGTAGTTTGTGATTTCTCGGTTTAAACCGGGCAACGTAAC	50699
QY	50700	GTCGCTAGAATTCGGGGCTTTCACAGCTAAGGGCGCGCATGCGTTCTTGAACCTCTCG	50759
Db	50700	GTCGCTAGAATTCGGGGCTTTCACAGCTAAGGGCGCGCATGCGTTCTTGAACCTCTCG	50759
QY	50760	GTCAGTTTAAAGTATATCTGCTTAAACCAAGCACTATGTGATTAACCGGCTGAATATCTCC	50819

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Db 50760 GTACCTTTGAGATATATGCTGTAAGCAAGAACTATATGATTAACCGCGTGAATACCTCC 50819
Oy 50820 CAAGCATGGGTGGCCATTTCGTCGTCCTGTCGTTGGCCGATATATATACGGCGGTG 50879
Db 50820 CAAGCATGGGTGGCCATTTCGTCGTCCTGTCGTTGGCCGATATATATACGGCGGTG 50879
Oy 50880 CCGAAGACAATTTGCGCAACACCGCTCGTGACCAACGCGCAAGTTATTTTGAAGACGTTG 50939
Db 50880 CCGAAGACAATTTGCGCAACACCGCTCGTGACCAACGCGCAAGTTATTTTGAAGACGTTG 50939
Oy 50940 GCGATAGCTGGTTAACAACATGTCCTTCAGTTTGTGATTAACGGGACCCCGCAAC 50999
Db 50940 GCGATAGCTGGTTAACAACATGTCCTTCAGTTTGTGATTAACGGGACCCCGCAAC 50999
Oy 51000 GGAACGCGCTTCGTTAAAGGCGTTCAGTTTGTGATTAACGGGACCCCGCAAC 51059
Db 51000 GGAACGCGCTTCGTTAAAGGCGTTCAGTTTGTGATTAACGGGACCCCGCAAC 51059
Oy 51060 ACAGTTTAACTAGTTGAAGCAACCTCTTAAATGTTTCTTCTGATCCACAGCTTCGCC 51119
Db 51060 ACAGTTTAACTAGTTGAAGCAACCTCTTAAATGTTTCTTCTGATCCACAGCTTCGCC 51119
Oy 51120 GGAATCGGCGCGGTTAGAGACTGTCGCGACGCGGAAGGTTTGACTTTGAACACATTTCA 51179
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Db 51300 TCTGCGCATGGACAGCAAGTAATGGGCGCTTCACGTTAAAGAAAGACAAGTGGT 51359
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Db 51420 TCCCTTACCGCTCATATGCGCTCTGTTTACGCTCCGCGTCTGTCGCGGAACACGA 51479
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Oy 51540 TGCCCCCAAAAGAGCATATGACTTTTGTCCATCATGTAAATTAAGTAAATTTT 51599
Db 51540 TGCCCCCAAAAGAGCATATGACTTTTGTCCATCATGTAAATTAAGTAAATTTT 51599
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Db 51600 ATAGGTGAACCGCGGTGGGGGCTGGAACGTAACCGTCCCGCGCTGAGCGCTCGG 51659
Oy 51660 GTTGGCGCAGCAATCGCTCGCTCGGGAGCGTGAACGATGACGATACCTCTCGC 51719
Db 51660 GTTGGCGCAGCAATCGCTCGCTCGGGAGCGTGAACGATGACGATACCTCTCGC 51719
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Db 51720 AAAAGCATGTTGTGTCACCTGTACAGCAAAAAGCATAGATTTGATTCATGAACACA 51779
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Db 52020 CCGAGCTCGAGTCGGAATTAACAAAAAATCTCCATCTCCGATATTTGACAGTTGGGG 52079
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Db 52080 ACAGCTTAAAAAAGAAAGACATCTGCGACCGCTTGTGGAAGCTAGAAAGTGCCTG 52139
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Oy 52560 GGCCTGCTGATTAACGATTTTGGACGCGCGCTGATTTTACGAGTGCATTTTAAAC 52619
Db 52560 GGCCTGCTGATTAACGATTTTGGACGCGCGCTGATTTTACGAGTGCATTTTAAAC 52619
Oy 52620 GATATAGTACGCGCTGCGGAGAAACATCCCTGAACCGCGGAGTACCGTATACGA 52679
Db 52620 GATATAGTACGCGCTGCGGAGAAACATCCCTGAACCGCGGAGTACCGTATACGA 52679
Oy 52680 TGTTCCTAGAGCGCGGTGATCATGTCGCGCTGATTTTCCGAGTAAACAGAGAA 52739
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Oy 52740 CTGCTAAACGCGGATCTTAACACGTAACCTGGAACGCGTGGCGTGAATTCCTGAG 52799
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Oy 52780 CTGCTAAACGCGGATCTTAACACGTAACCTGGAACGCGTGGCGTGAATTCCTGAG 52839
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Db 52800 CTGAGGAGAGCGGATTTTCTTAATATATATGTCGATGTCCTGACATGATCACT 52859
Oy 52860 CCAGAAATATATCTATTAAGGGAACGTAACCTGGAACGCGTGGCGTGAATTCCTGAG 52919
Db 52860 CCAGAAATATATCTATTAAGGGAACGTAACCTGGAACGCGTGGCGTGAATTCCTGAG 52919
Oy 52920 GATCTAGGTCGCGCTCTTTACACAGGGAACCTTGGACGAGTGTGATGACCTCC 52979
Db 52920 GATCTAGGTCGCGCTCTTTACACAGGGAACCTTGGACGAGTGTGATGACCTCC 52979
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OY	52980	AAACTGGGTTTCGTGCAGCACACGTAACCATTTTAAAGCACCGGCGCAGATTTATCTGAAG	53039
Db	52980	AAACTCGGGTTTCGTGCAGCACACGTAACCATTTTAAAGCACCGGCGCAGATTTATCTGAAG	53039
OY	53040	CACATTTACGGGGCGTCGTCTCCTACCCGCTGTCTGTCTGTGGCGGGGGGGCCG	53099
Db	53040	CACATTTACGGGGCGTCGTCTCCTACCCGCTGTCTGTCTGTGGCGGGGGGGCCG	53099
OY	53100	CAGGCGCATATGCTAAATCAGCCGTTTCCAAATACCTCCACAACCTGCGTCCAAATTTGAC	53159
Db	53100	CAGGCGCATATGCTAAATCAGCGGTTTCCAAATACCTCCACAACCTGCGTCCAAATTTGAC	53159
OY	53160	ATATTCGTCCCTGGGTTTATGTTTGTACATGCTCTAGAAATATCTTAGCCAGCTGAC	53219
Db	53160	ATATTCGTCCCTGGGTTTATGTTTGTACATGCTCTAGAAATATCTTAGCCAGCTGAC	53219
OY	53220	CCATTTTCCCGACGAGGAGGCGTTGGGGGAGCGTCTCCGAAATCCGCCACCATTTGTTTC	53279
Db	53220	CCATTTTCCCGACGAGGAGGCGTTGGGGGAGCGTCTCCGAAATCCGCCACCATTTGTTTC	53279
OY	53280	TATTTGCGTTGTCATGTTGTCACAGATGATCATCCCGAGATTTTTCGTGGCTGGGAC	53339
Db	53280	TATTTGCGTTGTCATGTTGTCACAGATGATCATCCCGAGATTTTTCGTGGCTGGGAC	53339
OY	53340	GTTTCCACTGCATTTTAGGCATATGCTCATCTGCGGCACGGGCGCAGATATCCCTGGAGAGA	53399
Db	53340	GTTTCCACTGCATTTTAGGCATATGCTCATCTGCGGCACGGGCGCAGATATCCCTGGAGAGA	53399
OY	53400	GCGTCACAGGGCGTTTTTGTGCCAACCAAGTAGTATTATATAGGGCGCAATACAAAGAGAT	53459
Db	53400	GCGTCACAGGGCGTTTTTGTGCCAACCAAGTAGTATTATATAGGGCGCAATACAAAGAGAT	53459
OY	53460	GCGTTTACAAAACGCATCCTCGGGCGTGTGTAATCTAAACTTAACTAGTCTCCAGAG	53519
Db	53460	GCGTTTACAAAACGCATCCTCGGGCGTGTGTAATCTAAACTTAACTAGTCTCCAGAG	53519
OY	53520	CTGTTGGTCAAGGAGACTACTTTAATCATTCATGCGGAAATCGCGGAGATCATGATTTTTCGC	53579
Db	53520	CTGTTGGTCAAGGAGACTACTTTAATCATTCATGCGGAAATCGCGGAGATCATGATTTTTCGC	53579
OY	53580	AGATGAGCCGATGTTTCAGGAGATGGCGCTTCTCCACATTCGATGAGCAGCAGCGCTCT	53639
Db	53580	AGATGAGCCGATGTTTCAGGAGATGGCGCTTCTCCACATTCGATGAGCAGCAGCGCTCT	53639
OY	53640	CTCGAAATAGCGCTGGCCAACTTTTAAACATAGCAGATAGGAGCGCTTTTAAAGCA	53699
Db	53640	CTCGAAATAGCGCTGGCCAACTTTTAAACATAGCAGATAGGAGCGCTTTTAAAGCA	53699
OY	53700	TAAACAAAAGAAATAAGATGCGCGCTATACGGTTCTGTATTAATTTTATCTATTCGC	53759
Db	53700	TAAACAAAAGAAATAAGATGCGCGCTATACGGTTCTGTATTAATTTTATCTATTCGC	53759
OY	53760	CAAGGTGGGAGATTTTATCGGCAACACCGACGTCAGATTTTACGTACATGGGTGT	53819
Db	53760	CAAGGTGGGAGATTTTATCGGCAACACCGAGTCAGATTTTATGTAAGTACATGGGTGT	53819
OY	53820	CAGGGGAGGCGCTGCAGCGCGCTGTGCGAAGTGTACGACGCGGTGCTTAACATGCACC	53879
Db	53820	CAGGGGAGGCGCTGCAGCGCGCTGTGCGAAGTGTACGACGCGGTGCTTAACATGCACC	53879
OY	53880	GCACGATTCGACACACAGCTGTGTGTCATTTGATAGAAACAGTCCAGCGGGCCAAAACATCAA	53939
Db	53880	GCACGATTCGACACACAGCTGTGTGTCATTTGATAGAAACAGTCCAGCGGGCCAAAACATCAA	53939
OY	53940	TCCCTCTGTGGAGCGTCTGAGGAGCGGCAATATTTGCTGTCGTCAAAATTTCACTGGGCCAT	53999
Db	53940	TCCCTCTGTGGAGCGTCTGAGGAGCGGCAATATTTGCTGTCGTCAAAATTTCACTGGGCCAT	53999
OY	54000	AAAAACAACAGATTTCTGCCAAAAAATTTTAAACCCGTGGCCTATATGTCACAAATCATTT	54059
Db	54000	AAAAACAACAGATTTCTGCCAAAAAATTTTAAACCCGTGGCCTATATGTCACAAATCATTT	54059

QY	54060	TGTAGCGGGCCCGCTGCGCTTGTGAGACTGCGTTGCCAGAGATGCTTAAAAAGATACTGGC	54119
Db	54060	TGTAGCGGGCCCGCTGCGCTTGTGAGACTGCGTTGCCAGAGATGCTTAAAAAGATACTGGC	54119
QY	54120	GAGTTGCTCCTATCCAGGGGAGCGACGTGTGAATACTAGGATTCATGACGAGTCCT	54179
Db	54120	GAGTTGCTCCTATCCAGGGGAGCGACGTGTGAATACTAGGATTCATGACGAGTCCT	54179
QY	54180	CAACGGGGTTTTGGGGTCTCCTTGGATTTTGGAAATTAACGTCAAGTCTGCACCCAAAGA	54239
Db	54180	CAACGGGGTTTTGGGGTCTCCTTGGATTTTGGAAATTAACGTCAAGTCTGCACCCAAAGA	54239
QY	54240	CGGTTTGGAGTTTCACCCAGACTGCAAAATCTATGAATTAATCCCGGTTTAACTACAC	54299
Db	54240	CGGTTTGGAGTTTCACCCAGACTGCAAAATCTATGAATTAATCCCGGTTTAACTACAC	54299
QY	54300	TTTTTCCAAATGAGCTGTGACCCGATTTAACCTGGTATTCGTAAACCTTTATCCAAACC	54359
Db	54300	TTTTTCCAAATGAGCTGTGACCCGATTTAACCTGGTATTCGTAAACCTTTATCCAAACC	54359
QY	54360	CAGCATGCAGACGCTTAAAGGGTTTTTGTACTCCATATCTAAACCGCGATCGAGTTTGT	54419
Db	54360	CAGCATGCAGACGCTTAAAGGGTTTTTGTACTCCATATCTAAACCGCGATCGAGTTTGT	54419
QY	54420	CGGAGAGACAGGCTCCCAAGTGAATCGGACTATCTTGTGGCATATGACAAAGATGGGA	54479
Db	54420	CGGAGAGACAGGCTCCCAAGTGAATCGGACTATCTTGTGGCATATGACAAAGATGGGA	54479
QY	54480	GGTGTGCCCGGGAAAAAGAGACGCTTAACTGCAGTACACCATCTAAGTTAAAAAGTGAT	54539
Db	54480	GGTGTGCCCGGGAAAAAGAGACGCTTAACTGCAGTACACCATCTAAGTTAAAAAGTGAT	54539
QY	54540	GATTACACAATCTACGGCGCCTTCTATGTGTATATATGTAGATTCGCGAGAAACCGG	54599
Db	54540	GATTACACAATCTACGGCGCCTTCTATGTGTATATATGTAGATTCGCGAGAAACCGG	54599
QY	54600	AGGCGAAATTAATTAATTAAGCTCATCTGAGCGCAACCTATTATTAACGTCAGGCACTCC	54659
Db	54600	AGGCGAAATTAATTAATTAAGCTCATCTGAGCGCAACCTATTATTAACGTCAGGCACTCC	54659
QY	54660	GTAATTATTACAGTGTGTCTCAGTCTCTCGTTGTACAGAGGTACATCAGTCTCCAA	54719
Db	54660	GTAATTATTACAGTGTGTCTCAGTCTCTCGTTGTACAGAGGTACATCAGTCTCCAA	54719
QY	54720	GGGAATTAATAATTTGGGAACCCAGAAAACTTTATAGGACTGGCTTTTATAGAAAACG	54779
Db	54720	GGGAATTAATAATTTGGGAACCCAGAAAACTTTATAGGACTGGCTTTTATAGAAAACG	54779
QY	54780	GCAAGTTTCAAGACCGAGTGTGTGACAGTCGGTGAATTTGCCCGGTTGGATCCACAGT	54839
Db	54780	GCAAGTTTCAAGACCGAGTGTGTGACAGTCGGTGAATTTGCCCGGTTGGATCCACAGT	54839
QY	54840	AGAGATACGACACCTTTTAATGTGTGACACCGGTGATTTTCCACGTCGGCCAAACCA	54899
Db	54840	AGAGATACGACACCTTTTAATGTGTGACACCGGTGATTTTCCACGTCGGCCAAACCA	54899
QY	54900	ACTGTGAACAGCAGCGACCGCAATTCGGCGGGGTAGTGTGTTGAGGCAATTTCCGAGCT	54959
Db	54900	ACTGTGAACAGCAGCGACCGCAATTCGGCGGGGTAGTGTGTTGAGGCAATTTCCGAGCT	54959
QY	54960	ACCATGGAGTTTATCTCTCTGTGTGCAACAGCCGCCACCAACACCGCTAGATGTGAAGGG	55019
Db	54960	ACCATGGAGTTTATCTCTCTGTGTGCAACAGCCGCCACCAACACCGCTAGATGTGAAGGG	55019
QY	55020	GAGCCATAGATGTATCCAAAGATTCGATCTTATATAGGAGAAAGCATGTCTTGG	55079
Db	55020	GAGCCATAGATGTATCCAAAGATTCGATCTTATATAGGAGAAAGCATGTCTTGG	55079
QY	55080	TTAAAGGCAGATGGAGTCGGCCCGGGGGCGGTGTCAAAACCCAAACCAAGCATCCAA	55139
Db	55080	TTAAAGGCAGATGGAGTCGGCCCGGGGGCGGTGTCAAAACCCAAACCAAGCATCCAA	55139
QY	55140	CATTAACCAATTAATTAATGTGCAGATTTTGTATTAAGCATTCGTATCTTATATGAGTGGGGT	55199

Db	55140	CAATAAAACAATAATTTGTCAGATTTTGTGTTAAGCATTCGTATCTTTATTTGAGATGGGCT	55199	
Qy	55200	GGATGGTGGGGGTGGGAAGGGAATGGGATTTGAGGGAGAGATGAATGCTGAATCATATA	55259	
Db	55200	GGATGGTGGGGGTGGGAAGGGAATGGGATTTGAGGGAGAGATGAATGCTGAATCATATA	55259	
Qy	55260	TGTATTTTGGATATGATCCTCTGTAATGCGTACAGCTCTTCTCTGTTTCAATATTAACGCT	55319	
Db	55260	TGTATTTTGGATATGATCCTCTGTAATGCGTACAGCTCTTCTCTGTTTCAATATTAACGCT	55319	
Qy	55320	TCAGTTCGGGGAGACTTAATCTTTGTCGTCTTCCTTTAGGGCTTGAGAGAGGGCTG	55379	
Db	55320	TCAGTTCGGGGAGACTTAATCTTTGTCGTCTTCCTTTAGGGCTTGAGAGAGGGCTG	55379	
Qy	55380	CGFATTTGGGGACCTTTGGGCACATTTCCAACTGTTTCTGATTAATCTTTAAGATGATGG	55439	
Db	55380	CGFATTTGGGGACCTTTGGGCACATTTCCAACTGTTTCTGATTAATCTTTAAGATGATGG	55439	
Qy	55440	CTAGATGCAAGTGTATCGGAATCATAGAGATGTTTCAAGCGCTATGACTTTGTCCAGGCTGG	55499	
Db	55440	CTAGATGCAAGTGTATCGGAATCATAGAGATGTTTCAAGCGCTATGACTTTGTCCAGGCTGG	55499	
Qy	55500	CAGATATGAATACCTTGTCTGTCGACAGAGGGAAGAAGCAGAAATCAGGTAACTGACAA	55559	
Db	55500	CAGATATGAATACCTTGTCTGTCGACAGAGGGAAGAAGCAGAAATCAGGTAACTGACAA	55559	
Qy	55560	AAACGCCAACGTAGATCCGATCTGGTCTTTAGGTACTTTACTAGAAATAGTTCTGTCT	55619	
Db	55560	AAACGCCAACGTAGATCCGATCTGGTCTTTAGGTACTTTACTAGAAATAGTTCTGTCT	55619	
Qy	55620	TGATTTACCAAGCTTTGTGAAGGACAAAAACAATTTATTAACCAAGACAAATATCGG	55679	
Db	55620	TGATTTACCAAGCTTTGTGAAGGACAAAAACAATTTATTAACCAAGACAAATATCGG	55679	
Qy	55680	AAACGAGCATATAGAACTGTTTCCATAGCCATCATGCTTCCGAGGGAGATTAATACA	55739	
Db	55680	AAACGAGCATATAGAACTGTTTCCATAGCCATCATGCTTCCGAGGGAGATTAATACA	55739	
Qy	55740	TCTCCATGGCTATTTAAGACAGATTAAGATTGGCCCAATCGTTTTCCGTAACGCACA	55799	
Db	55740	TCTCCATGGCTATTTAAGACAGATTAAGATTGGCCCAATCGTTTTCCGTAACGCACA	55799	
Qy	55800	GGGTGCTAGCAAGCTATTTCTCAGGAATCTGCTGCTTAAGCGGCTAGAACCCAGGTGG	55859	
Db	55800	GGGTGCTAGCAAGCTATTTCTCAGGAATCTGCTGCTTAAGCGGCTAGAACCCAGGTGG	55859	
Qy	55860	CCGAATTCACAGATATCATAGCCTGAGCGTGGTAAAGATAGGCAAAAATGTATACAT	55919	
Db	55860	CCGAATTCACAGATATCATAGCCTGAGCGTGGTAAAGATAGGCAAAAATGTATACAT	55919	
Qy	55920	ATACAACGAGGCTAAAGATATGTTTGTACAGACAGAACTGAATTAATACTGGATGG	55979	
Db	55920	ATACAACGAGGCTAAAGATATGTTTGTACAGACAGAACTGAATTAATACTGGATGG	55979	
Qy	55980	TCACAGGCTCAAAATAGACATTAATAAACTACACCTGGAGGCTTGAGCAACGATCCATG	56039	
Db	55980	TCACAGGCTCAAAATAGACATTAATAAACTACACCTGGAGGCTTGAGCAACGATCCATG	56039	
Qy	56040	TCTGAGAGCTGTCATTTGTTGCTGCTGACGCGCTTGCCCTTGAATATGGCCAGATGG	56099	
Db	56040	TCTGAGAGCTGTCATTTGTTGCTGCTGACGCGCTTGCCCTTGAATATGGCCAGATGG	56099	
Qy	56100	CCCAAGCATAGTAAACACAGCAGATATCCGTCACACCAAAAAGCCACAGATGTAGACA	56159	
Db	56100	CCCAAGCATAGTAAACACAGCAGATATCCGTCACACCAAAAAGCCACAGATGTAGACA	56159	
Qy	56160	ACATTTTGGTGGCTTCCAAAAACAAGTGGCGCTAGATGTTTACAGAACTTCTGACCG	56219	
Db	56160	ACATTTTGGTGGCTTCCAAAAACAAGTGGCGCTAGATGTTTACAGAACTTCTGACCG	56219	
Qy	56220	TTAGGTTTAAAGCGCTAGTGTGACCAAGTGTAAATAGACGGAATCCAAGTCCCG	56279	
Db	56220	TTAGGTTTAAAGCGCTAGTGTGACCAAGTGTAAATAGACGGAATCCAAGTCCCG	56279	

Db	56220	TTAGGTTTAAAGCGCTAGTGTGACCAAGTGTAAATAGACGGAATCCAAGTCCCG	56279	
Qy	56280	GGAATGTGGCGGTGTCAGTGGCACTACCGCTGACATTAATAAATAGTCCAGAAATACCA	56339	
Db	56280	GGAATGTGGCGGTGTCAGTGGCACTACCGCTGACATTAATAAATAGTCCAGAAATACCA	56339	
Qy	56340	GTAGTTTTTACCATGACGATTAAGATTAACGAGTCCGTCGGTAAATTTTCAATAGTTCAA	56399	
Db	56340	GTAGTTTTTACCATGACGATTAAGATTAACGAGTCCGTCGGTAAATTTTCAATAGTTCAA	56399	
Qy	56400	GAATCTGCTCGGGGGTGGCTTGGCAACTACAGTAATTAATGACAAAGTGGCTTCAATCT	56459	
Db	56400	GAATCTGCTCGGGGGTGGCTTGGCAACTACAGTAATTAATGACAAAGTGGCTTCAATCT	56459	
Qy	56460	TACGGAATTTAAATAGGCTCCGTTTAAATATCACATCTGTGCAAAAGGATTTGAGCCAC	56519	
Db	56460	TACGGAATTTAAATAGGCTCCGTTTAAATATCACATCTGTGCAAAAGGATTTGAGCCAC	56519	
Qy	56520	GGCACCATTGAACGCCCGGAGGTGGCAGTCAAGGGACATGTTTGCACATATCGCTGCAT	56579	
Db	56520	GGCACCATTGAACGCCCGGAGGTGGCAGTCAAGGGACATGTTTGCACATATCGCTGCAT	56579	
Qy	56580	AGCAGCAGCAGCGGAGAAATTAATTAATCTGGAGGTTCAATTTACTTTATGTCAACA	56639	
Db	56580	AGCAGCAGCAGCGGAGAAATTAATTAATCTGGAGGTTCAATTTACTTTATGTCAACA	56639	
Qy	56640	TGCGGAATTCAGGAGATGCCCATATCTATTTGTACCGAAACATTAAGCAATACGAC	56699	
Db	56640	TGCGGAATTCAGGAGATGCCCATATCTATTTGTACCGAAACATTAAGCAATACGAC	56699	
Qy	56700	TGGGGAATTTATCCGGCGGATTAACCGTCAAGCAGCGTCCATTAATAGACAGCGCGTAT	56759	
Db	56700	TGGGGAATTTATCCGGCGGATTAACCGTCAAGCAGCGTCCATTAATAGACAGCGCGTAT	56759	
Qy	56760	TATATGACGTGGGAATCCGTCCTGTTACGGAATCCCATATTTCAATTTGTAAGTGC	56819	
Db	56760	TATATGACGTGGGAATCCGTCCTGTTACGGAATCCCATATTTCAATTTGTAAGTGC	56819	
Qy	56820	CAGCCCGGTGCGTTAAGCTAAGGCTCAGCAGCCGGAATATGTAATAGTGGCTGCGAA	56879	
Db	56820	CAGCCCGGTGCGTTAAGCTAAGGCTCAGCAGCCGGAATATGTAATAGTGGCTGCGAA	56879	
Qy	56880	CGAGGTTGGATCAGTCCGTTGTTGCGGCGGAGCTGAGTATCTTCAATTTGGCATACC	56939	
Db	56880	CGAGGTTGGATCAGTCCGTTGTTGCGGCGGAGCTGAGTATCTTCAATTTGGCATACC	56939	
Qy	56940	ACTATGACCTTATGTTGATTTCTGTGTGTCCCAACCCCGGAATTTGTTCTCACAG	56999	
Db	56940	ACTATGACCTTATGTTGATTTCTGTGTGTCCCAACCCCGGAATTTGTTCTCACAG	56999	
Qy	57000	ATGTTTTCTCACTGTTTACTTTCCAACTTGAAGTTTACCTTTAAACAACGGGCGGTTA	57059	
Db	57000	ATGTTTTCTCACTGTTTACTTTCCAACTTGAAGTTTACCTTTAAACAACGGGCGGTTA	57059	
Qy	57060	TACTATAGGGCATTCAGATGCCAGCAATGCCAAAAAGGGCAAAAGATGGCCATTGGGT	57119	
Db	57060	TACTATAGGGCATTCAGATGCCAGCAATGCCAAAAAGGGCAAAAGATGGCCATTGGGT	57119	
Qy	57120	ATTTCTTGAATCTTTAATTTGGCAATCTCGTGAATTAACAAGTTCCGGGACAGAACTACAC	57179	
Db	57120	ATTTCTTGAATCTTTAATTTGGCAATCTCGTGAATTAACAAGTTCCGGGACAGAACTACAC	57179	
Qy	57180	TTGAGTATGCCACCGCAACATTTTACGTTCTCTGCGTGGAGCAGAGCGCTGATGTGGAAC	57239	
Db	57180	TTGAGTATGCCACCGCAACATTTTACGTTCTCTGCGTGGAGCAGAGCGCTGATGTGGAAC	57239	
Qy	57240	GGGCGCTTGGCGGAATTTTAAAGGCGCTGCACATTAAGTTTTCGGGACCGGGAAGGC	57299	
Db	57240	GGGCGCTTGGCGGAATTTTAAAGGCGCTGCACATTAAGTTTTCGGGACCGGGAAGGC	57299	
Qy	57300	GTAGCGCCCAACGTTAACTAGCTGCTGCTGGGGGACCATCCGAGAGGAACCCCTTCCCC	57359	
Db	57300	GTAGCGCCCAACGTTAACTAGCTGCTGCTGGGGGACCATCCGAGAGGAACCCCTTCCCC	57359	
Qy	57360	GTAGCGCCCAACGTTAACTAGCTGCTGCTGGGGGACCATCCGAGAGGAACCCCTTCCCC	57399	
Db	57360	GTAGCGCCCAACGTTAACTAGCTGCTGCTGGGGGACCATCCGAGAGGAACCCCTTCCCC	57399	

Qy 57360 CCCACTTTTCCGGCTTTCACACACTCCGGCTGTTTGGAGACCGCGAAGGCTGCAC 57419
|||
Db 57360 CCCACTTTTCCGGCTTTCACACACTCCGGCTGTTTGGAGACCGCGAAGGCTGCAC 57419
Qy 57420 GTAAACCGCGGTCAAGAACTCCAAAAGCACAAATTCGGGTACACTGGCCCCGTTTAA 57479
|||
Db 57420 GTAAACCGCGGTCAAGAACTCCAAAAGCACAAATTCGGGTACACTGGCCCCGTTTAA 57479
Qy 57480 GATTCATCTTAGGGGATGACGCTCTCATACCTGGCATTCCTAAACCCGATACC 57539
|||
Db 57480 GATTCATCTTAGGGGATGACGCTCTCATACCTGGCATTCCTAAACCCGATACC 57539
Qy 57540 GTACCCGTTGGGCGCTTTGGGTGGAGATGTTACTGATCTCTGGAGACGACA 57599
|||
Db 57540 GTACCCGTTGGGCGCTTTGGGTGGAGATGTTACTGATCTCTGGAGACGACA 57599
Qy 57600 GAAAGCGTTGGCCGATAGTCGACCCACATTCATAGTAATCATMAAATTTTCATCTG 57659
|||
Db 57600 GAAAGCGTTGGCCGATAGTCGACCCACATTCATAGTAATCATMAAATTTTCATCTG 57659
Qy 57660 TTGAGCCAGACCTAAATGCGACGTCGTTGTTAAATAGTTAGATACATAGCA 57719
|||
Db 57660 TTGAGCCAGACCTAAATGCGACGTCGTTGTTAAATAGTTAGATACATAGCA 57719
Qy 57720 ACCATCTGTTCCAGCGACCTTCGCTCTTCATCCAGAGAAATCAACCGGTTACTTGC 57779
|||
Db 57720 ACCATCTGTTCCAGCGACCTTCGCTCTTCATCCAGAGAAATCAACCGGTTACTTGC 57779
Qy 57780 ACCATTTTTCAGTGGGCGCGGCGAGCGGGGTATACCTGGCGCCATTTGATMAACA 57839
|||
Db 57780 ACCATTTTTCAGTGGGCGCGGCGAGCGGGGTATACCTGGCGCCATTTGATMAACA 57839
Qy 57840 GTATTCATCAAGGCTCCCGACGCTCAGGCGACGCTGATGTTCTGCGCATCTAAT 57899
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Db 57840 GTATTCATCAAGGCTCCCGACGCTCAGGCGACGCTGATGTTCTGCGCATCTAAT 57899
Qy 57900 AGTTGCGGTAGGAACAATGTTACGAAGTTMAAATPAACGTTTCTTTTCCACAG 57959
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Db 57900 AGTTGCGGTAGGAACAATGTTACGAAGTTMAAATPAACGTTTCTTTTCCACAG 57959
Qy 57960 AACGCAAAAGGTGTGACCCGCTTGAAGCGCATTTGGGCACTTCCGTACAGGAATTT 58019
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Db 57960 AACGCAAAAGGTGTGACCCGCTTGAAGCGCATTTGGGCACTTCCGTACAGGAATTT 58019
Qy 58020 CCCACCGGCTGACTGGCTCAAGTGTGAGTCTGCTCGGCTCGGTTTAAATAATAC 58079
|||
Db 58020 CCCACCGGCTGACTGGCTCAAGTGTGAGTCTGCTCGGCTCGGTTTAAATAATAC 58079
Qy 58080 CAGCCGGGGTTTGTATGCCGACTCGCAAGAGACCCACAGGGAAGCAAAAGCGGACT 58139
|||
Db 58080 CAGCCGGGGTTTGTATGCCGACTCGCAAGAGACCCACAGGGAAGCAAAAGCGGACT 58139
Qy 58140 CGTGGCTGAGACTGTCTAGTAGAAGCGGACGTTGTGCTTAAACACTCACTGTTACCGA 58199
|||
Db 58140 CGTGGCTGAGACTGTCTAGTAGAAGCGGACGTTGTGCTTAAACACTCACTGTTACCGA 58199
Qy 58200 TTGGGGGCGTGGGGGATATCTACCAACCTTTTGGCAACAGGCGGTGTATATTTT 58259
|||
Db 58200 TTGGGGGCGTGGGGGATATCTACCAACCTTTTGGCAACAGGCGGTGTATATTTT 58259
Qy 58360 GGTGCTGACCAAGCGCGGTGAAATCGGCGCCATATGCTCTCCCTACCGATGACT 58319
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Db 58360 GGTGCTGACCAAGCGCGGTGAAATCGGCGCCATATGCTCTCCCTACCGATGACT 58319
Qy 58320 GTGTACGCTCCACAGTTGTCTGTGACAAAGCGTGACCAATCTGCTGTGTAAGGAAT 58379
|||
Db 58320 GTGTACGCTCCACAGTTGTCTGTGACAAAGCGTGACCAATCTGCTGTGTAAGGAAT 58379
Qy 58380 GGGCGTTACGCGGTGAGTGTATTTATGTAACCTACAGAGGACACTATGTTTAA 58439
|||
Db 58380 GGGCGTTACGCGGTGAGTGTATTTATGTAACCTACAGAGGACACTATGTTTAA 58439

Qy 58440 GTGTGTGTCACACGGGAGGGTACGAGACTCACCGCGCAATATACGAAATTTAGAA 58499
|||
Db 58440 GTGTGTGTCACACGGGAGGGTACGAGACTCACCGCGCAATATATACGAAATTTAGAA 58499
Qy 58500 AGTTTGAAGGTCTATGTTTATTTTAAACAGAGTCTGTCTGGGATGCTGTAGGC 58559
|||
Db 58500 AGTTTGAAGGTCTATGTTTATTTTAAACAGAGTCTGTCTGGGATGCTGTAGGC 58559
Qy 58560 TGGTTATTTGAAATATTTTAAATACCGATGGGTATGAAAGGTGCTGTAAATTTGTC 58619
|||
Db 58560 TGGTTATTTGAAATATTTTAAATACCGATGGGTATGAAAGGTGCTGTAAATTTGTC 58619
Qy 58620 CGCATATAATATGTTAAAGTCTCCGGCTGCTCTTCTTCCAAAGTCTCTGTTA 58679
|||
Db 58620 CGCATATAATATGTTAAAGTCTCCGGCTGCTCTTCTTCCAAAGTCTCTGTTA 58679
Qy 58680 GACGAAAGATTTCCAAATAAATGGGTTTCAAGCCCTTTCATGTCTGCTGTTTTCGT 58739
|||
Db 58680 GACGAAAGATTTCCAAATAAATGGGTTTCAAGCCCTTTCATGTCTGCTGTTTTCGT 58739
Qy 58740 CCAACAGCTTATGGAGTTTGAACCGCACTAGGGGCGGAACGCGAAATTTGCGGGTG 58799
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Db 58740 CCAACAGCTTATGGAGTTTGAACCGCACTAGGGGCGGAACGCGAAATTTGCGGGTG 58799
Qy 58800 GGTTTAACTGCTGATGCGCCCAAGGTGACAGGCTATCATTGATCCCATACATACAA 58859
|||
Db 58800 GGTTTAACTGCTGATGCGCCCAAGGTGACAGGCTATCATTGATCCCATACATACAA 58859
Qy 58860 ACGGGAATCTATTACGATATACCTCTGCTGATAGTACCTGGCCCGGTCCAAAGCGGACA 58919
|||
Db 58860 ACGGGAATCTATTACGATATACCTCTGCTGATAGTACCTGGCCCGGTCCAAAGCGGACA 58919
Qy 58920 GGATAAATGATAGGGGGGGCTTATGCTGTTTTCAGCATGAAAGATGACGAGATT 58979
|||
Db 58920 GGATAAATGATAGGGGGGGCTTATGCTGTTTTCAGCATGAAAGATGACGAGATT 58979
Qy 58980 CTGTTACGCTGCGCTCGCCGCTTAAACAGCTGCACGCGGTACAGAAAAACGTCGGAT 59039
|||
Db 58980 CTGTTACGCTGCGCTCGCCGCTTAAACAGCTGCACGCGGTACAGAAAAACGTCGGAT 59039
Qy 59040 ATATGTCCAGTGGCTGATCATGTCTGTGTGTGACCCAGCAGCAAGCAAAAGCCAG 59099
|||
Db 59040 ATATGTCCAGTGGCTGATCATGTCTGTGTGTGACCCAGCAGCAAGCAAAAGCCAG 59099
Qy 59100 TAAAGTGGCCGACTGAAGCTGGTGGCCAGCTGACGCTAAATCAGAAAGTTAGTC 59159
|||
Db 59100 TAAAGTGGCCGACTGAAGCTGGTGGCCAGCTGACGCTAAATCAGAAAGTTAGTC 59159
Qy 59160 GTCTCGAACAACAGCTTAGGCGTATTTGAAGCCATGCAAAATGCTATTTTATGTA 59219
|||
Db 59160 GTCTCGAACAACAGCTTAGGCGTATTTGAAGCCATGCAAAATGCTATTTTATGTA 59219
Qy 59220 CTTCCACATCAGTCCGCGGAAAACTGGATTAATATAGGCGCTTGGACAGCATTTCTG 59279
|||
Db 59220 CTTCCACATCAGTCCGCGGAAAACTGGATTAATATAGGCGCTTGGACAGCATTTCTG 59279
Qy 59280 TTTGAGGATTAACGCGCTCAGATCGGTCTGCTGCCCATTTAGAGCTTCAGTATTTGCT 59339
|||
Db 59280 TTTGAGGATTAACGCGCTCAGATCGGTCTGCTGCCCATTTAGAGCTTCAGTATTTGCT 59339
Qy 59340 CCATCGGTTCCAGGCTGCTAATTTTTCGCAATATTTGTGGCCTATGCTATTTATATAC 59399
|||
Db 59340 CCATCGGTTCCAGGCTGCTAATTTTTCGCAATATTTGTGGCCTATGCTATTTATATAC 59399
Qy 59400 ACAGACAGCTGCTGCTCAGATACAGCTGTGCTGCAATATGCTGTAACTTAAGAAATG 59459
|||
Db 59400 ACAGACAGCTGCTGCTCAGATACAGCTGTGCTGCAATATGCTGTAACTTAAGAAATG 59459
Qy 59460 AGAGATGATTTATGAGTTCATGATTCAGTTTGGGATTTATGTTAGTAAAGGCGCT 59519
|||
Db 59460 AGAGATGATTTATGAGTTCATGATTCAGTTTGGGATTTATGTTAGTAAAGGCGCT 59519
Qy 59520 AAGAGATGAAACCGTGTCTCGAGTAGAGCGATGCTCTTCCGCTGCGCTGATTTGTC 59579
|||

Db	59520	AAGAGAAATGGAAACCGGTCTCTGCGAGTAGGCGATGCTCGTTCCCTGCCCCGTGATTGTGC	59579
Qy	59580	ACCAGGGGTGTGAGGTTGTACGTTTGAACAATTTCCCTTCCACAGGCTAAGTAGCTCT	59639
Db	59580	ACCAGGGGTGTGAGGTTGTACGTTTGAACAATTTCCCTTCCACAGGCTAAGTAGCTCT	59639
Qy	59640	TTGACACATCTCCATAAACGGGAGGAGCGATATGTGAAAAAAGCGTGTACTACGAGACTG	59699
Db	59640	TTGACACATCTCCATAAACGGGAGGAGCGATATGTGAAAAAAGCGTGTACTACGAGACTG	59699
Qy	59700	CCTTAGGAGATGTGACATTCGGATAGGTTAATGTTGGGTGCGCCACAGCGGATAAAGCC	59759
Db	59700	CCTTAGGAGATGTGACATTCGGATAGGTTAATGTTGGGTGCGCCACAGCGGATAAAGCC	59759
Qy	59760	TGCAACGATTTCTGAGTAGTAATTAATATCGTGTCTGGGCTTCGCTCTGTGTAA	59819
Db	59760	TGCAACGATTTCTGAGTAGTAATTAATATCGTGTCTGGGCTTCGCTCTGTGTAA	59819
Qy	59820	CTCTAAGCAACTGGGTTTCAATGATTAATCTTTTACGTAGTGTGCTCGTTCTTTC	59879
Db	59820	CTCTAAGCAACTGGGTTTCAATGATTAATCTTTTACGTAGTGTGCTCGTTCTTTC	59879
Qy	59880	TCAAGGTTAGAATTTATTCGAACTGCTGTTGATCTGTGATCTGTTCGTCAGGCAATTTGAAACG	59939
Db	59880	TCAAGGTTAGAATTTATTCGAACTGCTGTTGATCTGTGATCTGTTCGTCAGGCAATTTGAAACG	59939
Qy	59940	GTAATTTGAACCTGTTTCCGAGAACCCGGGTGCTACTTCCGATACCGGTCGCCAAGAC	59999
Db	59940	GTAATTTGAACCTGTTTCCGAGAACCCGGGTGCTACTTCCGATACCGGTCGCCAAGAC	59999
Qy	60000	TTGTTTTTGTCCACAAATGTTTTTGAGAGACGTCGTGAGCAAAATCCTCAACAGCTCTGT	60059
Db	60000	TTGTTTTTGTCCACAAATGTTTTTGAGAGACGTCGTGAGCAAAATCCTCAACAGCTCTGT	60059
Qy	60060	ATGCCGCTCACTGTTTGTCTCCGCGAGCTTTATCAGCAAGTTTAGAGAGTCCCTCTTG	60119
Db	60060	ATGCCGCTCACTGTTTGTCTCCGCGAGCTTTATCAGCAAGTTTAGAGAGTCCCTCTTG	60119
Qy	60120	GGGTGCGTTTTTTAGACGATTTGCTTAAGCGAGCCAAATATGCTTTATACATGCTGTG	60179
Db	60120	GGGTGCGTTTTTTAGACGATTTGCTTAAGCGAGCCAAATATGCTTTATACATGCTGTG	60179
Qy	60180	CACGTGCTACCGAGCAGCGCTTTTATAGAGCGCGGATTTAGTAATGACATTAACCTTTGCG	60239
Db	60180	CACGTGCTACCGAGCAGCGCTTTTATAGAGCGCGGATTTAGTAATGACATTAACCTTTGCG	60239
Qy	60240	TGCTCCGGGTCCTGTGATGTCATTAATCGCGGTAATTAACCGGTACAGAGGCGCTATCA	60299
Db	60240	TGCTCCGGGTCCTGTGATGTCATTAATCGCGGTAATTAACCGGTACAGAGGCGCTATCA	60299
Qy	60300	AAGCGAGCGCTCATTTGTAAATTAATAGCGCGTGAACAACCTTCACCTGTTATATCTTT	60359
Db	60300	AAGCGAGCGCTCATTTGTAAATTAATAGCGCGTGAACAACCTTCACCTGTTATATCTTT	60359
Qy	60360	TGTCGTATGATGCGGAGTATAGACCGCTTATCTCCGTTAAATCTCCAGACACCTCGCGCG	60419
Db	60360	TGTCGTATGATGCGGAGTATAGACCGCTTATCTCCGTTAAATCTCCAGACACCTCGCGCG	60419
Qy	60420	TAGTCTGGAATTAATTAAGACATCGGTCAATTAATCGAGTAATCTCCTGCGCAGT	60479
Db	60420	TAGTCTGGAATTAATTAAGACATCGGTCAATTAATCGAGTAATCTCCTGCGCAGT	60479
Qy	60480	TTGTGTCGAAATCCGCGATATGTAACGTCCTCCGGAAGCGTACGCTTTTCCATCTATGTTGA	60539
Db	60480	TTGTGTCGAAATCCGCGATATGTAACGTCCTCCGGAAGCGTACGCTTTTCCATCTATGTTGA	60539
Qy	60540	CAGTGTGTTTATATCCGCGATGCTGTGCGCGGGGGTGCCTTGACAAATAGGCAACC	60599
Db	60540	CAGTGTGTTTATATCCGCGATGCTGTGCGCGGGGGTGCCTTGACAAATAGGCAACC	60599
Qy	60600	AACCCAAAGGCGACACCACTGACGATATGTTGCTGATACGATTAACAGTCTGCTGTGT	60659
Db	60600	AACCCAAAGGCGACACCACTGACGATATGTTGCTGATACGATTAACAGTCTGCTGTGT	60659
Qy	60660	AGTACCTGATTAATAGTGTTCAGTAACAGTGTGATGCACTGTTATAGCAAGGTACTGTGCC	60719
Db	60660	AGTACCTGATTAATAGTGTTCAGTAACAGTGTGATGCACTGTTATAGCAAGGTACTGTGCC	60719
Qy	60720	CACGATTCAAACGTATAGCCGTTTGAATTCGCGGCTAGAGTGTCTCGACACCGCGCAACGG	60779
Db	60720	CACGATTCAAACGTATAGCCGTTTGAATTCGCGGCTAGAGTGTCTCGACACCGCGCAACGG	60779
Qy	60780	GTCCTTGAAGGTGTCTCGAAGTTTGTCCAGTCCCTTTTAAAGCGTTGTCTATGTGACCTC	60839
Db	60780	GTCCTTGAAGGTGTCTCGAAGTTTGTCCAGTCCCTTTTAAAGCGTTGTCTATGTGACCTC	60839
Qy	60840	CCCAATGCCGCTCTTTGACAGGTATGAAACAGTGTCTTCCAAAGATCCCTGGAATTTGCA	60899
Db	60840	CCCAATGCCGCTCTTTGACAGGTATGAAACAGTGTCTTCCAAAGATCCCTGGAATTTGCA	60899
Qy	60900	AGACTGGAGTGTAGCTTTGACCGCAAGATAGCGCTACTTCCCGTATGAGATTCGAAA	60959
Db	60900	AGACTGGAGTGTAGCTTTGACCGCAAGATAGCGCTACTTCCCGTATGAGATTCGAAA	60959
Qy	60960	AGCGAGATGAGAGTTCCTCGATGAGCAACACGTCGAAACCAATCCGGGTTTCATC	61019
Db	60960	AGCGAGATGAGAGTTCCTCGATGAGCAACACGTCGAAACCAATCCGGGTTTCATC	61019
Qy	61020	TTGACATGACGTCGATGCAAAAGTCAGGGGTTGTGTGATACAGTCAAGTCCGCTGTCA	61079
Db	61020	TTGACATGACGTCGATGCAAAAGTCAGGGGTTGTGTGATACAGTCAAGTCCGCTGTCA	61079
Qy	61080	AATATTAACATACAGCCACCGGAATAGGTTGTGTACAGCTGCGCTTGATCCGCGTGAA	61139
Db	61080	AATATTAACATACAGCCACCGGAATAGGTTGTGTACAGCTGCGCTTGATCCGCGTGAA	61139
Qy	61140	GACTCCGGGCGCTTGTGCGCTTTACGTTTATCTAATTAAGGGAACGTGCTGTGCG	61199
Db	61140	GACTCCGGGCGCTTGTGCGCTTTACGTTTATCTAATTAAGGGAACGTGCTGTGCG	61199
Qy	61200	AAAAGTACAGCATATCGGCCCTGTACCAAAATTTAACTGCTGTATCAAGGGCGCGAAC	61259
Db	61200	AAAAGTACAGCATATCGGCCCTGTACCAAAATTTAACTGCTGTATCAAGGGCGCGAAC	61259
Qy	61260	ACCATAGCCGACAGAACTATTCGCGCTCCCTTAAGAGCTTGTGTCACGATCTTTCAGC	61319
Db	61260	ACCATAGCCGACAGAACTATTCGCGCTCCCTTAAGAGCTTGTGTCACGATCTTTCAGC	61319
Qy	61320	GCTTTTGGCTTTAAGAGCCGACACATCAATATAGCGCTAGAGAAAGCTCATAGACCGGA	61379
Db	61320	GCTTTTGGCTTTAAGAGCCGACACATCAATATAGCGCTAGAGAAAGCTCATAGACCGGA	61379</

Dd	6060d	AACCAGGGGACACCACCACAGTGCAGCTATCGTACAGATTAACAACTCCTGGGTGT	60659d
Oy	60660	AGTACGCTGATTAAATAGTGTTCAGTAAACAGTTGATGCATGTGTAAGCAAGCGTAGCTGCC	60719d
Dd	60660	AGTACGCTGATTAAATAGTGTTCAGTAAACAGTTGATGCATGTGTAAGCAAGCGTAGCTGCC	60719d
Oy	60720	CACAGTTCCAAACGATAGACCGCTTGGAAATTCGGGGGTACAGGTCGTGCACACCGGCCCAAGG	60779d
Dd	60720	CACAGTTCCAAACGATAGACCGCTTGGAAATTCGGGGGTACAGGTCGTGCACACCGGCCCAAGG	60779d
Oy	60780	GTCCTTCAGGGGTGTCTCGAAGTTGGTCCAGTCCCTTTAAGACGTTGTGATGTGCAGCTC	60839d
Dd	60780	GTCCTTCAGGGGTGTCTCGAAGTTGGTCCAGTCCCTTTAAGACGTTGTGATGTGCAGCTC	60839d
Oy	60840	CCCAATGCGCTCTGTGTACAGGTGTATGAAACAGCTGTCTTCCAAAGATCCCTGGATTTCGA	60899d
Dd	60840	CCCAATGCGCTCTGTGTACAGGTGTATGAAACAGCTGTCTTCCAAAGATCCCTGGATTTCGA	60899d
Oy	60900	AGACTGAGAGTGTAGCGCTTTACCGCGACGATAGCGCTACTTGGCCCTGTAGATCTCGAAA	60959d
Dd	60900	AGACTGAGAGTGTAGCGCTTTACCGCGACGATAGCGCTACTTGGCCCTGTAGATCTCGAAA	60959d
Oy	60960	AGCGAGATGTGAAGATTCCTGTGCGATGACCAAAACAGTGTGAACCAATCCGGGGTTTCATC	61019d
Dd	60960	AGCGAGATGTGAAGATTCCTGTGCGATGACCAAAACAGTGTGTGATACGTGACGTCGCTGTCA	61019d
Oy	61020	TTGAAACATGTAGCGTCCGATGGCCAAAGATGAGGGGTGTGTGGATACGTGACGTCGCTGTCA	61079d
Dd	61020	TTGAAACATGTAGCGTCCGATGGCCAAAGATGAGGGGTGTGTGGATACGTGACGTCGCTGTCA	61079d
Oy	61080	AATATTAACCTACCCAGCCACCAGAAATGGTTGGTATGACCTGGCCCTTCATCCGGCTGAAA	61139d
Dd	61080	AATATTAACCTACCCAGCCACCAGAAATGGTTGGTATGACCTGGCCCTTCATCCGGCTGAAA	61139d
Oy	61140	GACATCCGGCGCTTCTGCGGTGTACCGCTTATCTAATTAACGGGAACGTGCTGGTGGG	61199d
Dd	61140	GACATCCGGCGCTTCTGCGGTGTACCGCTTATCTAATTAACGGGAACGTGCTGGTGGG	61199d
Oy	61200	AAAATGTACCAAGCATATGCGCCCTGTACCAAAATTTAAACTGCTGTATCAGCGGGCGGAC	61259d
Dd	61200	AAAATGTACCAAGCATATGCGCCCTGTACCAAAATTTAAACTGCTGTATCAGCGGGCGGAC	61259d
Oy	61260	ACCATACCGGCACAGAACCTATGCGCGCTGCTTAAACAGCTGTCTGTCCACATCTTTCAGC	61319d
Dd	61260	ACCATACCGGCACAGAACCTATGCGCGCTGCTTAAACAGCTGTCTGTCCACAGCTTTCAGC	61319d
Oy	61320	GCTTTTGGCTTTAAGAACCCGACACATCAATATAGCGGTGAGAAAGCTCATAGACCGGA	61379d
Dd	61320	GCTTTTGGCTTTAAGAACCCGACACATCAATATAGCGGTGAGAAAGCTCATAGACCGGA	61379d
Oy	61380	GCGGTATTCATATAGACAATTCAGCAACAGAGACTATGCAAGTATTGGCCGGTTATAGTG	61439d
Dd	61380	GCGGTATTCATATAGACAATTCAGCAACAGAGACTATGCAAGTATTGGCCGGTTATAGTG	61439d
Oy	61440	GACCTTTATGAAAGGGTTATGGGGAAGAAAAACCAATGGGATGTAGCGGACTATATTCACAC	61499d
Dd	61440	GACCTTTATGAAAGGGTTATGGGGAAGAAAAACCAATGGGATGTAGCGGACTATATTCACAC	61499d
Oy	61500	GCGAATTTTGAACCCCTCTGAGAAATGACCGGACGCTGTTATGACCTTCACAATATATT	61559d
Dd	61500	GCGAATTTTGAACCCCTCTGAGAAATGACCGGACGCTGTTATGACCTTCACAATATATT	61559d
Oy	61560	GTAATTCAGACGAGCGCGGAACCCGTCTCTTATATATCTACACACGCTGTGTCTTTTATAC	61619d
Dd	61560	GTAATTCAGACGAGCGCGGAACCCGTCTCTTATATATCTACACACGCTGTGTCTTTTATAC	61619d
Oy	61620	TGATTCCTAAACAGCTGGCTAAATATACCCCTCTTTACCGCAGGGGGGTTCGGTGACATA	61679d
Dd	61620	TGATTCCTAAACAGCTGGCTAAATATACCCCTCTTTACCGCAGGGGGGTTCGGTGACATA	61679d
Oy	61680	GTAATGCTGTGGTGGCCACGACGACAAAGCGCTTCAGTCAACTTACACACAGGGAGAC	61739d
Dd	61680	GTAATGCTGTGGTGGCCACGACGACAAAGCGCTTCAGTCAACTTACACACAGGGAGAC	61739d

QY	61740	CAAAAGACGAGATATGTCGTGCGAGAACATCTTAACATTCATGATAGGAGAAAGGTC	61799
Db	61740	CAAAAAGACGAGATATGTCGTGCGAGAACATCTTAACATTCATGATAGGAGAAAGGTC	61799
QY	61800	GTATCTGAGTACGTACACCTTGGAGAAACTGGGCGCTGTTTATAAACCAACAGCGTCG	61859
Db	61800	GTATCTGAGTACGTACACCTTGGAGAAACTGGGCGCTGTTTATAAACCAACAGCGTCG	61859
QY	61860	ACCGATTCGACGAGTTCGACACCTCTTAATAAGTATATCTTCCATCTCCGAC	61919
Db	61860	ACCGATTCGACGAGTTCGACACCTCTTAATAAGTATATCTTCCATCTCCGAC	61919
QY	61920	GAACTCATGAGTTACGTACGACAGATTTGTCCTTAAAGTAAGTATATGATCTTTTA	61979
Db	61920	GAACTCATGAGTTACGTACGACAGATTTGTCCTTAAAGTAAGTATATGATCTTTTA	61979
QY	61980	GAAATACATTTGGCTGGACCCGACCTTTTGTACATAGCGAGTAAGGGGATCTAAC	62039
Db	61980	GAAATACATTTGGCTGGACCCGACCTTTTGTACATAGCGAGTAAGGGGATCTAAC	62039
QY	62040	AACCTACACACATGCTTACCGCTAGGGGCGGATACAGGGACACGAAGCTCTTACCTGT	62099
Db	62040	AACCTACACACATGCTTACCGCTAGGGGCGGATACAGGGACACGAAGCTCTTACCTGT	62099
QY	62100	CCCGTGTGTGCGGAGGTGTTGTGAAGCCGTTTGAAGATACAAAGGGGCGCTACCTC	62159
Db	62100	CCCGTGTGTGCGGAGGTGTTGTGAAGCCGTTTGAAGATACAAAGGGGCGCTACCTC	62159
QY	62160	ACCAACCTCACGAGACCGAGTGGGTGACAAAAACCTTAAGTTAAGTAATATATCG	62219
Db	62160	ACCAACCTCACGAGACCGAGTGGGTGACAAAAACCTTAAGTTAAGTAATATATCG	62219
QY	62220	CAGTTTGTGACACGAGACATGTCATAGTCGCCACGGATCCTACTGAAAGCTTCGACCAG	62279
Db	62220	CAGTTTGTGACACGAGACATGTCATAGTCGCCACGGATCCTACTGAAAGCTTCGACCAG	62279
QY	62280	GTTACCTTTATCACCAGTTGTTTAAAAACAGCCAGCTGCTTTTAAATGGAAAAACAAA	62339
Db	62280	GTTACCTTTATCACCAGTTGTTTAAAAACAGCCAGCTGCTTTTAAATGGAAAAACAAA	62339
QY	62340	AAATGCAATATGTGGGTTTCAGGAGTACGTAAGTTGATTCAAAAAGAACCTTAGACAGGAA	62399
Db	62340	AAATGCAATATGTGGGTTTCAGGAGTACGTAAGTTGATTCAAAAAGAACCTTAGACAGGAA	62399
QY	62400	CTCTTCGTGAGAGCGCATTCGCAAGACCGTCCGGAATACGTATACGGTTCTTTAAACAGC	62459
Db	62400	CTCTTCGTGAGAGCGCATTCGCAAGACCGTCCGGAATACGTATACGGTTCTTTAAACAGC	62459
QY	62460	CTACTGTACACGCGCATGTACTGCTTTCACGCGTACGCGGCTGAGTACACAGCAAAA	62519
Db	62460	CTACTGTACACGCGCATGTACTGCTTTCACGCGTACGCGGCTGAGTACACAGCAAAA	62519
QY	62520	TATCTGCAAGACCTAAAAATTTGCACCCCTCCGCGCCTCTGGCAACCGGCGGTAGAC	62579
Db	62520	TATCTGCAAGACCTAAAAATTTGCACCCCTCCGCGCCTCTGGCAACCGGCGGTAGAC	62579
QY	62580	CTTCAAAACGTTTCTGTAAGAGTTAAACCTGGAAAGACACATCTTCTACACAGTGTGAGT	62639
Db	62580	CTTCAAAACGTTTCTGTAAGAGTTAAACCTGGAAAGACACATCTTCTACACAGTGTGAGT	62639
QY	62640	CCCCCGCACCCGGGGGATACACTCCCTCCAGGTTTGGTGCACACAGTACTGGGCCCTA	62699
Db	62640	CCCCCGCACCCGGGGGATACACTCCCTCCAGGTTTGGTGCACACAGTACTGGGCCCTA	62699
QY	62700	AAGGACGTGTTGCGCTCCAGAAATAAAGGTGGCGTGTGCTGTTTGGCGGGAGATTGAG	62759
Db	62700	AAGGACGTGTTGCGCTCCAGAAATAAAGGTGGCGTGTGCTGTTTGGCGGGAGATTGAG	62759
QY	62760	AAGGAAACGTTTCCGCGTTTACGTTTAAACATGAGTCTAAAGGACGAGATTGACTTTGTC	62819
Db	62760	AAGGAAACGTTTCCGCGTTTACGTTTAAACATGAGTCTAAAGGACGAGATTGACTTTGTC	62819
QY	82820	TCCCTTCAGAAAGCTCACAAGGGCGTGTGGCGTTGCAATCAACCGTGTAAATCTATAA	62879
Db	82820	TCCCTTCAGAAAGCTCACAAGGGCGTGTGGCGTTGCAATCAACCGTGTAAATCTATAA	62879
QY	62880	ATTAAAGGGGACACGTTTTTTTACCGGATAGGGTTTCGGTCCGTACAGGTTTGGCACTAGT	62939
Db	62880	ATTAAAGGGGACACGTTTTTTTACCGGATAGGGTTTCGGTCCGTACAGGTTTGGCACTAGT	62939
QY	62940	GATGACCTCAGAGAAAGATAGCCCTCCCTGTCGTACAGAGCTTACAGCGTTTATCCGC	62999
Db	62940	GATGACCTCAGAGAAAGATAGCCCTCCCTGTCGTACAGAGCTTACAGCGTTTATCCGC	62999
QY	63000	TGCTTAGAGATATACATTAACCAATTGACCGAAACCATGAGAGCGGAGCGTTTCCAA	63059
Db	63000	TGCTTAGAGATATACATTAACCAATTGACCGAAACCATGAGAGCGGAGCGTTTCCAA	63059
QY	63060	GTGTGCTGTGCGGGGACATATGGGGTACACTCAAAATTTAGCATGACATGCTTAAAGCA	63119
Db	63060	GTGTGCTGTGCGGGGACATATGGGGTACACTCAAAATTTAGCATGACATGCTTAAAGCA	63119
QY	63120	CAGGGAATGTCTGTTGGAGGAGTAGCCGTATATTTGGGTCCACAAAGACCTCCAGACA	63179
Db	63120	CAGGGAATGTCTGTTGGAGGAGTAGCCGTATATTTGGGTCCACAAAGACCTCCAGACA	63179
QY	63180	AGCCAGTGTATGTACCAATATCAGGCGTGTTAACCTCAAAATTTATTTGGTCAATGACAC	63239
Db	63180	AGCCAGTGTATGTACCAATATCAGGCGTGTTAACCTCAAAATTTATTTGGTCAATGACAC	63239
QY	63240	AACCCCTTTAAAAACCTCCGTCAGAGAACCAAGTCGATTAACACCTCCGCAAGACATTATGTC	63299
Db	63240	AACCCCTTTAAAAACCTCCGTCAGAGAACCAAGTCGATTAACACCTCCGCAAGACATTATGTC	63299
QY	63300	CGCGCCCTCCACAAACCCAAACACAAACCTCATCTACTTAATTAATTAATAACCAAGCAATG	63359
Db	63300	CGCGCCCTCCACAAACCCAAACACAAACCTCATCTACTTAATTAATTAATAACCAAGCAATG	63359
QY	63360	GAAAAATTTGTGTTTTTATTTACGTCCAACACAGGCGCAGGATATGTTGATTTCCACACA	63419
Db	63360	GAAAAATTTGTGTTTTTATTTACGTCCAACACAGGCGCAGGATATGTTGATTTCCACACA	63419
QY	63420	CCGGGGGGGTGGCGGCATAGTTTGACGACAGAAACGCGCGGCGCTCTGGGTTTGAAG	63479
Db	63420	CCGGGGGGGTGGCGGCATAGTTTGACGACAGAAACGCGCGGCGCTCTGGGTTTGAAG	63479
QY	63480	TAGCCCGGCCCGCGTGTGAGAGTACATGCTCTTAAAGGCGCTGGGTTGTAACCAAT	63539
Db	63480	TAGCCCGGCCCGCGTGTGAGAGTACATGCTCTTAAAGGCGCTGGGTTGTAACCAAT	63539
QY	63540	AAATTCACGTGCTATACACCGTTGACATCCCTGCGTACGCCGGGCTCTTGACAGGGGAC	63599
Db	63540	AAATTCACGTGCTATACACCGTTGACATCCCTGCGTACGCCGGGCTCTTGACAGGG	

Db 63900 TTTTCATCAGATGTCCTCGTAGTCATCTATAAAAAAATCGCTTCGTGCTGATTCAGATG 63959
QY 63960 ACTGGGGTGGGGGTTGGCCAGTAACCAACCGCAACGGGCGCGGACCAACAAAGCGG 64019
Db 63960 ACTGGGGTGGGGGTTGGCCAGTAACCAACCGCAACGGGCGCGGACCAACAAAGCGG 64019
QY 64020 TCAGTGGCGGGGCGGCTGGGTGGTGGTGCGACCTCTCGAAGTAATGACGTAAGTA 64079
Db 64020 TCAGTGGCGGGGCGGCTGGGTGGTGGTGCGACCTCTCGAAGTAATGACGTAAGTA 64079
QY 64080 GCGGCGCGCTGGTTAAAGAACTCACCGCTCCGCTGGCGGATCTATCTGAGTGGG 64139
Db 64080 GCGGCGCGCTGGTTAAAGAACTCACCGCTCCGCTGGCGGATCTATCTGAGTGGG 64139
QY 64140 AAGAGACCGGCGGTTGCTCTTTCATCCACATCACTGATGTCGCTTCCGAAATGAG 64199
Db 64140 AAGAGACCGGCGGTTGCTCTTTCATCCACATCACTGATGTCGCTTCCGAAATGAG 64199
QY 64200 ACTCGGTTTCGTCGCGGTTTGGAGTAGTGGGAGGGAATCTTGTCAAAAACATCT 64259
Db 64200 ACTCGGTTTCGTCGCGGTTTGGAGTAGTGGGAGGGAATCTTGTCAAAAACATCT 64259
QY 64260 CAGGTGCAATGATCAATCACTGGGGGCGCTCCGTAACCGGCGGTACCGGACCCG 64319
Db 64260 CAGGTGCAATGATCAATCACTGGGGGCGCTCCGTAACCGGCGGTACCGGACCCG 64319
QY 64320 TACGGGACCCGGGGAACAAAAAGCTGTGTTCTCTTTTCTAGGTGCCCGGGAATCG 64379
Db 64320 TACGGGACCCGGGGAACAAAAAGCTGTGTTCTCTTTTCTAGGTGCCCGGGAATCG 64379
QY 64380 GCAGCATCTCTGGGAGTGGCGGCGGCGGCTCTGACGGTGGGATAGAACATAGCCATG 64439
Db 64380 GCAGCATCTCTGGGAGTGGCGGCGGCGGCTCTGACGGTGGGATAGAACATAGCCATG 64439
QY 64440 CCGAAACGTTCACTGTAAAGACGACTGCTATCCCGATCACTGATATTTCCAGTCAAC 64499
Db 64440 CCGAAACGTTCACTGTAAAGACGACTGCTATCCCGATCACTGATATTTCCAGTCAAC 64499
QY 64500 GGCACCCCTCGATCTGTAAGTATGTCATTCGCAAGTTTAAATGGTTGACGCTAG 64559
Db 64500 GGCACCCCTCGATCTGTAAGTATGTCATTCGCAAGTTTAAATGGTTGACGCTAG 64559
QY 64560 AAACGTGGGCGGGAACCGGTTGCGCGGGGGGTAGCCAGGGGAGCGAATGGG 64619
Db 64560 AAACGTGGGCGGGAACCGGTTGCGCGGGGGGTAGCCAGGGGAGCGAATGGG 64619
QY 64620 CGCCTTGAGAGAGATGTCGTGCTGCTTATCAGCGTCCGCTTGTATAGCCTTCT 64679
Db 64620 CGCCTTGAGAGAGATGTCGTGCTGCTTATCAGCGTCCGCTTGTATAGCCTTCT 64679
QY 64680 TCCCCACAGCATAAAAACGACCTCGAAGCTTGAGAAAGGACACTTATTATGAGCT 64739
Db 64680 TCCCCACAGCATAAAAACGACCTCGAAGCTTGAGAAAGGACACTTATTATGAGCT 64739
QY 64740 GGTGAACCAATCCACGCAAGGTGGCGGTGACCCCGCTTCCCTTTCCACCTCGAG 64799
Db 64740 GGTGAACCAATCCACGCAAGGTGGCGGTGACCCCGCTTCCCTTTCCACCTCGAG 64799
QY 64800 AATGGGTTTAAAGCAGAACTCCCGTTTGGCCAAAGCTTAAGCACCCGAGAGAAG 64859
Db 64800 AATGGGTTTAAAGCAGAACTCCCGTTTGGCCAAAGCTTAAGCACCCGAGAGAAG 64859
QY 64860 ACGGTGAACCCAGGTACAGTATTTGGCTATCTCTTAAAAATATTTTGAAGGTTGAGG 64919
Db 64860 ACGGTGAACCCAGGTACAGTATTTGGCTATCTCTTAAAAATATTTTGAAGGTTGAGG 64919
QY 64920 TATCTGTAAGTCGGAAGCAAGCGTAAAGGCTAGTCCGCTTGACCCGAGTGAAGG 64979
Db 64920 TATCTGTAAGTCGGAAGCAAGCGTAAAGGCTAGTCCGCTTGACCCGAGTGAAGG 64979
QY 64980 ATCCGGAAGATACGACTTTATATTCCTCCGTTGGCAACATTAAGACACACAT 65039
Db 64980 ATCCGGAAGATACGACTTTATATTCCTCCGTTGGCAACATTAAGACACACAT 65039

Db 64980 ATCCGGAAGATACGACTTTATATTCCTCCGTTGGCAACATTAAGACACACAT 65039
QY 65040 AATTCTATCTATCGGTGATTAATTCACGGTTAGCTTGCATATTCATAACGGCTTCAG 65099
Db 65040 AATTCTATCTATCGGTGATTAATTCACGGTTAGCTTGCATATTCATAACGGCTTCAG 65099
QY 65100 CAGAGCCGGAGCTTCTGTTTAAAAATGGAAGAAATTTAAATTTCAAGCCTAGATC 65159
Db 65100 CAGAGCCGGAGCTTCTGTTTAAAAATGGAAGAAATTTAAATTTCAAGCCTAGATC 65159
QY 65160 GCTAATGACAACTTTGTTGGTGGAGGTTCTTAACTCTGGTGACATTTTACTCCA 65219
Db 65160 GCTAATGACAACTTTGTTGGTGGAGGTTCTTAACTCTGGTGACATTTTACTCCA 65219
QY 65220 AACTATGTTTAAAGCAACCTCATTAATCCCGCTCGTGTAAATTAAGTATAGATTA 65279
Db 65220 AACTATGTTTAAAGCAACCTCATTAATCCCGCTCGTGTAAATTAAGTATAGATTA 65279
QY 65280 CGTGAACCTTTTACTTCTGCTGAGAAATCCACAGAGTGGCCGCTAATAGCAT 65339
Db 65280 CGTGAACCTTTTACTTCTGCTGAGAAATCCACAGAGTGGCCGCTAATAGCAT 65339
QY 65340 CCGCTTCACTACCGTTTATGTAAGTCTTCAAACTCGGCTAAAAACTATCAAGACTA 65399
Db 65340 CCGCTTCACTACCGTTTATGTAAGTCTTCAAACTCGGCTAAAAACTATCAAGACTA 65399
QY 65400 TATTCATATTAATTCACAAATGAGCTCTCTGCGGACACTGTAATTTAACTGTAC 65459
Db 65400 TATTCATATTAATTCACAAATGAGCTCTCTGCGGACACTGTAATTTAACTGTAC 65459
QY 65460 AAATCCTTATAAAAACGCTTAAGTGAATCCATTTACATATTTCTGAGTAG 65519
Db 65460 AAATCCTTATAAAAACGCTTAAGTGAATCCATTTACATATTTCTGAGTAG 65519
QY 65520 CGATCAGCTTATATGCAATGTTGCTGTAACAGCCCTGAGACATTAAGCTAATTTGTT 65579
Db 65520 CGATCAGCTTATATGCAATGTTGCTGTAACAGCCCTGAGACATTAAGCTAATTTGTT 65579
QY 65580 AAATGAAAAGCAATTCACAAAGCGCTCGGGAATATTAAGTCACTAAGTATTAAT 65639
Db 65580 AAATGAAAAGCAATTCACAAAGCGCTCGGGAATATTAAGTCACTAAGTATTAAT 65639
QY 65640 TTACAACATGATTTCTACAAAGCCCGGTACCAACATGTAATTTAAAAATTCACATGTA 65699
Db 65640 TTACAACATGATTTCTACAAAGCCCGGTACCAACATGTAATTTAAAAATTCACATGTA 65699
QY 65700 ATAAATAACTTAAGGTATACATTTCTCATGTTTATTAATTAATGAAAGCTAATGC 65759
Db 65700 ATAAATAACTTAAGGTATACATTTCTCATGTTTATTAATTAATGAAAGCTAATGC 65759
QY 65760 TGTACTTATATTAATGATATGATTAATGCAATTAAGTCAATTAAGTCAATTAATTAAG 65819
Db 65760 TGTACTTATATTAATGATATGATTAATGCAATTAAGTCAATTAAGTCAATTAATTAAG 65819
QY 65820 CATTAATGCAACCTCAATTAATTAACAAATGACGCTTCGGAATTCGCCAGCT 65879
Db 65820 CATTAATGCAACCTCAATTAATTAACAAATGACGCTTCGGAATTCGCCAGCT 65879
QY 65880 GTTAAACCGAAATATACAGAAATGACTACAAACACACCTGAAACCAATTTTATTCGA 65939
Db 65880 GTTAAACCGAAATATACAGAAATGACTACAAACACACCTGAAACCAATTTTATTCGA 65939
QY 65940 CATATCAACAAATATTTAGGGTAAACCATGTTAATAAATAGCAGATGACATTTT 65999
Db 65940 CATATCAACAAATATTTAGGGTAAACCATGTTAATAAATAGCAGATGACATTTT 65999
QY 66000 TAGCTAAGCTCCGCAAGCAATTTCTCTTCAATTAAGTCAATCAACCTGCTGTTCC 66059
Db 66000 TAGCTAAGCTCCGCAAGCAATTTCTCTTCAATTAAGTCAATCAACCTGCTGTTCC 66059
QY 66060 GTGTTAATGTCGGAATTAATGATGTCAGAGTATCCCTGCAATCGGCACAAATTAATTC 66119
Db 66060 GTGTTAATGTCGGAATTAATGATGTCAGAGTATCCCTGCAATCGGCACAAATTAATTC 66119

QY	66120	AGGGCTTGTA	AAATAT	CATCCAGT	CAATCA	AGCTGCT	TAATGTA	AGAGAT	GTGTTTCT	TAAT	66179	
Db	66120	AGGGCTTGTA	AAATAT	CATCCAGT	CAATCA	AGCTGCT	TAATGTA	AGAGAT	GTGTTTCT	TAAT	66179	
QY	66180	TTT	AGCCAT	CCAA	ATG	TG	TGAG	TGGG	TGAC	ACTTTTGG	GA	66239
Db	66180	TTT	AGCCAT	CCAA	ATG	TG	TGAG	TGGG	TGAC	ACTTTTGG	GA	66239
QY	66240	CGCTCCAC	AAACG	GAAG	GATCAT	TTGATCG	TTCCAC	AGGGG	GCAGCAT	TAATTTATTTT	66299	
Db	66240	CGCTCCAC	AAACG	GAAG	GATCAT	TTGATCG	TTCCAC	AGGGG	GCAGCAT	TAATTTATTTT	66299	
QY	66300	ATTAAC	ATCAG	AGAAC	CGGAC	CCGCTCA	TAGAC	CAATAT	GTCCATTA	TAGATTG	GA	66359
Db	66300	ATTAAC	ATCAG	AGAAC	CGGAC	CCGCTCA	TAGAC	CAATAT	GTCCATTA	TAGATTG	GA	66359
QY	66360	ACACTGGT	TAAAT	TGAC	GGTGA	AAAAAAT	TGTAAT	TGTGTCA	ATGCGCAT	TAATTTT	66419	
Db	66360	ACACTGGT	TAAAT	TGAC	GGTGA	AAAAAAT	TGTAAT	TGTGTCA	ATGCGCAT	TAATTTT	66419	
QY	66420	AACCA	CACG	AGGGG	CGAAT	AAAAAG	GGGTCC	CGGCGCT	TAAGG	CCGTGA	TGCGAG	66479
Db	66420	AACCA	CACG	AGGGG	CGAAT	AAAAAG	GGGTCC	CGGCGCT	TAAGG	CCGTGA	TGCGAG	66479
QY	66480	CGGCTCAT	TG	CCATTTT	CGAC	ATTGTT	TAAATCT	GTTCGA	ACAT	TAGAGTCT	TAAT	66539
Db	66480	CGGCTCAT	TG	CCATTTT	CGAC	ATTGTT	TAAATCT	GTTCGA	ACAT	TAGAGTCT	TAAT	66539
QY	66540	TAT	AACAC	AGCA	AGTTCA	AAACG	AGGAG	GGGAC	GGGCTG	TTCCAC	CCGCGAC	66599
Db	66540	TAT	AACAC	AGCA	AGTTCA	AAACG	AGGAG	GGGAC	GGGCTG	TTCCAC	CCGCGAC	66599
QY	66600	CTC	CAAA	CCG	GAAC	CTCTAG	AGAC	AGC	ATCAAA	AGCCTT	GCAG	66659
Db	66600	CTC	CAAA	CCG	GAAC	CTCTAG	AGAC	AGC	ATCAAA	AGCCTT	GCAG	66659
QY	66660	GAA	AC	CCT	AGT	CTG	AG	AC	CCATCT	GTGTTA	AACTG	66719
Db	66660	GAA	AC	CCT	AGT	CTG	AG	AC	CCATCT	GTGTTA	AACTG	66719
QY	66720	CAC	AG	CTG	CTT	GTG	AG	ATTA	AGG	GGCCTC	AG	66779
Db	66720	CAC	AG	CTG	CTT	GTG	AG	ATTA	AGG	GGCCTC	AG	66779
QY	66780	TG	CTG	GG	CGG	CGCTCG	CGAC	CTTT	GA	CCG	CA	66839
Db	66780	TG	CTG	GG	CGG	CGCTCG	CGAC	CTTT	GA	CCG	CA	66839
QY	66840	CG	CT	CTT	GA	AG	CGG	CCCAT	CTG	GGCAT	TAG	66899
Db	66840	CG	CT	CTT	GA	AG	CGG	CCCAT	CTG	GGCAT	TAG	66899
QY	66900	TG	CA	TAT	AT	AT	CTG	TG	GGT	TA	AA	66959
Db	66900	TG	CA	TAT	AT	AT	CTG	TG	GGT	TA	AA	66959
QY	66960	CTT	TC	AT	CG	TTTTCT	CTG	AT	CT	TA	AG	67019
Db	66960	CTT	TC	AT	CG	TTTTCT	CTG	AT	CT	TA	AG	67019
QY	67020	AA	CC	C	AG	AT	GT	CG	AC	CTT	TA	67079
Db	67020	AA	CC	C	AG	AT	GT	CG	AC	CTT	TA	67079
QY	67080	TTT	CA	G	AT	GT	CG	AC	CTT	TA	AG	67139
Db	67080	TTT	CA	G	AT	GT	CG	AC	CTT	TA	AG	67139
QY	67140	AC	AC	CTT	TA	CT	GA	T	GA	AA	GC	67199
Db	67140	AC	AC	CTT	TA	CT	GA	T	GA	AA	GC	67199

QY	67200	CTAACCCCGAAACAGAGCTAAATACCAATGACTGTACCCCTTACCCCAAGCACGCCCCC	67259
Db	67200	CTAACCCCGAAACAGAGCTAAATACCAATGACTGTACCCCTTACCCCAAGCACGCCCCC	67259
QY	67260	GTACTATTACCAAGGGGTAGTAACACAGCTATCCCTTTAAAAACCATAACGAGAGTTTG	67319
Db	67260	GTACTATTACCAAGGGGTAGTAACACAGCTATCCCTTTAAAAACCATAACGAGAGTTTG	67319
QY	67320	TAAAGTAAACAGCTCGTGTATATTTTACAGACGCCGTGCATTAATAAGGATACGACACAAT	67379
Db	67320	TAAAGTAAACAGCTCGTGTATATTTTACAGACGCCGTGCATTAATAAGGATACGACACAAT	67379
QY	67380	CAGGTATTAACTTTTTTTTATTCAGAGATTACAGAGGGCGTGTTCACAGTGTGTAGGTG	67439
Db	67380	CAGGTATTAACTTTTTTTTATTCAGAGATTACAGAGGGCGTGTTCACAGTGTGTAGGTG	67439
QY	67440	GGACCAATATCCGCAGATGGGATGGCTGTGTATCCACACTTAGCGCCGATACAGGTG	67499
Db	67440	GGACCAATATCCGCAGATGGGATGGCTGTGTATCCACACTTAGCGCCGATACAGGTG	67499
QY	67500	CTCTGTGTACTTTACTAGTGCCCATTAACCTAAATTTGGCGTGTATAGGTCGTACCAAC	67559
Db	67500	CTCTGTGTACTTTACTAGTGCCCATTAACCTAAATTTGGCGTGTATAGGTCGTACCAAC	67559
QY	67560	AAAAAAGCTGCGTCCCTGCGCTTTTGAAGCTCTATGACAGCTTATATCGTCCAAATAG	67619
Db	67560	AAAAAAGCTGCGTCCCTGCGCTTTTGAAGCTCTATGACAGCTTATATCGTCCAAATAG	67619
QY	67620	CTTGCTTTTAAAAATGCACTGTGTGTACATCTTTATGACAGTGTGCCAAAAAACAAAG	67679
Db	67620	CTTGCTTTTAAAAATGCACTGTGTGTACATCTTTATGACAGTGTGCCAAAAAACAAAG	67679
QY	67680	ATTTTAAAAACAGTTAAACTGCGTGCCTGTAGTCTCGTATATTAACCTCCCTCAACAG	67739
Db	67680	ATTTTAAAAACAGTTAAACTGCGTGCCTGTAGTCTCGTATATTAACCTCCCTCAACAG	67739
QY	67740	AAAAAATTTTTTAAACCAACTGCCAGGTACTGAAGAATGTTAGCGAGAGGTGCTGAAT	67799
Db	67740	AAAAAATTTTTTAAACCAACTGCCAGGTACTGAAGAATGTTAGCGAGAGGTGCTGTAAT	67799
QY	67800	AGTGTATATATCCCTTCACACCTCCCTTTGAAGGTTTGGTTTACACGACCATGTGAGA	67859
Db	67800	AGTGTATATATCCCTTCACACCTCCCTTTGAAGGTTTGGTTTACACGACCATGTGAGA	67859
QY	67860	TAGGACACAGCTCAGGGGGAGGTGCGGATCTGTGAGGGGTAAACAATTCGTGGCGTGGGG	67919
Db	67860	TAGGACACAGCTCAGGGGGAGGTGCGGATCTGTGAGGGGTAAACAATTCGTGGCGTGGGG	67919
QY	67920	GTACTCCAGTTTATAGATCTCCGGCAGAGCGGTACAGATCTTGCTCAATCTCAACGA	67979
Db	67920	GTACTCCAGTTTATAGATCTCCGGCAGAGCGGTACAGATCTTGCTCAATCTCAACGA	67979
QY	67980	GCCCGCATTCACAGGGGGAGTACTGAGTTAATACTCCCGGAATCTATACGTTCTGTAT	68039
Db	67980	GCCCGCATTCACAGGGGGAGTACTGAGTTAATACTCCCGGAATCTATACGTTCTGTAT	68039
QY	68040	TTTTTGGAGGTCCTTTAGACAGTAAACCAATGTTGCTCCACACACTCGGTACANTAAACG	68099
Db	68040	TTTTTGGAGGTCCTTTAGACAGTAAACCAATGTTGCTCCACACACTCGGTACANTAAACG	68099
QY	68100	CTCTCTCTGTCTGTGTGATGAGACACTGAGATCTTTAGACAGGTAATAGGCCCGTTTC	68159
Db	68100	CTCTCTCTGTCTGTGTGATGAGACACTGAGATCTTTAGACAGGTAATAGGCCCGTTTC	68159
QY	68160	CACCTTAAGGGTGGCCGCTGTGTAGAGCGGATTTGGCGGATTTGACGGTACAGTGTTCAT	68219
Db	68160	CACCTTAAGGGTGGCCGCTGTGTAGAGCGGATTTGGCGGATTTGACGGTACAGTGTTCAT	68219
QY	68220	TTTCCACAGTATATATGCGCAGTGGCGAGTATAGTGAACCTGTACATATGATTTTAAAAAGT	68279
Db	68220	TTTCCACAGTATATATGCGCAGTGGCGAGTATAGTGAACCTGTACATATGATTTTAAAAAGT	68279
QY	68280	GTCCTTTCGCTTAATGGCGACTCATGGTCTGTTTAAAGTTCACAGGCTGTTTAAAAAACT	68339

Db 68280 GTCCTCCGCTATGCGACTATGCTGTGTTTAACTTCACAGGGTGTAAAAACT 68339
QY 68340 CAGAAAGTCTCTGCTGAGCAACTTTTTCGCGACTCTCCGAACCGCTAGGGATTAAGCTGA 68399
Db 68340 CAGAAAGTCTCTGCTGAGCAACTTTTTCGCGACTCTCCGAACCGCTAGGGATTAAGCTGA 68399
QY 68400 CCACGGGTGCTTCTTATTAACGAAAGATACGTCAAAAAACATGACCACTGACCTAAA 68459
Db 68400 CCACGGGTGCTTCTTATTAACGAAAGATACGTCAAAAAACATGACCACTGACCTAAA 68459
QY 68460 TAAGCTCAGAAAGATGCTGTGATGATTAAGTAAGTAAGTGTCTCTCCCTGGTCCCAT 68519
Db 68460 TAAGCTCAGAAAGATGCTGTGATGATTAAGTAAGTAAGTGTCTCTCCCTGGTCCCAT 68519
QY 68520 CTCGGGCTCATCGCGGATCTGAATCTCTTAACTGTCTGCTTACCGGGGTCCCG 68579
Db 68520 CTCGGGCTCATCGCGGATCTGAATCTCTTAACTGTCTGCTTACCGGGGTCCCG 68579
QY 68580 GGTAAACCCCGGGGGCCGCACTGTAAAGTCCCGTCCGCAAGATGCGCCAGGGCAT 68639
Db 68580 GGTAAACCCCGGGGGCCGCACTGTAAAGTCCCGTCCGCAAGATGCGCCAGGGCAT 68639
QY 68640 CCGTGAAGATTCACCGAGAGGGCCCTTGTGTACGGAAGATGTCATAGCCGTCCG 68699
Db 68640 CCGTGAAGATTCACCGAGAGGGCCCTTGTGTACGGAAGATGTCATAGCCGTCCG 68699
QY 68640 CCGTGAAGATTCACCGAGAGGGCCCTTGTGTACGGAAGATGTCATAGCCGTCCG 68699
Db 68640 CCGTGAAGATTCACCGAGAGGGCCCTTGTGTACGGAAGATGTCATAGCCGTCCG 68699
QY 68700 CTGCAAGCGGGGTCTTATACCGCCCGAGTTGGCCAGATTCGACAGAGCTACCGGA 68759
Db 68700 CTGCAAGCGGGGTCTTATACCGCCCGAGTTGGCCAGATTCGACAGAGCTACCGGA 68759
QY 68760 AATGAAGGCCAAGTGTGGGGGGCGTGTCTCATATGTGCAAGCGCTATCAT 68819
Db 68760 AATGAAGGCCAAGTGTGGGGGGCGTGTCTCATATGTGCAAGCGCTATCAT 68819
QY 68820 GGTATTTGCGAGTGGTCTCTGTCTATATATACCTGATGCGGAGGAAATGGA 68879
Db 68820 GGTATTTGCGAGTGGTCTCTGTCTATATATACCTGATGCGGAGGAAATGGA 68879
QY 68880 ACTTAGACTCAAGAGCACTGTGCAAACTTTTTCACCCCATCTTCTTCAAGATCTT 68939
Db 68880 ACTTAGACTCAAGAGCACTGTGCAAACTTTTTCACCCCATCTTCTTCAAGATCTT 68939
QY 68940 ACCCCCTATGCACTACTGTGCAAGGAGATGGTCTCTGACATTTATTTACATCAC 68999
Db 68940 ACCCCCTATGCACTACTGTGCAAGGAGATGGTCTCTGACATTTATTTACATCAC 68999
QY 69000 CCGTACGGCGGAGAGAGGCGCTGTGCTGATGGAATGCTAGGCGGATGACGCTCC 69059
Db 69000 CCGTACGGCGGAGAGAGGCGCTGTGCTGATGGAATGCTAGGCGGATGACGCTCC 69059
QY 69060 GGGAAAGCAGCTTGTCCCGATCTCTTAATCTCTGCAATGCAACCGGGCTTCTCC 69119
Db 69060 GGGAAAGCAGCTTGTCCCGATCTCTTAATCTCTGCAATGCAACCGGGCTTCTCC 69119
QY 69120 GGCACCCCTGCTGCTGACTAGTAATGTCTTAAAGAAATCCAGAAATATCTTCAAGCCCC 69179
Db 69120 GGCACCCCTGCTGCTGACTAGTAATGTCTTAAAGAAATCCAGAAATATCTTCAAGCCCC 69179
QY 69180 ACCCCGATCAATTTGTATACAAACAGCAGCCCATGTCGCTCAGTCCAGTCCGAT 69239
Db 69180 ACCCCGATCAATTTGTATACAAACAGCAGCCCATGTCGCTCAGTCCAGTCCGAT 69239
QY 69240 TATTAAGCCCAACCCAGGGGCTTGTCCCGCAATGTTTATGACACCTGGAAGCGGT 69299
Db 69240 TATTAAGCCCAACCCAGGGGCTTGTCCCGCAATGTTTATGACACCTGGAAGCGGT 69299
QY 69300 GTCAAGAGCATTTACACAGGCAAGAGCGCTTATTTGGCGCGCACTAAACGGGTT 69359
Db 69300 GTCAAGAGCATTTACACAGGCAAGAGCGCTTATTTGGCGCGCACTAAACGGGTT 69359
QY 69360 GACATCTGGGGCGCTGGCGGCATATGCAATGTTCCAGTTGCCGAGCTCTCGGA 69419
Db 69360 GACATCTGGGGCGCTGGCGGCATATGCAATGTTCCAGTTGCCGAGCTCTCGGA 69419
QY 69420 GGTGAAGGGTCCGCGGGGTGATTTGCGGAAACAGCATGCTTCCGACCGCGTT 69479
Db 69420 GGTGAAGGGTCCGCGGGGTGATTTGCGGAAACAGCATGCTTCCGACCGCGTT 69479
QY 69480 ACCGCCAATGTCCCCCGCAAGAGATGGAACCGTAGACAGTTGGAAAGCTCCCT 69539
Db 69480 ACCGCCAATGTCCCCCGCAAGAGATGGAACCGTAGACAGTTGGAAAGCTCCCT 69539
QY 69540 AAAAAAGTCCCATGAGAGGCGGCTATACGCTCAGTGTAAATATACATATAGA 69599
Db 69540 AAAAAAGTCCCATGAGAGGCGGCTATACGCTCAGTGTAAATATACATATAGA 69599
QY 69600 CTTAAGCTCCCGTCAGGGTCCGCGAGATCCGCGCATATGCGCAACCTCCAGATC 69659
Db 69600 CTTAAGCTCCCGTCAGGGTCCGCGAGATCCGCGCATATGCGCAACCTCCAGATC 69659
QY 69660 CCGCATGCGCGGCTCTCCGCTTCCGCGCAACCGCGCATACGCTTCCGCTTAAG 69719
Db 69660 CCGCATGCGCGGCTCTCCGCTTCCGCGCAACCGCGCATACGCTTCCGCTTAAG 69719
QY 69720 AAAAGCAGCGAGAGAGTGGCAGAAAAAGACTGAAGGGGAGCTTCGGGCGCCG 69779
Db 69720 AAAAGCAGCGAGAGAGTGGCAGAAAAAGACTGAAGGGGAGCTTCGGGCGCCG 69779
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Db 69780 AACAGTAAACCAACCTTCTCCGGGACGTCGGGATGCGCTTCCGAGCGGCTTAT 69839
QY 69840 CCAATTTAATCGAAAGTCCACGATTAACCCGGAACGATCTGGAACCCAAACGACGA 69899
Db 69840 CCAATTTAATCGAAAGTCCACGATTAACCCGGAACGATCTGGAACCCAAACGACGA 69899
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Db 69900 CGACATGTAGCGGCTATCTACAGAGCTGTATGAGTACAGTCCCGCGGCATCA 69959
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Db 69960 TTCGCCCTCAGCACTGCGGACATGAGAGATATTTCCAGAGTATGTCGCGCATCTAG 70019
QY 70020 CGGCCAGGATGCTTGAAGATGACCCCAAGCAGATACACACCGAGACATG 70079
Db 70020 CGGCCAGGATGCTTGAAGATGACCCCAAGCAGATACACACCGAGACATG 70079
QY 70080 CCGCCAGGATGCTTGAAGATGACCCCAAGCAGATACACACCGAGACATG 70139
Db 70080 CCGCCAGGATGCTTGAAGATGACCCCAAGCAGATACACACCGAGACATG 70139
QY 70140 CGACAAATGAGCTTCAAACTTCTGCTATTTCCGAGACCTAAAAAT 70199
Db 70140 CGACAAATGAGCTTCAAACTTCTGCTATTTCCGAGACCTAAAAAT 70199
QY 70200 GTCCGAGTGGGACAAATTTTAAAGTCTGTAAATGTCACCTTCTCAAGTTCTGTC 70259
Db 70200 GTCCGAGTGGGACAAATTTTAAAGTCTGTAAATGTCACCTTCTCAAGTTCTGTC 70259
QY 70260 CTAGAAATTTCAATCCATTTCAATATATATAAAGACACCTGTTTCTGTAATC 70319
Db 70260 CTAGAAATTTCAATCCATTTCAATATATATATAAAGACACCTGTTTCTGTAATC 70319
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Db 70320 TGGCGTGTATCTTGAAGAGGCGCCCTAAAAACATGCGCTGCTGTAAGAACACCA 70379
QY 70380 AGAGACCCCAAGTGTGTAATTTATGCAATTTATGATGTCACAGGTGGAACACAGGAGA 70439
Db 70380 AGAGACCCCAAGTGTGTAATTTATGCAATTTATGATGTCACAGGTGGAACACAGGAGA 70439
QY 70440 TGGATTTCAAAACCGTGTCTGACGGCGCAGAGATGCTCGGGTTTATATATACG 70499
Db 70440 TGGATTTCAAAACCGTGTCTGACGGCGCAGAGATGCTCGGGTTTATATATACG 70499

QY 70500 AGAATAACGGCCCGTTTCCCAATATGACAAATGAGACAGACCAATACCGGGAGAGGTG 70559
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Db 70500 AGAATAACGGCCCGTTTCCCAATATGACAAATGAGACAGACCAATACCGGGAGAGGTG 70559
QY 70560 AAAGCTTCGGACACTACGCTGCGGCGAGCGGTTTCTGGGCGGTCTGTGTCAAGGATGT 70619
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Db 70560 AAAGCTTCGGACACTACGCTGCGGCGAGCGGTTTCTGGGCGGTCTGTGTCAAGGATGT 70619
QY 70620 ATGGAACAACACCGGAGAGGGCGGTCTAAAGACCGTCCGGCTGGCCGTAACCGCT 70679
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Db 70620 ATGGAACAACACCGGAGAGGGCGGTCTAAAGACCGTCCGGCTGGCCGTAACCGCT 70679
QY 70680 CGGCTCAGCTAATTCACGGGCGTCCGAGGCGCTGTGTGGCCGAGCAAGGACCTTCACAG 70739
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Db 70680 CGGCTCAGCTAATTCACGGGCGTCCGAGGCGCTGTGTGGCCGAGCAAGGACCTTCACAG 70739
QY 70740 GGGACATGCGCTATCTGACCGGATAGGACAGAGCGGTGGCGCTGACAAATAGACTCTCA 70799
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Db 70740 GGGACATGCGCTATCTGACCGGATAGGACAGAGCGGTGGCGCTGACAAATAGACTCTCA 70799
QY 70800 AGGTGATGCGGCGCTGCGACAAACAAAGACCGCTTCCGACGCACTCTGCTTGC 70859
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Db 70800 AGGTGATGCGGCGCTGCGACAAACAAAGACCGCTTCCGACGCACTCTGCTTGC 70859
QY 70860 GTTGCTAATCTTTGATGTTTAAACAGTAATGTCTGTTTATATTAACCTTCGATAGCCG 70919
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Db 70860 GTTGCTAATCTTTGATGTTTAAACAGTAATGTCTGTTTATATTAACCTTCGATAGCCG 70919
QY 70920 AACCGAAGCTGTGCGATGCGGATTAATAACGACACTGGAAGCTGATGAGAGCG 70979
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Db 70920 AACCGAAGCTGTGCGATGCGGATTAATAACGACACTGGAAGCTGATGAGAGCG 70979
QY 70980 CAAACGCGGCGGAGTGCAGACCTCAGGAAAAATAAGGCCAAGACACTGCAACAG 71039
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Db 70980 CAAACGCGGCGGAGTGCAGACCTCAGGAAAAATAAGGCCAAGACACTGCAACAG 71039
QY 71040 TACAAATAGCAAAATTTAGTAATTTTAAAGTTTCCGAGGTTTCCCGTGCCCT 71099
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Db 71040 TACAAATAGCAAAATTTAGTAATTTTAAAGTTTCCGAGGTTTCCCGTGCCCT 71099
QY 71100 GCGGCAACCGGTCGCTGCTTAACTGGAATACCTCTCCCTAACAAGCAGATTCACAAG 71159
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Db 71100 GCGGCAACCGGTCGCTGCTTAACTGGAATACCTCTCCCTAACAAGCAGATTCACAAG 71159
QY 71160 GAGCTGGAAGTAATAACAAGCAAGTACCGCTCTCAACGACGAAAGCCCTTCAA 71219
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Db 71160 GAGCTGGAAGTAATAACAAGCAAGTACCGCTCTCAACGACGAAAGCCCTTCAA 71219
QY 71220 AAGCAGCGATCAATTTTACAGAAAGATGATGATGATGTCAAAAACGGGAACAGTAA 71279
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Db 71220 AAGCAGCGATCAATTTTACAGAAAGATGATGATGATGTCAAAAACGGGAACAGTAA 71279
QY 71280 AAAAGCAGCTGATGATTTAAAGCCAGCTGCGGTTACTAGTTTAAACTGCTTAATGAT 71339
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Db 71280 AAAAGCAGCTGATGATTTAAAGCCAGCTGCGGTTACTAGTTTAAACTGCTTAATGAT 71339
QY 71340 CTAATCACCCTTAATAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 71399
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Db 71340 CTAATCACCCTTAATAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 71399
QY 71400 TAAACTATTTAACTATTTGGAATTAAGATTTATGGAATTAAGGATTAAGGATTAATTT 71459
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Db 71400 TAAACTATTTAACTATTTGGAATTAAGATTTATGGAATTAAGGATTAAGGATTAATTT 71459
QY 71460 TTTGGATTCATGATTTGGGAATACATGCTGGGATGAGGATTAATGCTTCTGCGG 71519
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Db 71460 TTTGGATTCATGATTTGGGAATACATGCTGGGATGAGGATTAATGCTTCTGCGG 71519
QY 71520 TGGCGTGCATGACGAGGAGCGGTGCTGTCGCAACCTGGACACTGACAGATGGGAAT 71579
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Db 71520 TGGCGTGCATGACGAGGAGCGGTGCTGTCGCAACCTGGACACTGACAGATGGGAAT 71579

QY 71580 ACGAGCGGTATACAGGCACTACCTGCAAGAGTGCAGCAAAATGAAGCTCGGGAGCC 71639
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Db 71580 ACGAGCGGTATACAGGCACTACCTGCAAGAGTGCAGCAAAATGAAGGCTCGGGAGCC 71639
QY 71640 TGGACGTTTCGGACAGCAAAAGGCTCTGGAACCAAGCAACCAAGCTAATATAT 71699
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Db 71640 TGGACGTTTCGGACAGCAAAAGGCTCTGGAACCAAGCAACCAAGCTAATATAT 71699
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Db 71700 CGATTAAGACCTAAGTGTGTCATGACATGAAATTAAGAGCCGCTGGGACAGCAGCA 71759
QY 71760 GGGCCGAAATCATCACAGGACCTGCGACGATCAAGAGGTTAAAGCTCTCGATTAACA 71819
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Db 71760 GGGCCGAAATCATCACAGGACCTGCGACGATCAAGAGGTTAAAGCTCTCGATTAACA 71819
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Db 71820 CCCCCGAATTTGGCGCAACCACTCCGCTAGTAAATGACATCCGCGGAGTCAACATCAG 71879
QY 71880 GTGGGACACCGTGAACGGCGGCCCGGCGGCTTATGACACAAAGACATGCTCA 71939
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Db 71880 GTGGGACACCGTGAACGGCGGCCCGGCGGCTTATGACACAAAGACATGCTCA 71939
QY 71940 ACCCATCTGTGCTCTGCTTTCAGACCACTCCGTCGCGGTCACACGAGTACCGAGC 71999
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Db 71940 ACCCATCTGTGCTCTGCTTTCAGACCACTCCGTCGCGGTCACACGAGTACCGAGC 71999
QY 72000 AGTCGCTGCGGATCGGAACAGGTCACGACAGCTATGCTACCCCTGCGGCCCTTCCC 72059
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Db 72000 AGTCGCTGCGGATCGGAACAGGTCACGACAGCTATGCTACCCCTGCGGCCCTTCCC 72059
QY 72060 TCTTTCAGGACAGCCCTGCTCAGAGTGCAGGCTGACCCCTGCGGCCGGAAGCATG 72119
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Db 72060 TCTTTCAGGACAGCCCTGCTCAGAGTGCAGGCTGACCCCTGCGGCCGGAAGCATG 72119
QY 72120 CAAGATACGCGGAGTGCAGCAATATGACCAAAATTAAGCCGAAGAATACAGCC 72179
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Db 72120 CAAGATACGCGGAGTGCAGCAATATGACCAAAATTAAGCCGAAGAATACAGCC 72179
QY 72180 GTCCGTTGAGCGAGTGCAGGCTGACGAGTGCAGGAGCTCAAGGCTCGGTGACAG 72239
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Db 72180 GTCCGTTGAGCGAGTGCAGGCTGACGAGTGCAGGAGCTCAAGGCTCGGTGACAG 72239
QY 72240 CCAATTCCTCCCTTGCAGGAGCGGCTGACCTGTTTACCCCTGTGGCTATGAGCCGA 72299
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Db 72240 CCAATTCCTCCCTTGCAGGAGCGGCTGACCTGTTTACCCCTGTGGCTATGAGCCGA 72299
QY 72300 ATATTGGGCTCAGATGCGCTTGTACAGCATATATCAAAATATATGACATAGAACTAC 72359
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Db 72300 ATATTGGGCTCAGATGCGCTTGTACAGCATATATCAAAATATATGACATAGAACTAC 72359
QY 72360 ACGAGCTTACAGCGCAATTAAGGTTTATTTTTCACACTAGTCCGGTCTGATTTT 72419
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Db 72360 ACGAGCTTACAGCGCAATTAAGGTTTATTTTTCACACTAGTCCGGTCTGATTTT 72419
QY 72420 CTGCTCTGAGCTGAGGCGGCTCTCTCTAGGCGCCGTCGCGGCTGAGGATTCG 72479
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Db 72420 CTGCTCTGAGCTGAGGCGGCTCTCTCTAGGCGCCGTCGCGGCTGAGGATTCG 72479
QY 72480 CTTCTGCTGCTCTGCTCATTTGACAGCTGACGCGGATTAATTCGCGGAGGCGTCT 72539
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Db 72480 CTTCTGCTGCTCTGCTCATTTGACAGCTGACGCGGATTAATTCGCGGAGGCGTCT 72539
QY 72540 TCCATGCGCGGCGGCTGAGGCGCTGCGGCTGCGGCGCTGACCTTAAGCTTA 72599
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Db 72540 TCCATGCGCGGCGGCTGAGGCGCTGCGGCTGCGGCGCTGACCTTAAGCTTA 72599
QY 72600 CCGGTTTGCAGCTTACATTAAGGCGGAAGCGAGCTGATTTTGGCCTCTTTCGCTG 72659
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Db 72600 CCGGTTTGCAGCTTACATTAAGGCGGAAGCGAGCTGATTTTGGCCTCTTTCGCTG 72659
QY 72660 TTAGAGATGACGAGGCTGAGAGCCGAGCTGTGTGGATCCCAAGATTTATCAGCTTTTG 72719
|||||

D	b	72660	TTAGAGATGACGGGGTCCGAGCCGAGCTGTGGGATCCCAAGATTTATCAGCTTTTGG	72719	D	b	73740	TGAGTTGTATTATAGAGTCCACAGCTCAGACCCGCCAGCTCCCACTAATCGTGGGC	73799
O	y	72720	AGCTGCTTGTTTTCAACCGACAAATTTTTCACCTGAGCGGCTAATCCTCCATTGTACG	72779	O	y	73800	GCTGTGACGTGGCGCAAAAGGGGCTTACCGTGCAGCGACCAATGAGCCAGTGTGG	73859
D	b	72720	AGCTGCTTGTTTTCAACCGACAAATTTTTCACCTGAGCGGCTAATCCTCCATTGTACG	72779	D	b	73800	GCTGTGACGTGGCGCAAAAGGGGCTTACCGTGCAGCGACCAATGAGCCAGTGTGG	73859
O	y	72780	TCTTTTGGGGGCGCGCTCTGGGACCGCTGAGACATGGCAGCTACTACGCAATAC	72839	O	y	73860	TACATCTAGGTTTATTAACCTTACCAAGAGCCCAATGATATACACCAACAGCCGCA	73919
D	b	72780	TCTTTTGGGGGCGCGCTCTGGGACCGCTGAGACATGGCAGCTACTACGCAATAC	72839	D	b	73860	TACATCTAGGTTTATTAACCTTACCAAGAGCCCAATGATATACACCAACAGCCGCA	73919
O	y	72840	AGAGTACAGCGGGAGCTTAAATCTTTCAGGGGCGCCCTGAGGTCATCGGCGCCAG	72899	O	y	73920	TATGTACAGTGTATTTATCCAGAAAGACACAGCTCCCAAGGGGGGGAACATTTAGAT	73979
D	b	72840	AGAGTACAGCGGGAGCTTAAATCTTTCAGGGGCGCCCTGAGGTCATCGGCGCCAG	72899	D	b	73920	TATGTACAGTGTATTTATCCAGAAAGACACAGCTCCCAAGGGGGGGAACATTTAGAT	73979
O	y	72900	GTTTCAACAAATTTAAAAAGCACATATATGTAGTACAGAAATGTTGCAACCGCAGC	72959	O	y	73980	CCCGGTACAACTCGCGAGCACACCTCCAGATATCGTGGGCCAAATACGTTTACCGAG	74039
D	b	72900	GTTTCAACAAATTTAAAAAGCACATATATGTAGTACAGAAATGTTGCAACCGCAGC	72959	D	b	73980	CCCGGTACAACTCGCGAGCACACCTCCAGATATCGTGGGCCAAATACGTTTACCGAG	74039
O	y	72960	AGAACAGATTGATCAGCCCATATCTCGAAAACTAGACAGCAGCGGCTGTAGCTG	73019	O	y	74040	TGGCAGCGCTCCCAAAACCCACCGCTCAACTCCCGCCACACTCAAGCCAAACCGAAC	74099
D	b	72960	AGAACAGATTGATCAGCCCATATCTCGAAAACTAGACAGCAGCGGCTGTAGCTG	73019	D	b	74040	TGGCAGCGCTCCCAAAACCCACCGCTCAACTCCCGCCACACTCAAGCCAAACCGAAC	74099
O	y	73020	TCCGCGGAGCAATCATAGTCAATAAAAAGGGCGTTAGGAGGAGCGCGGAGGGGTTT	73079	O	y	74100	CGGAGACCGCCCGCGCCCAAAAGGGGTTGGGGTGTGAGGGTTATATTTTAAAAACATGG	74159
D	b	73020	TCCGCGGAGCAATCATAGTCAATAAAAAGGGCGTTAGGAGGAGCGCGGAGGGGTTT	73079	D	b	74100	CGGAGACCGCCCGCGCCCAAAAGGGGTTGGGGTGTGAGGGTTATATTTTAAAAACATGG	74159
O	y	73080	GTAATCAGAGAGGCGTCCGCTCTCTAGTTCGAGAGAGTGAGTACGCTGGCGCACAC	73139	O	y	74160	CATTATTTTAAAGTTTATTTTATTTTAAATAAAAACAATCCAAATTTACGTTAACATCAGCT	74219
D	b	73080	GTAATCAGAGAGGCGTCCGCTCTCTAGTTCGAGAGAGTGAGTACGCTGGCGCACAC	73139	D	b	74160	CATTATTTTAAAGTTTATTTTATTTTAAATAAAAACAATCCAAATTTACGTTAACATCAGCT	74219
O	y	73140	GGCAGACACATATATAGCAGCCCAACAGGGCTTAAACGAGACATTTGACCTGTCAAT	73199	O	y	74220	TGCGATCCTGTATTTATTTTCTGCGACGATATATCCGACCGCCACACTGGGGCTGC	74279
D	b	73140	GGCAGACACATATATAGCAGCCCAACAGGGCTTAAACGAGACATTTGACCTGTCAAT	73199	D	b	74220	TGCGATCCTGTATTTATTTTCTGCGACGATATATCCGACCGCCACACTGGGGCTGC	74279
O	y	73200	TTCAAGCGGGGTTTCGGAGGCAACCCCTCACTTTGGAGCGGCGCTCTCTTATATACT	73259	O	y	74280	GTTTGTCAATCACCGGATGGAGGGGTTGAGAGAGCGCTTGGTGTCTACAGCACATTA	74339
D	b	73200	TTCAAGCGGGGTTTCGGAGGCAACCCCTCACTTTGGAGCGGCGCTCTCTTATATACT	73259	D	b	74280	GTTTGTCAATCACCGGATGGAGGGGTTGAGAGAGCGCTTGGTGTCTACAGCACATTA	74339
O	y	73260	ACGAGTTAAACATTATGGCAGAGTGCAGCGCCCATACGGTTCCGTACGCCCTTGTGACTCT	73319	O	y	74340	TTAATTTCCGAGCCCGACGTGCAGACATATCGAGCGGATCGTGTGACCAAGTTTTC	74399
D	b	73260	ACGAGTTAAACATTATGGCAGAGTGCAGCGCCCATACGGTTCCGTACGCCCTTGTGACTCT	73319	D	b	74340	TTAATTTCCGAGCCCGACGTGCAGACATATCGAGCGGATCGTGTGACCAAGTTTTC	74399
O	y	73320	GTAAGTTGAATATATACCAAAAAACAATCTATCTCGTATAGCGTTACGCCAACAATTTTC	73379	O	y	74400	ATTTCAGAGTGCAGCGGTCCTGCGGGCCGTTTATTCAAAAGCGGTGAAGGCGCTC	74459
D	b	73320	GTAAGTTGAATATATATACCAAAAAACAATCTATCTCGTATAGCGTTACGCCAACAATTTTC	73379	D	b	74400	ATTTCAGAGTGCAGCGGTCCTGCGGGCCGTTTATTCAAAAGCGGTGAAGGCGCTC	74459
O	y	73380	CCGTGCTGTCAAAACCGGGAGAACCTTGTGCTGCGCCCTGGGACTAAAAATTTATCCGCG	73439	O	y	74460	TCGTCCACCGTAATATCCCTATAGCCAGGAGCAACATGAGGCTTCCAGATTAACGTTCTGT	74519
D	b	73380	CCGTGCTGTCAAAACCGGGAGAACCTTGTGCTGCGCCCTGGGACTAAAAATTTATCCGCG	73439	D	b	74460	TCGTCCACCGTAATATCCCTATAGCCAGGAGCAACATGAGGCTTCCAGATTAACGTTCTGT	74519
O	y	73440	CGCCCGAGTGGCATTTCTTCTCAGCGGAGCGCGAGGATGAGGTATTTACACACACG	73499	O	y	74520	ATPAGACTTTAGCTTAGATATTTGAATCTTAACCGTCTCTGCGACCCCGGGTACCTTA	74579
D	b	73440	CGCCCGAGTGGCATTTCTTCTCAGCGGAGCGCGAGGATGAGGTATTTACACACACG	73499	D	b	74520	ATPAGACTTTAGCTTAGATATTTGAATCTTAACCGTCTCTGCGACCCCGGGTACCTTA	74579
O	y	73500	GACTTATATGATCAAGGGATATGTGGAGAAATATAACTATGCTTCTCAATAAGACTAAC	73559	O	y	74580	GCCGCGTCAAAACGACGAAATPACTCGGTTATTTTATGGAATGGAACGGCCACAGATAC	74639
D	b	73500	GACTTATATGATCAAGGGATATGTGGAGAAATATAACTATGCTTCTCAATAAGACTAAC	73559	D	b	74580	GCCGCGTCAAAACGACGAAATPACTCGGTTATTTTATGGAATGGAACGGCCACAGATAC	74639
O	y	73560	AGGTGCTACACTTTACCGGGGAGAGTCAACGTCCTCATGCGCTTATATGATACGCT	73619	O	y	74640	GTCGTCCGAAGGGGCGGTGCACATCTCTGCTTCCATATCCCACTACCTCC	74699
D	b	73560	AGGTGCTACACTTTACCGGGGAGAGTCAACGTCCTCATGCGCTTATATGATACGCT	73619	D	b	74640	GTCGTCCGAAGGGGCGGTGCACATCTCTGCTTCCATATCCCACTACCTCC	74699
O	y	73620	CGCCCGGGCCCTTAAATGCGCGATCTAGAACCTACACATTTACTCTTGGACGCTGAT	73679	O	y	74700	GGGGGACAGCCATATGCTATTTTGGTCCGCGAGTGTAGTAGACACTCGTTAAGAGATCT	74759
D	b	73620	CGCCCGGGCCCTTAAATGCGCGATCTAGAACCTACACATTTACTCTTGGACGCTGAT	73679	D	b	74700	GGGGGACAGCCATATGCTATTTTGGTCCGCGAGTGTAGTAGAGACTCGTTAAGAGATCT	74759
O	y	73680	TTGATTTTACGTGGCGCATCTGCATGACATATACCCCAACGAGACAAAGCCCGTTTACGT	73739	O	y	74760	GGCAGGGAGCATATTTGACATCCCAACGCGTCCAAAGGACTTAACCCGCAACAGCTCAA	74819
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RESULT 2
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DEFINITION complete sequence.
ACCESSION AF210726
VERSION AF210726.1 GI:7329990
KEYWORDS Macaca mulatta rhadinovirus 26-95
SOURCE Macaca mulatta rhadinovirus 26-95
ORGANISM Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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REFERENCE 1 (bases 1 to 130733)
AUTHORS Alexander,L., Denekamp,L., Knapp,A., Auerbach,M.R., Damania,B. and
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TITLE The primary sequence of rhesus monkey rhadinovirus isolate 26-95:
       sequence similarities to Kaposi's sarcoma-associated herpesvirus
       and rhesus monkey rhadinovirus isolate 17517
       J Virol. 74 (7), 3388-3398 (2000)
JOURNAL MEDLINE 20173730
PUBMED 10708456
REFERENCE 2 (bases 1 to 130733)
AUTHORS Alexander,L., Denekamp,L.M., Knapp,A., Auerbach,M., Czajak,S.,
          Damania,B. and Desrochers,R.C.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1999) Microbiology, New England Regional Primate
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OY	49318	CGCCATAAGGAGACTGCTTGTAGGGGAGACTGTGTTAATTCGTTTGTGTACCTTTTC	49377	OY	50398	AACTGTGTGTCTTTTCCGGGTCTTTGATAGACGGCATTAATAATTAACGTGTGATGATT	50457
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OY	49378	TAATGCGCGGAGAGCGTTCGATACCCGGGCGCTTAACCCACATCCGGGAGAAACGCT	49437	OY	50458	AATTGTTGTGAAGAGGCTCAAGGCAACAAACCCGGGACAGTAACCTCCATTTTAAAT	50517
Db	47386	TAATGCGCGGAGAGCGCTTCGATACCCGGGCGCTTAACCCACATCCGGGAGAAACGCT	47445	Db	48466	AATTGTTGTGAAGAGGCTCAAGGCAACAAACCCGGGACAGTAACCTCCATTTTAAAT	48525
OY	49438	GCCCGGGCTAACAAACAGAGAAATTAATACACTTCGCAACACAGTGGCAAGAGACAGAT	49497	OY	50518	GACGACAGGTGGCTAAAAACGTCCGCACTTCTGCATTAACCGGGGCACTCTAGAAAGCT	50577
Db	47446	GCCCGGGCTAACAAACAGAGAAATTAATACACTTCGCAACACAGTGGCAAGAGACAGAT	47505	Db	48526	GACGACAGGTGGCTAAAAACGTCCGCACTTCTGCATTAACCGGGGCACTCTAGAAAGCT	48585
OY	49498	ACCGATGTCCATAAAGGGGAAAGTTCACCAATAATCCGTTTGTGTGTGACGG	49557	OY	50578	TGCTGGGTCCGTTTGGGCCCATTTGGATTTCCATAGTAAGTGGTCCCTTGGCGTTTCCATTGG	50637
Db	47506	ACCGATGTCCATAAAGGGGAAAGTTCACCAATAATCCGTTTGTGTGTGACGG	47565	Db	48586	TGCTGGGTCCGTTTGGGCCCATTTGGATTTCCATAGTAAGTGGTCCCTTGGCGTTTCCATTGG	48645
OY	49558	AGGGGCGTTTGGGCAAGTTCCTCTGTGGATTTATGTGCTGTCTGTCCCGACATCGA	49617	OY	50638	ACCCGACAACATGTTTGTTTTAAGATGTAGTTGTGAGTTCCTCTGCTTAACCGGGGCAACGTA	50697
Db	47566	AGGGGCGTTTGGGCAAGTTCCTCTGTGGATTTATGTGCTGTCTGTCCCGACATCGA	47625	Db	48646	ACCCGACAACATGTTTGTTTTAAGATGTAGTTGTGAGTTCCTCTGCTTAACCGGGGCAACGTA	48705
OY	49618	CACAGTTCCTGCTCTGGCCAGAAATGTTTGGGCTTCTTACACAGTGCATTAAGACACAGTG	49677	OY	50698	GGGTGGCTAGAAATTCGGGGCTTTTCCCAACGTAGGGGCCGGCATGGGTTCTTGAACCTGTG	50757
Db	47626	CACAGTTCCTGCTCTGGCCAGAAATGTTTGGGCTTCTTACACAGTGCATTAAGACACAGTG	47685	Db	48706	GGGTGGCTAGAAATTCGGGGCTTTTCCCAACGTAGGGGCCGGCATGGGTTCTTGAACCTGTG	48765
OY	49678	TAAATTTTGTACGGGGGCCCAACGTACACAGTTAACCCGTATCCGGGATACACAGCCACTGA	49737	OY	50758	CGGTAGCTTTGAAATATCGTCTAATAACAGAACTATATGCAATTAACCCGCGTAATACT	50817
Db	47686	TAAATTTTGTACGGGGGCCCAACGTACACAGTTAACCCGTATCCGGGATACACAGCCACTGA	47745	Db	48766	CGGTAGCTTTGAAATATCGTCTAATAACAGAACTATATGCAATTAACCCGCGTAATACT	48825
OY	49738	CTCGCAAGGAGACTACACCTCTGTGCCCCCTGCTTATCTGTGCGGGGCCAAGCGCGCGGC	49797	OY	50818	CCCAACATATGGGTGGGCCAATTCGTTGCTGTCTGTCTTCCCGATATTAATAACGGGCGGT	50877
Db	47746	CTCGCAAGGAGACTACACCTCTGTGCCCCCTGCTTATCTGTGCGGGGCCAAGCGCGCGGC	47805	Db	48826	CCCAACATATGGGTGGGCCAATTCGTTGCTGTCTGTCTTCCCGATATTAATAACGGGCGGT	48885
OY	49798	GGATGTCTGTGTTACCGGACACAGTTAATCTTTTGGGCTGTCTTTTACCCCAAAAGCTTC	49857	OY	50878	TGCGGAAACCAAGTTTTCGCAACCAACCGCTCGGTGACACACGGAAGTTATTGGAAGAGCT	50937
Db	47806	GGATGTCTGTGTTACCGGACACAGTTAATCTTTTGGGCTGTCTTTTACCCCAAAAGCTTC	47865	Db	48886	TGCGGAAACCAAGTTTTCGCAACCAACCGCTCGGTGACACACGGAAGTTATTGGAAGAGCT	48945
OY	49858	CCCCAAAGTGAACAGCGCTTTAAAAAAGAAACCCACGGCCGGTACGATAGAGAGCGC	49917	OY	50938	TGCGATATCTGGTTTAACAAACATGTTCCCTTCAAGTTTAAATTAACGGGACCCCGAA	50997
Db	47866	CCCCAAAGTGAACAGCGCTTTAAAAAAGAAACCCACGGCCGGTACGATAGAGAGCGC	47925	Db	48946	TGCGATATCTGGTTTAACAAACATGTTCCCTTCAAGTTTAAATTAACGGGACCCCGAA	49005
OY	49918	CATGTCCGGGCGTCAAGCGCCGAAGGAGCCGAGGTGCAACCACTTGCTACCGTGGGCGCT	49977	OY	50998	ACGGAAGCGCGCTTCTTTAAAGCGTTTCAAGTTTATGACCTGTGTGACAAACCTCGC	51057
Db	47926	CATGTCCGGGCGTCAAGCGCCGAAGGAGCCGAGGTGCAACCACTTGCTACCGTGGGCGCT	47985	Db	49006	ACGGAAGCGCGCTTCTTTAAAGCGTTTCAAGTTTATGACCTGTGTGACAAACCTCGC	49065
OY	49978	CATTTCGCCCTCGCGGATTTAGCCAGTCCGCTGTATCTATACGGCTGCCAGAACTTTAAAG	50037	OY	51058	GGACATTTTAACTACTTGAACCACTCTTAATAGTTTCTTCTGTGTATCCAAAGCTTCG	51117
Db	47986	CATTTCGCCCTCGCGGATTTAGCCAGTCCGCTGTATCTATACGGCTGCCAGAACTTTAAAG	48045	Db	49066	GGACATTTTAACTACTTGAACCACTCTTAATAGTTTCTTCTGTGTATCCAAAGCTTCG	49125
OY	50038	CATTCGCTTACGTTCTTATTGAAGCAGCTGCACACATCAAGCCGAGCCGCGCTCGC	50097	OY	51118	CCGGAATTCGCCGCCGGTTTGAAGACTGTCCGCAAGCCGAAGGGTTTGACTTTAAACATTT	51177
Db	48046	CATTCGCTTACGTTCTTATTGAAGCAGCTGCACACATCAAGCCGAGCCGCGCTCGC	48105	Db	49126	CCGGAATTCGCCGCCGGTTTGAAGACTGTCCGCAAGCCGAAGGGTTTGACTTTAAACATTT	49185
OY	50098	GGGCTCGCGTACACAGATGTTCGCTTTCTTTTATGTTCAAGTTCTTTCGCGCGAAGAC	50157	OY	51178	CACCTCCCAAAACTAACACAGCATGACGCTGTCTCTGTGGCGATAGCGCACCATGTTAAC	51237
Db	48106	GGGCTCGCGTACACAGATGTTCGCTTTCTTTTATGTTCAAGTTCTTTCGCGCGAAGAC	48165	Db	49186	CACCTCCCAAAACTAACACAGCATGACGCTGTCTCTGTGGCGATAGCGCACCATGTTAAC	49245
OY	50158	CACCTGATATACGTTGGGAGATGACTCGGAGAAAAAGGCAATTTGGGAGAGTGTGTTGGTGG	50217	OY	51238	AACGACAGACAGTGGCTTTAACGTAAGGAAGCAATTCCTCGCAATTCACAGGGTGCCTTGT	51297
Db	48166	CACCTGATATACGTTGGGAGATGACTCGGAGAAAAAGGCAATTTGGGAGAGTGTGTTGGTGG	48225	Db	49246	AACGACAGACAGTGGCTTTAACGTAAGGAAGCAATTCCTCGCAATTCACAGGGTGCCTTGT	49305
OY	50218	GCCACGTAAACCAGTGAACGTTTTCAAACGACGAGAGAAAGAAAGCTGATTAATGGCACCC	50277	OY	51298	TATCTCCGTTATGGAGACAGACGAATGGAATTTGGGCGCTCTACGTTTAAAGAAACAAAGTTGG	51357
Db	48226	GCCACGTAAACCAGTGAACGTTTTCAAACGACGAGAGAAAGAAAGCTGATTAATGGCACCC	48285	Db	49306	TATCTCCGTTATGGAGACAGACGAATGGAATTTGGGCGCTCTACGTTTAAAGAAACAAAGTTGG	49365
OY	50278	ACGATTCATGTTTTCGCGTGACGACGCGGGATTAACAAAAAACGCTGCTTTCTGCGTTAAAC	50337	OY	51358	GTTTAAATGGCTGTAGAGGGCTTGTCAAATTCACAGCACTGGAAAGGTTTAGAGCCCGTG	51417
Db	48286	ACGATTCATGTTTTCGCGTGACGACGCGGGATTAACAAAAAACGCTGCTTTCTGCGTTAAAC	48345	Db	49366	GTTTAAATGGCTGTAGAGGGCTTGTCAAATTCACAGCACTGGAAAGGTTTAAAGCCCGTG	49425
OY	51418	GATCCCTTTACCGGCTCAATGAGGCTTCGTTTAAAGGTTTCCGGGTGCTGTGTGGGAAACCA	51477	OY	51478	GATCCCTTTACCGGCTCAATGAGGCTTCGTTTAAAGGTTTCCGGGTGCTGTGTGGGAAACCA	51547

D	49426	GATCCTTTACCGCTCATATATGGCTTCTGTTTAAAGCGTTCCGGTCTGTTCTGTCGGGAACCA	49485
Q	51478	GAGTGCCTATATGAACGCAATTTTGGTATGTAAGGAGACCATATCTTTACCGCCACATATG	51537
D	49486	GAGTGCCTATATGAACGCAATTTTGGTATGTAAGGAGACCATATCTTTACCGCCACATATG	49545
Q	51538	TATGCCCCCAAAAGAGCTAATGACTTTTGCATCATGTAAATTAAGTACGTTAAATTT	51597
D	49546	TATGCCCCCAAAAGAGCTAATGACTTTTGCATCATGTAAATTAAGTACGTTAAATTT	49605
Q	51598	TTATACGTGAACGCGGTGGGGGTCTTGAACCTGAACCGTCCCGCGCTTCGAGCGCTCG	51657
D	49606	TTATACGTGAACGCGGTGGGGGTCTTGAACCTGAACCGTCCCGCGCTTCGAGCGCTCG	49665
Q	51658	CGGTTGCGCGAGCATTCGCTCTGTCGGGAGCTGGAGGGGATGACGATACCTCTCC	51717
D	49666	CGGTTGCGCGAGCATTCGCTCTGTCGGGAGCTGGAGGGGATGACGATACCTCTCC	49725
Q	51718	GCAAAAGTGCATGTTGTGTACACCTGTACAAAGCAAAACATACGATTTGATTCATGAACA	51777
D	49726	GCAAAAGTGCATGTTGTGTACACCTGTACAAAGCAAAACATACGATTTGATTCATGAACA	49785
Q	51778	CACGTGGCGGAGTCATCGCATTTAGCGCGAGAGCGTGGAGATATATACGCTATGCTT	51837
D	49786	CACGTGGCGGAGTCATCGCATTTAGCGCGAGAGCGTGGAGATATATACGCTATGCTT	49845
Q	51838	CGGGCTCAACGGTGCACAGAGTCGGGGAGATTTGTTTAAATCCCGCTGACAAATGAA	51897
D	49846	CGGGCTCAACGGTGCACAGAGTCGGGGAGATTTGTTTAAATCCCGCTGACAAATGAA	49905
Q	51898	GGGCTCGTAAAGCATATAGGGAACATGGCCTCGGACAGCACTAAAAATGTTAATTA	51957
D	49906	GGGCTCGTAAAGCATATAGGGAACATGGCCTCGGACAGCACTAAAAATGTTAATTA	49965
Q	51958	GTCGAGCTGAGTGGGAAATCAACAAAAAATCTGCATCTCCGTATTTGACAGGTTGG	52017
D	49966	GTCGAGCTGAGTGGGAAATCAACAAAAAATCTGCATCTCCGTATTTGACAGGTTGG	50025
Q	52018	GGCGACAGTCGCTGTTTAAACGCGCAGTATTAAGGAGCAACAGGAAATCGTGCCTGTA	52077
D	50026	GGCGACAGTCGCTGTTTAAACGCGCAGTATTAAGGAGCAACAGGAAATCGTGCCTGTA	50085
Q	52078	CAAAAGCCTAAAAAAGAGACGATCTGGGACCGTGTGGAAACCTAGAAACGTGCT	52137
D	50086	CAAAAGCCTAAAAAAGAGACGATCTGGGACCGTGTGGAAACCGTGTAGAAACGTGCT	50145
Q	52138	GCGTGAAGAAACAAAGCAATGGGATGACTTAAAGGGTTTAAACGAGAAAAAATTTGAGA	52197
D	50146	GCGTGAAGAAACAAAGCAATGGGATGACTTAAAGGGTTTAAACGAGAAAAAATTTGAGA	50205
Q	52198	GTTTGACGCTGTGGCGGACGCGTTGCGGACCTCAAGAGACGCTGTAGAGAACTGGA	52257
D	50206	GTTTGACGCTGTGGCGGACGCGTTGCGGACCTCAAGAGACGCTGTAGAGAACTGGA	50265
Q	52258	GATTCCTAGGCTGCTGCAATGAATGTTCCCGTGGAAAGAGTCCCGCAAGGACGA	52317
D	50266	GATTCCTAGGCTGCTGCAATGAATGTTCCCGTGGAAAGAGTCCCGCAAGGACGA	50325
Q	52318	CATTATTAAGTGAATTTGAGCGCTGCCAGAGTGGCCCAAAAAGCCCTTGATCCCA	52377
D	50326	CATTATTAAGTGAATTTGAGCGCTGCCAGAGTGGCCCAAAAAGCCCTTGATCCCA	50385
Q	52378	TTCCCAAGGTTCAACACTGAGAGTGCAGAGAACAGCATGTCCTCATATACCGTCTTAAA	52437
D	50386	TTCCCAAGGTTCAACACTGAGAGTGCAGAGAACAGCATGTCCTCATATACCGTCTTAAA	50445
Q	52438	CACGTAAGAGCATGGCCCACTGAAGATACCTAAACAATGGGGCACTGTAGTACACAGG	52497
D	50446	CACGTAAGAGCATGGCCCACTGAAGATACCTAAACAATGGGGCACTGTAGTACACAGG	50505
Q	52498	CGACGCACTGACCGCGCTGCTGAGAGCGGCTGTATGTTGGTGAAGGTCATGTC	52557
D	50506	CGACGCACTGACCGCGCGTCTGAGAGCGGCTGTATGTTGGTGAAGGTCATGTC	50565
Q	52558	TCGGCGCTGCGTTTAAAGCATTTTGGACGCGCGCTGATGTTTTTAAAGATGCATTTTA	52617
D	50566	TCGGCGCTGCGTTTAAAGCATTTTGGACGCGCGCTGATGTTTTTAAAGATGCATTTTA	50625
Q	52618	ACGATATAGACGCGCTGCGGAGCAAAACATCCCTGAAACCGCGGGGTGACCGATAC	52677
D	50626	ACGATATAGACGCGCTGCGGAGCAAAACATCCCTGAAACCGCGGGGTGACCGATAC	50685
Q	52678	TATGTTTCTTAGACCGCTGCGTACATGTGCGCCCTGTATTTCCCGAGTTAACAGGGA	52737
D	50686	TATGTTTCTTAGACCGCTGCGTACATGTGCGCCCTGTATTTCCCGAGTTAACAGGGA	50745
Q	52738	ATCTGCTAAACGGGGATCTTAAACAGCTGAACCCCTGAACCGGCGCTGTAATCTCG	52797
D	50746	ATCTGCTAAACGGGGATCTTAAACAGCTGAACCCCTGAACCGGCGCTGTAATCTCG	50805
Q	52798	AGCTGAGGAGAGCGGTAGTTTCTTAAATATATATGTGCAATCTGTCACCTGACATCA	52857
D	50806	AGCTGAGGAGAGCGGTAGTTTCTTAAATATATATGTGCAATCTGTCACCTGACATCA	50865
Q	52858	GTCAGAAAAATATCTGATTAAGGGGAACTGACAACCTCGTACGGGACCTTATGATCG	52917
D	50866	GTCAGAAAAATATCTGATTAAGGGGAACTGACAACCTCGTACGGGACCTTATGATCG	50925
Q	52918	GAGATCTAAGGCTCGGCTCTTTACACAGGGAACCCCTTGACCGGAGATGTGACCT	52977
D	50926	GAGATCTAAGGCTCGGCTCTTTACACAGGGAACCCCTTGACCGGAGATGTGACCT	50985
Q	52978	CCAACTCGGGTGTGTCAGACACAGCTACCATTTTAAAGCACCGCGCAGATTTATCTGTA	53037
D	50986	CCAACTCGGGTGTGTCAGACACAGCTACCATTTTAAAGCACCGCGCAGATTTATCTGTA	51045
Q	53038	AGCACATTTAACGGCGCTGCTGCTCTACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	53097
D	51046	AGCACATTTAACGGCGCTGCTGCTCTCTACCGGCTGCTGCTGCTGCTGCTGCTGCTG	51105
Q	53098	CGCAGCGCATATGCTTAAATACGCGCTTCCAAATCACTCCACACTCGGCTCACAAATG	53157
D	51106	CGCAGCGCATATGCTTAAATACGCGCTTCCAAATCACTCCACACTCGGCTCACAAATG	51165
Q	53158	ACATATCTGCTCCGCTTATATGTTGCTAGCATGCTTAAAGAAATATCTGACCGACGCG	53217
D	51166	ACATATCTGCTCCGCTTATATGTTGCTAGCATGCTTAAAGAAATATCTGACCGACGCG	51225
Q	53218	ACCCATTTCCCGACAGGAGAGGTTGGCGAGAGCTCCCTCCAAATCCGCCACCCATGCT	53277
D	51226	ACCCATTTCCCGACAGGAGAGGTTGGCGAGAGCTCCCTCCAAATCCGCCACCCATGCT	51285
Q	53278	TCTATTTGCGTTGATGTTGTCACAGATATGATGCGCGAGATTTTCTGTTGCTGCGG	53337
D	51286	TCTATTTGCGTTGATGTTGTCACAGATATGATGCGCGAGATTTTCTGTTGCTGCGG	51345
Q	53338	ACGTTCCACGATTTTAAAGCATTTGATGCTGCGACACGCGCAGCTATTTCCCTGAGAG	53397
D	51346	ACGTTCCACGATTTTAAAGCATTTGATGCTGCGACACGCGCAGCTATTTCCCTGAGAG	51405
Q	53398	AAGCGTACAGGCGGTTTTTGGCAACAGTATATATAGGGCGCAATCAAAAGAGG	53457
D	51406	AAGCGTACAGGCGGTTTTTGGCAACAGTATATATAGGGCGCAATCAAAAGAGG	51465
Q	53458	ATGCGTTTAAAAACGATCCTCGCGCTGTGTAACTCAAAACTTAAACTGATTCGAGA	53517
D	51466	ATGCGTTTAAAAACGATCCTCGCGCTGTGTAACTCAAAACTTAAACTGATTCGAGA	51525
Q	53518	AGCTGTTGGTCAAGGACTACTTTAGCATTTGGGAAACGCGGAGATCATGATTTTTC	53577
D	51526	AGCTGTTGGTCAAGGACTACTTTAGCATTTGGGAAACGCGGAGATCATGATTTTTC	51585
Q	53578	TCAGATAGCCGATGGTTGAGAGATGCGGCTTCTGACATCGATAGACGACGCGCTC	53637
D	51586	TCAGATAGCCGATGGTTGAGAGATGCGGCTTCTGACATCGATAGACGACGCGCTC	51645

OY	53638	CTCTCGAAATATGAGCTTGCCCAACTTTTAAAAATGACGAGTAAGGGCGTTTTTATGAC	53697
Db	51646	CTCTCGAAATATGAGCTTGCCCAACTTTTAAAAATGAGCGAGTAAGGGCGTTTTTATGAC	51705
OY	53698	GATATACAAAAGAAATTAAGCATGCGCGGTATACGGTGTGCTATATAATTTTATATATTC	53757
Db	51706	GATATACAAAAGAAATTAAGCATGCGCGGTATACGGTGTGCTATATAATTTTATATATTC	51765
OY	53758	GCCAAAGTGGAGATTTTATTCGGCAACACGACGTGTACGATTTTTTACGTCACTTGCGTG	53817
Db	51766	GCCAAAGTGGAGATTTTATTCGGCAACACGACGTGTACGATTTTTTACGTCACTTGCGTG	51825
OY	53818	TTTCAGGGGAGGGGCGCTGACGCGCGCTGTGCGAAGTGTACGACGCGTGGCTTAACATATGAC	53877
Db	51826	TTTCAGGGGAGGGGCGCTGACGCGCGCTGTGCGAAGTGTACGACGCGTGGCTTAACATATGAC	51885
OY	53878	CCGCACATATGACACACACGATGTGTGCTATGATAGAACAGTGTACGCGCGCGCCAAACATTC	53937
Db	51886	CCGCACATATGACACACACGATGTGTGCTATGATAGAACAGTGTACGCGCGCGCCAAACATTC	51945
OY	53938	AATTCCTGTGGGACCGCTGTGAGGACCGCATATTTTGTGTCTCAAAATTTTACTTGGGCC	53997
Db	51946	AATTCCTGTGGGACCGCTGTGAGGACCGCATATTTTGTGTCTCAAAATTTTACTTGGGCC	52005
OY	53998	ATTAACAACAGAAATTCGTCCAAAAAAATTTTAAACCCGTGGCTATATGATCAACATATAC	54057
Db	52006	ATTAACAACAGAAATTCGTCCAAAAAAATTTTAAACCCGTGGCTATATGATCAACATATAC	52065
OY	54058	TTTTGTACGGGCGCCGCTCGGTTTGGACGTGCGTTGGGAGAAGTGGTTAAAAAGATATGTG	54117
Db	52066	TTTTGTACGGGCGCCGCTCGGTTTGGACGTGCGTTGGGAGAAGTGGTTAAAAAGATATGTG	52125
OY	54118	GCGACGTGTGTCATCCAGGCGAGGGGCACTGTGAAGTAAGTACGAAATCCAGAGTCTCT	54177
Db	52126	GCGACGTGTGTCATCCAGGCGAGGGGCACTGTGAAGTAAGTACGAAATCCAGAGTCTCT	52185
OY	54178	CTCAACGGGGTTTTTGGCGTCTCTTGGATTTTGGAAATTAACGTACGCTGACCCCAAA	54237
Db	52186	CTCAACGGGGTTTTTGGCGTCTCTTGGATTTTGGAAATTAACGTACGCTGACCCCAAA	52245
OY	54238	GACGGTTTGGAGTTTCAACCCAGACCTGCAAAATCTATGAATTAAGTCCGGTTTAAATGAC	54297
Db	52246	GACGGTTTGGAGTTTCAACCCAGACCTGCAAAATCTATGAATTAAGTCCGGTTTAAATGAC	52305
OY	54298	ACTTTTCCAAAGATGAGTGTGACGCCGATTTACGCGTGTATGCTTAACTTATATACAGAG	54357
Db	52306	ACTTTTCCAAAGATGAGTGTGACGCCAATTTACGCGTGTATGCTTAACTTATATACAGAG	52365
OY	54358	CCACAGATGACAGACCGCTTAAAGGGTTTTTGTACTCCATATCTAAGACGGCGATGAGATTT	54417
Db	52366	CCACAGATGACAGACCGCTTAAAGGGTTTTTGTACTCCATATCTAAGACGGCGATGAGATTT	52425
OY	54418	GTCGGAGAGGACAGGCTCCCAAGATGAATGGGACTATCTGTGGCATATGACAAAGAAATGG	54477
Db	52426	GTCGGAGAGGACAGGCTCCCAAGATGAATGGGACTATCTGTGGCATATGACAAAGAAATGG	52485
OY	54478	GAGGTGTGTCGGCGGAAAAAGAACGCTTAACTGACAGTACACCATCTAGTTAAAAAGTGC	54537
Db	52486	GAGGTGTGTCGGCGGAAAAAGAACGCTTAACTGACAGTACACCATCTAGTTAAAAAGTGC	52545
OY	54538	ATGATTTACAACTGTACGGGCTTGTGATGTGTATATTTGTACAGATCCGACAGAAAC	54597
Db	52546	ATGATTTACAACTGTACGGGCTTGTGATGTGTATATTTGTACAGATCCGACAGAAAC	52605
OY	54598	GGAAGCCAAATTTAATATTAAGCTCATCTGAGAGCGCAACCTTTTATTAAGCTCAGGAT	54657
Db	52606	GGAAGCCAAATTTAATATTAAGCTCATCTGAGAGCGCAACCTTTTATTAAGCTCAGGAT	52665
OY	54658	CCGTATTTATATCAAGTGTGTGCTCAAGTCTCTCGTTGTACAGAGTACATCACTGTCTCC	54717
Db	52666	CCGTATTTATATCAAGTGTGTGCTCAAGTCTCTCGTTGTACAGAGTACATCACTGTCTCC	52725

QY	54718	AAGGAACTAAAAATTTGGAGACCCAGAAAAACTTTATATGCGACTGCTTTTATGAAAA	547777
Db	52726	AAGGAACTAAAAATTTGGAGACCCAGAAAAACTTTATATGCGACTGCTTTTATGAAAA	527859
QY	54778	CGGAGTTTCAAGACCCGAGCTGCTGACATGCGGGAATTTTCCCGCTGGGTCACAC	548937
Db	52786	CGGAGTTTCAAGACCCGAGCTGCTGACATGCGGGAATTTTCCCGCTGGGTCACAC	52845
QY	54838	GTAGAGATACCGACCTTTTAAATCGTAGACCCGCTATTTTCCAGCTGGCCAAACAC	548937
Db	52846	GTAGAGATACCGACCTTTTAAATCGTAGACCCGCTATTTTCCAGCTGGCCAAACAC	529059
QY	54898	CAACTGCTGAAGCAGCGCGACCCAAATTCCTGGCGGCTAGTCTCTGAGGCATTTCCGAG	54957
Db	52906	CAACTGCTGAAGCAGCGCGACCCAAATTCCTGGCGGCTAGTCTCTGAGGCATTTCCGAG	529655
QY	54958	CTACCATGGGATTTATCCTCTGCTGTGGCAACGCCCCACCAACCGTAGATGTGAAG	550177
Db	52966	CTACCATGGGATTTATCCTCTGCTGTGGCAACGCCCCACCAACCGTAGATGTGAAG	530253
QY	55018	GGGAGCCCATATGATGTATCCAAAGAAATTCGATCCTATTTATAGAGAAAGACATGTCT	550777
Db	53026	GGGAGCCCATATGATGTATCCAAAGAAATTCGATCCTATTTATAGAGAAAGACATGTCT	530859
QY	55078	TGTTTACGGCAGATGGAGCTGCCCCCGCGCTGTACAAACCCAAACCAAGCCATCCA	551377
Db	53086	TGTTTACGGCAGATGGAGCTGCCCCCGCGCTGTACAAACCCAAACCAAGCCATCCA	531454
QY	55138	AACATAAAAACAATAATTTGTCAATTTTGTTTTATAGCATTCGTATCTTTATTTGGAGTGGG	551977
Db	53146	AACATAAAAACAATAATTTGTCAATTTTGTTTTATAGCATTCGTATCTTTATTTGGAGTGGG	532059
QY	55198	GTGATGGTGTGGGGTTGGGAAGGAATGGGATTTGAGAGGAGGATGAATGCTAGATCA	55257
Db	53206	GTGATGGTGTGGGGTTGGGAAGGAATGGGATTTGAGAGGAGGATGAATGCTAGATCA	532656
QY	55258	TATGATTTTGGATATGCAATCCTCGTATATGCTACGCTCTTCTTCTGTTTCATATACGC	553177
Db	53266	TATGATTTTGGATATGCAATCCTCGTATATGCTACGCTCTTCTTCTGTTTCATATACGC	533253
QY	55318	GTTCAGTTCCGGGAGACTTAACTTTTGTGCTCTCTTTAGGGCCTTGAGAGAGGGG	553777
Db	53326	GTTCAGTTCCGGGAGACTTAACTTTTGTGCTCTCTTTAGGGCCTTGAGAGAGGGG	533859
QY	55378	TGCGATTTCCGGGACCTTTGGGACCAATTTCCATGCTTTCTATTAATTTTAAATGAT	554377
Db	53386	TGCGATTTCCGGGACCTTTGGGACCAATTTCCATGCTTTCTATTAATTTTAAATGAT	534454
QY	55438	GGCTTAGATGCAAGTGTATCGGAATCATAGAGATGTTACACGCTATGACTTGTGACGGCT	554977
Db	53446	GGCTTAGATGCAAGTGTATCGGAATCATAGAGATGTTACACGCTATGACTTGTGACGGCT	535059
QY	55498	GGCAGATATGAATACCTTGTCTGTATGCAACGACGGGAGAAAGCAGATCAGGTAACTGAC	555577
Db	53506	GGCAGATATGAATACCTTGTCTGTATGCAACGACGGGAGAAAGCAGATCAGGTAACTGAC	535655
QY	55558	AAAAACGCCAAGTAGAATCCGATCCTGCTTATAGTACTTTACTAGAAATGTTCTGT	556177
Db	53566	AAAAACGCCAAGTAGAATCCGATCCTGCTTATAGTACTTTACTAGAAATGTTCTGT	536253
QY	55618	GTTGATATACCAAGCTATTTGTATAGGACAAAAACAAGTTTATTTGAACCAAGCAATATC	556777
Db	53626	GTTGATATACCAAGCTATTTGTATAGGACAAAAACAAGTTTATTTGAACCAAGCAATATC	536859
QY	55678	GGAAACGAGCATATAGAAACTGTTTCCAAATAGCCATATCTGTTCCGAGGAGATATCTAA	557377
Db	53686	GGAAACGAGCATATAGAAACTGTTTCCAAATAGCCATATCTGTTCCGAGGAGATATCTAA	537454
QY	55738	CATCTCCATGGCTATTTAAGGACAGATTAAGATTTGGGCGCAATGGTTTTCCGTAACGCA	557977
Db	53746	CATCTCCATGGCTATTTAAGGACAGATTAAGATTTGGGCGCAATGGTTTTCCGTAACGCA	538059
QY	55798	CAGGGTGTCTAGCAAGCTATTTCTCAGGAATCTCTGCTCAACACCGCTAGAGACCGCT	558577

D	53806																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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QY	58018	TTCCACCCGCGCTGACGTGGCTCAAGTGTGAGGTCTGCTCCGCGCTCGGTGTTTTAAAAAT	58077
Db	56026	TTCCCGCCCAACGTACGCTGAAGTGTGAGGTCTGCTCCGCGCTCGGTGTTTTAAAAAT	56085
QY	58078	ACCAAGCCGGGGTTTTGTATGCCGAGCTCGCAAGAGACCCACCAGGGAGCAAAACGGGA	58137
Db	56086	ACCAAGCCGGGGTTTTGTATGCCGAGCTCGCAAGAGACCCACCAGGGAGCAAAACGGGA	56145
QY	58138	CTCCTGGCTGAGCTGTATTAGAAAGCGGAGCTGTGTCTTAACATCAAGTGTATAC	58197
Db	56146	CTCCTGGCTGAGCTGTATTAGAAAGCGGAGCTGTGTCTTAACATCAAGTGTATAC	56205
QY	58198	GATTGGGGCGCTGGCGGGGTATCTTACCCACCCCTTTTGGCAAGCGGTGTGTAAATT	58257
Db	56206	GATTGGGGCGCTGGCGGGGTATCTTACCCACCCCTTTTGGCAAGCGGTGTGTAAATT	56265
QY	58258	TTGGCTCTGCTGCACAGCGCGCTGGGTAAATTTGGCGCCCATATGCGCTTCCCTTACCATTTGA	58317
Db	56366	TTGGCTCTGCTGCACAGCGCGCTGGGTAAATTTGGCGCCCATATGCGCTTCCCTTACCATTTGA	56335
QY	58318	CTGTGTACGCTCCACAGATTTTGTCTGACAAAGCGTGGACCAATCTGCTGTACAAAGA	58377
Db	56326	CTGTGTACGCTCCACAGATTTTGTGTAGTACAAAGCGTGGACCAATCTGCTGTACAAAGA	56385
QY	58378	ATGGCGCTTACCGGTGACGTGATTTTATGTACTACTACACAGAGGACATATGTGTTTT	58437
Db	56386	ATGGCGCTTACCGGTGACGTGATTTTATGTACTACTACACAGAGGACATATGTGTTTT	56445
QY	58438	TAGTGTGTGTCCACAGCGGAGGGTACGAGACTCACAGCGGACAAATATACGAATTA	58497
Db	56446	TAGTGTGTGTCCACAGCGGAGGGTACGAGAGTCAAGCGGACAAATATACGAATTA	56505
QY	58498	GAACTTTGAAAGGTACTATGTTTATTTTAAACAGAGTCTGTGCGGATGCTGTGTAG	58557
Db	56506	GAACTTTGAAAGGTACTATGTTTATTTTAAACAGAGTGTGTGCGGATGCTGTGTAG	56565
QY	58558	GCTGTGTTATTTGAAATATTTTATTAATACCGATGCGTTATGAGGTGTCTGTAAATTTGT	58617
Db	56566	GCTGTGTTATTTGAAATATTTTATTAATACCGATGCGTTATGAGAGTGTCTGTAAATTTGT	56625
QY	58618	GCCGCAATTAATATGTTTAAAGTCCGCGGTGCGCCTTCTCTCCAAAGCTTCTGTGT	58677
Db	56626	GCCGCAATTAATATGTTTAAAGTCTCCGCGGTGCGCCTTCTCTCTCCAAAGCTTCTGTGT	56685
QY	58678	TAGACGAAGGATTCAAATAAATGGGTTTCAAGTAAGCCCTTCATGCTGTGCGTTTTC	58737
Db	56686	TAGACGAAGGATTCCAAAATAAATGGGTTTCAAGTAAGCCCTTCATGCTGTGCGTTTTC	56745
QY	58738	GTCCACACGCTTATGAGAGTTTGAACCGCACTAGGGGGGGAACCGCAAAATGCTTGGGG	58797
Db	56746	GTCCACACGCTTATGAGAGTTTGAACCGCACTAGGGGGGGAACCGCAAAATGCTTGGGG	56805
QY	58798	TGGGTTTAACGTCGTGATGCGCGCAAGGTGCAAGGATCACTTGCATCCCATACAAATAC	58857
Db	56806	TGGGTTTAACCTCGTGTATGCGCGCAAGGTGCAAGGATCACTTGCATCCCATACAAATAC	56865
QY	58858	AAACGCGGAATTCATACAGCTATACCTCTCTGTAGTAGTACCTGGCCCGTCAAGCGGGA	58917
Db	56866	AAACGCGGAATTCATACAGGATATACCTCTCTGTAGTAGTACCTGGCCCGGTCAAAGCGGGA	56925
QY	58918	CAGATTAATATGATAGGGGGGGCTTATGCTAGTTTTCAGCATAGAAAGATGACAGAG	58977
Db	56926	CAGATTAATATGATAGGGGGGGCTTATGCTAGTTTTCAGCATAGAAAGATGACAGAG	56985
QY	58978	TTCTGTATACGCTGCGCTCGCGGCTTAAACAGCTGACGCGGTGCAAAAAACGTCGGG	59037
Db	56986	TTCTGTATACGCTGCGCTCGCGGCTTAAACAGCTGACGCGGTGCAAAAAACGTCGGG	57045
QY	59038	ATATATGTCCAGTGCATGATGTCCTGTGTGACACACGACGCAAAAGCAAAACC	59097
Db	57046	ATATATGTCCAGTGCATGATGTCCTGTGTGACACACGACGCAAAAGCAAAACC	57105

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Db 58186 TGCACGTGCTACCGACACGCGCTTTTATAGAGCGCGGCTATTTATTAATGACATTAACCTTATG 58245
QY 60238 CGTGCTCCGCGGTCTGTGACATGTCATTAATCCGGTAATAATTAACCGGTACAGAGGCTTAT 60297
Db 58246 CGTGCTCCGCGGTCTGTGACATGTCATTAATCCGGTAATAATTAACCGGTACAGAGGCTTAT 58305
QY 60298 CAAAGCGACGCGTCCATTGTAAATTAATAGCCCGTAAACAACTTCACTGTTATATCTT 60357
Db 58306 CAAAGCGACGCGTCCATTGTAAATTAATAGCCCGTAAACAACTTCACTGTTATATCTT 58365
QY 60358 TTTGTCTGATAGTCCGATATAAGACGCTTATCTCCGTTAAACCTCCACAGACCTCGG 60417
Db 58366 TTTGTCTGATAGTCCGATATAAGACGCTTATCTCCGTTAAACCTCCACAGACCTCGG 58425
QY 60418 CGTAGTCTGGAATATAAATAGAGAGTCATCCGTCATTATCGAGGTAATCTCTGTGCA 60477
Db 58426 CGTAGTCTGGAATATAAATAGAGAGTCATCCGTCATTATCGAGGTAATCTCTGTGCA 58485
QY 60478 GTTTGTCGACAAATCCGCGATATCGTAACTCTCCGAAACGTCATCTTTCTCATCTGTT 60537
Db 58486 GTTTGTCGACAAATCCGCGATATCGTAACTCTCCGAAACGTCATCTTTCTCATCTGTT 58545
QY 60538 GACAGTGTCTGTATCTGCGGATGTCGCGCGTCCGCGGCGGCGCTGACAATATGGA 60597
Db 58546 GACAGTGTCTGTATCTGCGGATGTCGCGCGTCCGCGGCGGCGCTGACAATATGGA 58605
QY 60598 CCAACCCAAAGGCGACACCCAGTCGACGTCATCTGTTCTGACGATTAACAGTCCTGCTGT 60657
Db 58606 CCAACCCAAAGGCGACACCCAGTCGACGTCATCTGTTCTGACGATTAACAGTCCTGCTGT 58665
QY 60658 GTAGTACCTGATTAATAGTGTTCAGTAACAGTTGATCGACTGTATAGACAGAGGTACGTT 60717
Db 58666 GTAGTACCTGATTAATAGTGTTCAGTAACAGTTGATCGACTGTATAGACAGAGGTACGTT 58725
QY 60718 CCCACGATTCAAACGATAGACGCTTGTGAATTCGCGCTCAGTGTCTGACACCGCGCAAC 60777
Db 58726 CCCACGATTCAAACGATAGACGCTTGTGAATTCGCGCTCAGTGTCTGACACCGCGCAAC 58785
QY 60778 GGGTCTTCAGGGTGGTCTCGAAGTTGGTCCAGTCTTTAAGACGTTGTCGATGTGACAC 60837
Db 58786 GGGTCTTCAGGGTGGTCTCGAAGTTGGTCCAGTCTTTAAGACGTTGTCGATGTGACAC 58845
QY 60838 TCCCAATGCGCTTGTACAGGTGTATAGACGTCGTCCTCCAAAGATCCCTGGAATTC 60897
Db 58846 TCCCAATGCGCTTGTATGACAGGTGTATAGACGTCGTCCTCCAAAGATCCCTGGAATTC 58905
QY 60898 GAAGACTGGAGTGTAGCGCTTTGACCGGACGTCAGCTACTTGCCCTGTAGAGTCTGA 60957
Db 58906 GAAGACTGGAGTGTAGCGCTTTGACCGGACGTCAGCTACTTGCCCTGTAGAGTCTGA 58965
QY 60958 AAAAGGAGATGAGAGATTCCGTGCGATGGACCAAAACAGTCGAACCAAAATCCGGGGTCA 61017
Db 58966 AAAAGGAGATGAGAGATTCCGTGCGATGGACCAAAACAGTCGAACCAAAATCCGGGGTCA 59025
QY 61018 TCTTGAACATGACGTCGCGATGCAAAAGTCAGGGGCTGTGATGATCAGTCAGTCGCTCT 61077
Db 59026 TCTTGAACATGACGTCGCGATGCAAAAGTCAGGGGCTGTGATGATCAGTCAGTCGCTCT 59085
QY 61078 CAAATATTAATCTACAGCCACCGGAATGGTTGGTACAGCTGGCTTCGATCCGCGCTG 61137
Db 59086 CAAATATTAATCTACAGCCACCGGAATGGTTGGTACAGCTGGCTTCGATCCGCGCTG 59145
QY 61138 AAGACTCCGGGCGCTTCTTCCGTTTACCCTTTATCTAATATACGGGAATCTGCTGGGCTG 59205
Db 59146 AAGACTCCGGGCGCTTCTTCCGTTTACCCTTTATCTAATATACGGGAATCTGCTGGGCTG 59257
QY 61198 GGAAGAGTACAGCAATATCGGCTCTGATCCAAATTTAATACGTCGATCAGAGGCGCA 61257
Db 59206 GGAAGAGTACAGCAATATCGGCTCTGATCCAAATTTAATACGTCGATCAGAGGCGCA 59265
QY 61258 CCACCATAGCCGACAGAACTATGCGCTGCTAAAGACGTTCTGCCACAGACTTCA 61317
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Db 59266 CCACCATAGCCGACAGAACTATGCGCTGCTTAAAGACGTTCTGCCACAGATCTGA 59325
QY 61318 GCGCTTTTGGCTTTAAGAGCCGACACATCAATATAGCCGTGAGAAAAAGCTCATACAGCG 61377
Db 59326 GCGCTTTTGGCTTTAAGAGCCGACACATCAATATAGCCGTGAGAAAAAGCTCATACAGCG 59385
QY 61378 GAGCCGTATCCATAGAGCAAAATTCAGCAACAGAGAGCTATCGAAGTATTGGCCGGTTATAG 61437
Db 59386 GAGCCGTATCCATAGAGCAAAATTCAGCAACAGAGAGCTATCGAAGTATTGGCCGGTTATAG 59445
QY 61438 TGGACATTAATGAAAGAGTTATAGCGAAAAAACCCATGAGTACGGGACTATATCA 61497
Db 59446 TGGACATTAATGAAAGAGTTATAGCGAAAAAACCCATGAGTACGGGACTATATCA 59505
QY 61498 ACGCAATTTTGAACCTCTCTGAGATACCGGACCGTGTATTAGGACTTCCAAATATTA 61557
Db 59506 ACGCAATTTTGAACCTCTCTGAGATACCGGACCGTGTATTAGGACTTCCAAATATTA 59565
QY 61558 TTTGATTCGACGAGCGCGGAACCTGCTCTTACTACTCAACACCGTCTGTTCTTT 61617
Db 59566 TTTGATTCGACGAGCGCGGAACCTGCTCTTACTACTCAACACCGTCTGTTCTTT 59625
QY 61618 ACTGTTCTTAAACAGCTGGCTAAATACCCTCTTTACCGCGAGGGGCGGTTCCGTGA 61677
Db 59626 ACTGTTCTTAAACAGCTGGCTAAATACCCTCTTTACCGCGAGGGGCGGTTCCGTGA 59685
QY 61678 TAGTATGCGTGGTTCGCCACGACGACAAACGCGTTCCAGTCATCAACACGAGGA 61737
Db 59686 TAGTATGCGTGGTTCGCCACGACGACAAACGCGTTCCAGTCATCAACACGAGGA 59745
QY 61738 CCGAAAAGAGGAGATATGCTGTGCGAACAATCTAATCAATGATAGGGAAGAAG 61797
Db 59746 CCGAAAAGAGGAGATATGCTGTGCGAACAATCTAATCAATGATAGGGAAGAAG 59805
QY 61798 TCGTATCTGATACGTACACTTGGAGAGAACTGGCGCTGTTTATTAACAACAACGCGT 61857
Db 59806 TCGTATCTGATACGTACACTTGGAGAGAACTGGCGCTGTTTATTAACAACAACGCGT 59865
QY 61858 GCACGATTCGACGTTCCGACACCTCTTAATAATTTTACAGTATTAATCTTCCATCTCTG 61917
Db 59866 GCACGATTCGACGTTCCGACACCTCTTAATAATTTTACAGTATTAATCTTCCATCTCTG 59925
QY 61918 ACGAAGTCATGATTAACGTACGACAGATTTGTGTCCTTAAAGTATGATTAAGATCTT 61977
Db 59926 ACGAAGTCATGATTAACGTACGACAGATTTGTGTCCTTAAAGTATGATTAAGATCTT 59985
QY 61978 TAGAATACATTTGGCTGGACCCGACCTTTTGTCAATATAGCAGGTAAGGCTATCTAA 62037
Db 59986 TAGAATACATTTGGCTGGACCCGACCTTTTGTCAATATAGCAGGTAAGGCTATCTAA 60045
QY 62038 CAAACCTACACATGTCCTAACGCTTAGGGGCGATACAGGACACGAAAGCTTTTACCT 62097
Db 60046 CAAACCTACACATGTCCTAACGCTTAGGGGCGATACAGGACACGAAAGCTTTTACCT 60105
QY 62098 GTCCCGTGGTGGCGAGGTGTTTGAACCCGTTTGAGAGATATACAGGCGGCGTCACAC 62157
Db 60106 GTCCCGTGGTGGCGAGGTGTTTGAACCCGTTTGAGAGATATACAGGCGGCGTCACAC 60165
QY 62158 TCACCAACCTCAACCGTGAACGAGTGGGTGACAAAAAACCTCTTAAATTAATTAAT 62217
Db 60166 TCACCAACCTCAACCGTGAACGAGTGGGTGACAAAAAACCTCTTAAATTAATTAAT 60225
QY 62218 CGCAGTTTGTGACACGACATGTCATATGTCGCCACGGAATTCACGTAAGCTTGACGCC 62277
Db 60226 CGCAGTTTGTGACACGACATGTCATATGTCGCCACGGAATTCACGTAAGCTTGACGCC 60285
QY 62278 AGTTTACCTTTATCAACAAAGTTTGTAAACACGACACGCTGCTTAAATGAAAAACA 62337
Db 60286 AGTTTACCTTTATCAACAAAGTTTGTAAACACGACACGCTGCTTAAATGAAAAACA 60345
QY 62338 AAAAATGATATGTGGGTTTACAGGTACGTTAGTTGAGTTCAAAAGAAATCTTACAGACG 62397
Db 60346 AAAAATGATATGTGGGTTTACAGGTACGTTAGTTGAGTTCAAAAGAAATCTTACAGACG 60405
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QY	62398	AACCTCTTGAGAGACGATTCGCAAGACCGCTCCGGAAATACGTATACGGTTTCTTAACA	62457
Db	60406	AACCTCTTGAGAGACGATTCGCAAGACCGCTCCGGAAATACGTATACGGTTTCTTAACA	60465
QY	62458	CGGTACTGTCAACGGCATGTACTGCTTTCAGCGGTACGGCGTACGTACTAGTCACACGACA	62517
Db	60466	CGGTACTGTCAACGGCATGTACTGCTTTCAGCGGTACGGCGTACGTACTAGTCACACGACA	60529
QY	62518	AATATCTGCAAGACCTTAAATTTTGACACCCCTCCGGCCCGCTCGACACCGGGCGGTAG	62577
Db	60526	AATATCTGCAAGACCTTAAATTTTGACACCCCTCCGGCCCGCTCGACACCGGGCGGTAG	60585
QY	62578	ACCTTCAACGGTTTCGTGAAGATTTAACTGGAAGACGACATCTTCTACCACTGTGCA	62637
Db	60586	ACCTTCAACGGTTTCGTGAAGATTTAACTGGAAGACGACATCTTCTACCACTGTGCA	60645
QY	62638	GTCGCCCGCACCCCGCGGGTATACCTCCCTCCAGGTTTGGTCGACACTGTACTGGGCC	62697
Db	60646	GTCGCCCGCACCCCGCGGGTATACCTCCCTCCAGGTTTGGTCGACACTGTACTGGGCC	60705
QY	62698	TAAAGACGTTGTCGCTCCAGAAATAAAGTGGCGTGTGCTGCTGGCGGGAGTTTG	62757
Db	60706	TAAAGACGTTGTCGCTCCAGAAATAAAGTGGCGTGTGCTGCTGGCGGGAGTTTG	60765
QY	62758	AGAAAGAAACGTTTCCGGCTTAACTGGTTCGTAAGGGGACGAGTTGACTTTG	62817
Db	60766	AGAAAGAAACGTTTCCGGCTTAACTGGTTCGTAAGGGGACGAGTTGACTTTG	60825
QY	62818	TCTCCCTTCAGAACGTCCTCAAGGGCTGTTGGCTGATCGACCGTTGAATCGTATA	62877
Db	60826	TCTCCCTTCAGAACGTCCTCAAGGGCTGTTGGCTGATCGACCGTTGAATCGTATA	60885
QY	62878	AAATTAAGGGGTACACTTTTACCGGTACGGTGGCGTGCAGGGTTTGCACATCA	62937
Db	60886	AAATTAAGGGGTACACTTTTACCGGTACGGTGGCGTGCAGGGTTTGCACATCA	60945
QY	62938	GTCATGACCTCAGAGAAAGAGATCCCTCCCTGGTCCGTGACAGACTCTACCGGTTTATCG	62997
Db	60946	GTCATGACCTCAGAGAAAGAGATCCCTCCCTGGTCCGTGACAGACTCTACCGGTTTATCG	61005
QY	62998	CGTGCTTAAGAAATTAACATTAACCAATTGACGGAACCATGAGACGGGAGCGTTTCC	63057
Db	61006	CGTGCTTAAGAAATTAACATTAACCAATTGACGGAACCATGAGAGCGGGAGCGTTTCC	61065
QY	63058	AAGTGTCTGTGGCGGGGACTATGAGGATGCTCAAAATTAGCGATGACCATCGTTAAG	63117
Db	61066	AAGTGTCTGTGGCGGGGACTATGAGGATGCTCAAAATTAGCGATGACCATCGTTAAG	61125
QY	63118	CACAGGGAATGTGCTTGAGAGAGTAGCGGTAGTTTGGGTCCCAAGAACGTCAGA	63177
Db	61126	CACAGGGAATGTGCTTGAGAGAGTAGCGGTAGTTTGGGTCCCAAGAACGTCAGA	61185
QY	63178	CAAGCCACGTTATGTATGCAATTTCAAGGGCTGTTAACTCAAAATTTTTGGTCATGGACA	63237
Db	61186	CAAGCCACGTTATGTATGCAATTTCAAGGGCTGTTAACTCAAAATTTTTGGTCATGGACA	61245
QY	63238	GCAACCCCTTAAAAACCTCTCTAGAGAACCACTGATTAACACCTCCGGCAAGCATATAG	63297
Db	61246	GCAACCCCTTAAAAACCTCTCTCTAGAGAACCACTGATTAACACCTCCGGCAAGCATATAG	61305
QY	63298	TTCGGCGCTTCACAAACCCAAACCAACCTCATCTATCTAATTAATTAACCAAGCAAA	63357
Db	61306	TTCGGCGCTTCACAAACCCAAACCAACCTCATCTAATTAATTAACCAACCAAA	61365
QY	63358	TGGAATAACATTTGTTTATATCAATGTCACACAGGCGACAGATGTTGTCATTTCCACA	63417
Db	61366	TGGAATAACATTTGTTTATATCAATGTCACACAGGCGACAGATGTTGTCATTTCCACA	61425
QY	63418	CACCGGGGGGTGGCGGCATAGTTTGACGACAGCAAAAGCCCGGGCCCTCTGGGTTAGA	63477
Db	61426	CACCGGGGGGTGGCGGCATAGTTTGACGACAGCAAAAGCCCGGGCCCTCTGGGTTAGA	61485

OY	63478	AGTAGCCCCCCCCCGGTGTCAGAGTCATACGTCCTCTTAAGGCCCTGGGTGTACCAAC	63537
Db	61486	AGTAGCCCCCCCCCGGTGTCAGAGTCATACGTCCTCTTAAGGCCCTGGGTGTACCAAC	61545
OY	63538	ATAAATACGTCGATACACCGTTGGAGAGTCCGCGGTGACGGCGGCTTTGCACGGCGC	63597
Db	61546	ATAAATACGTCGATACACCGTTGGAGAGTCCGCGGTGACGGCGGCTTTGCACGGCGC	61605
OY	63598	ACGAAACCCCGCTGTTAGACGTGATCTGCACTGTCGTGCTGTGAAAGATGAACACAG	63657
Db	61606	ACGAAACCCCGCTGTTAGACGTGATCTGCACTGTCGTGCTGTGAAAGATGAACACAG	61665
OY	63658	GTCATACATCACTAGTGGCGCCGCTCCATACGCGCTGATTCGTCCATGTCTCAAC	63717
Db	61666	GTCATACATCACTAGTGGCGCCGCTCCATACGCGCTGATTCGTCCATGTCTCAAC	61725
OY	63718	AGAGCCCGGTCGTCACCTTCGTCGATCTGTGAATAATTAATGATCTCTGTGTCGACGT	63777
Db	61726	AGAGCCCGGTCGTCACCTTCGTCGATCTGTGAATAATTAATGATCTCTGTGTCGACAT	61785
OY	63778	TGATCGACGAACAACAG--TCTCTCTTCATGGAAGACCATCCGCGCTTCGCGGTGA	63834
Db	61786	TGATCGACGAACAACAGTCTCTCTTCATGGAAGACCATCCGCGCTTCGCGGTGA	61845
OY	63835	TCTAGATATATCACTGACCGCGCGCGCGCTGCGCGAANAACGTCACGTTCTCC	63894
Db	61846	TCTAGATATATCACTGACCGCGCGCGCGCTGCGCGAANAACGTCACGTTCTCC	61905
OY	63895	GCACCTTCATCATGTCCTGTCGATCATCTATAAANAATGTCCTGTCGTCGATTC	63954
Db	61906	GCACCTTCATCATGTCCTGTCGATCATCTATAAANAATGTCCTGTCGTCGATTC	61965
OY	63955	AGAGACTGGGGGTGCGGGGTGTGGCAGTAACACACGACGGCGCGGACCAACAA	64014
Db	61966	AGAGACTGGGGGTGCGGGGTGTGGCAGTAACACACGACGGCGCGGACCAACAA	62025
OY	64015	CGCGGTACGTCGCGCGGGCGCTCGGTGTGTGTGGCACTGTGGAATGACGCT	64074
Db	62026	CGCGGTACGTCGCGGGCGGGCGCTCGGTGTGTGTGGCACTGTGGAATGACGCT	62085
OY	64075	AGTAGGCGGGCGCTCGGTGTAAAGACACACGCTCCGCGGTGGGATCTAATCTAGG	64134
Db	62086	AGTAGGCGGGCGCTCGGTGTAAAGACACACGCTCCGCGGTGGGATCTAATCTAGG	62145
OY	64135	TGGGAGAGAACCGCGCGGTCTGCTTCTTCATCACATCACTAGTATCCCTTTCCGA	64194
Db	62146	TGGGAGAGAACCGCGCGGTCTGCTTCTTCATCACATCACTAGTATCCCTTTCCGA	62205
OY	64195	ATGAGAGTCGGTTCGTCGTGGCTTTTGGAGTAGTGGAGGGGAATCTTGGTCAAAAC	64254
Db	62206	ATGAGAGTCGGTTCGTCGTGGCTTTTGGAGTAGTGGAGGGGAATCTTGGTCAAAAC	62265
OY	64255	ATCTCTAGGTGCACTATGTCATATCACTGGGGGGCTCCGTAACCGGGGGGTACCGGCA	64314
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OY	64315	CCCCGTACGGGACCCGCGCAACAAAAACGTCCTTGTCTCTTTTCTTCTAGTCCCGGG	64374
Db	62326	CCCCGTACGGGACCCGCGCAACAAAAACGTCCTTGTCTCTTTTCTTCTAGTCCCGGG	62385
OY	64375	AATCGGACGATCCTGGGAGTGGCGGGCGGTCCTTGAACGGGTGCGATTAAGACATAC	64434
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OY	64435	CATGGCCGAAACGTTCACTGT-AAAAAGCACTGCTATTCGCCGATTAATATTCCA	64493
Db	62446	CATGGCCGAAACGTTCACTGTAAAAAGCACTGCTATTCGCCGATTAATATTCCA	62505
OY	64494	GTCACAGGCAACCCCTCGATTCGAAGTAATGATTCGCAAGTTTAAATATGTTGCA	64553
Db	62506	GTCACAGGCAACCCCTCGATTCGAAGTAATGATTCGCAAGTTTAAATATGTTGCA	62565
OY	64554	GCCCTAGTAAC-TGCGGCAAGGAGAACCGGTTCCCGCTGGGCGGTAGCCAGGGAGAGC	64612

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Db 63106 CGCTTACAGAGCGCGGAGCTTCT 63130
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RESULT 3
AF241163 1945 bp mRNA linear VRL 23-OCT-2002
LOCUS
DEFINITION Cercopithecine herpesvirus 17 Immediate-early transcription factor
ACCESSION AF241163
VERSION
KEYWORDS
SOURCE
ORGANISM
Cercopithecine herpesvirus 17
Cercopithecine herpesvirus 17
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
AUTHORS Lin,S.F., Robinson,D.R., Oh,J., Jung,J.U., Luciw,P.A. and Kung,H.J.
TITLE Identification of the bZIP and Rta homologues in the genome of
Rhesus monkey rhadinovirus
JOURNAL Virology 298 (2), 181-188 (2002)
MEDLINE 22127395
PUBMED 12127781
REFERENCE
AUTHORS Lin,S.F., Robinson,D.R., Oh,J., Kung,H.J. and Luciw,P.A.
TITLE Cloning and characterization of cDNAs encoding Rhesus Rhadinovirus
(RRV) ORF50
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1945)
AUTHORS Lin,S.F., Robinson,D.R., Oh,J., Kung,H.J. and Luciw,P.A.
TITLE Direct Submission
JOURNAL Submitted (02-MAR-2000) Biological Chemistry, School of Medicine,
UC Davis, 4645 Second Avenue, Rm. 2400, Sacramento, CA 95831, USA
FEATURES
Source
1. 1945
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CDS
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BASE COUNT 471 a 581 c 490 g 403 t
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 83 CAGGCTGTTAAAACTCAGAGGTCCTGCGGAGCAACTTTTGGCACTCCGACCG 142
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Db 143 CTCAGGATAGCTGTACCGCGGCTCTTTATTAACGAAACATPAGCTCAAAAACAT 202
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Db 203 GACCACGTCACCTAAATAGCTCAGAGAGAGTGTGCGATGATGTAATGGAATGT 262
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QY 68503 GCCTCCCTGGGTCCCATCTCCGCGGCTCATCGCGGATCTGAATCTTTAAACCTGTTCTGC 68562
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QY 68743 CACGACGCTACGCGGGAATGAAGGCAAGTCTTGGGGGCGTCCGCTGCTCATATGT 68802
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Qy	69103	GAACCGGGGGCTTCTCCGGGACCCCTGGTGTGACCTCAGTAATGTCTTAGAAATCCAGAA	69162
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Qy	69163	ATCATCTCAGGGGCCCCACCCCTGATGCAATTTGTCTATCAACAAACAGCACCAGTCTG	69222
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Qy	69283	GACACGTGGAAAGCGGTGTACAGAGCATTCACACAGCAGCAGACGCTATTTTGGCC	69342
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Qy	69343	GCCGCATTAACCGGTTGACATCTGCGGCGCCCTGGCCGCTATTCGATTCGCTCCCAATT	69402
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Qy	69403	GCCGGCAGCTCTCGGCAAGGTGGAAGGTCGCGGGCGCTGATTCGCGGGAACCAAGATGC	69462
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Qy	69523	TTGGGAAACGCTCCCGTAAACAGTCCACATCCGAGGCGCGGATACGCTCCCACTGCTT	69582
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Qy	69583	AATATACCAATATATAGACTTAATACCTCCCGTCAAGGTCGCGCAGAGTCCGCGGATATC	69642
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Qy	69643	GCCAACTCCAGAGTCCCGCATGGCGGCGGCTCTCCGCTTCGCGGAAACCGCGCA	69702
Db	1403	GCCAACTCCAGAGTCCCGCATGGCGGCGGCTCTCCGCTTCGCGGAAACCGCGCA	1462
Qy	69703	ACGGTCCCGCTTAGAGAAACGACGACGCGAGAGACGTGGAGACAAAGACTGAAGGC	69762
Db	1463	ACGGTCCCGCTTAGAGAAACGACGACGCGAGAGACGTGGAGACAAAGACTGAAGGC	1522
Qy	69763	GACGTTGGGGGCGCGCAACAGTAAACACACCTTTTCCCGGAGCGTCCGGATGGCGCTT	69822
Db	1523	GACGTTGGGGGCGCGCAACAGTAAACACACCTTTTCCCGGAGCGTCCGGATGGCGCTT	1582
Qy	69823	CGCGAGCAGGGCTTATTCGATTTAATCGAAAAGCTCCACGAGTGAACCGCGACGATCT	69882
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Qy	70003	GTTAGTCCGCATCTAGCGGCGCAAGATGCTTGAAGATGACCCCAAGACGCAAGATC	70062
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Qy 70183 CGG 70185
 Db 1943 CGG 1945

RESULT 4
 AF241164 819 bp mRNA linear VRL 23-OCT-2002
 LOCUS Cercopithecine herpesvirus 17 bzip transcription factor mRNA,
 DEFINITION complete cds.
 ACCESSION AF241164
 VERSION AF241164.1 GI:13506780
 KEYWORDS
 SOURCE Cercopithecine herpesvirus 17
 ORGANISM Cercopithecine herpesvirus 17
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae; Rhadinovirus.

REFERENCE 1 (bases 1 to 819)
 Lin,S.F., Robinson,D.R., Oh,J., Jung,J.U., Luciw,P.A. and Kung,H.J.
 Identification of the bzip and Rta homologues in the genome of
 rhesus monkey rhadinovirus
 Virology 298 (2), 181-188 (2002)
 MEDLINE 22127395
 PUBMED 12127781
 REFERENCE 2 (bases 1 to 819)
 Lin,S.F., Robinson,D.R., Oh,J., Kung,H.J. and Luciw,P.A.
 Cloning and characterization of cDNAs encoding Rhesus Rhadinovirus
 (RVV) regulatory genes
 Unpublished

JOURNAL 3 (bases 1 to 819)
 REFERENCE Lin,S.F., Robinson,D.R., Oh,J., Kung,H.J. and Luciw,P.A.
 AUTHORS Direct Submission
 TITLE Submitted (02-MAR-2000) Biological Chemistry, School of Medicine,
 JOURNAL UC Davis, 4645 Second Avenue, Rm. 2400, Sacramento, CA 95831, USA
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BASE COUNT 247 a 208 c 201 g 163 t
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Query Match 1.2%; Score 481; DB 1; Length 819;
 Best Local Similarity 100.0%; Pred. No. 1.9e-280;
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 Qy 70441 GGATTCACAAACCTGTGTCTGACGCGCAGAGATCTGCTGGGTCTTATATCTATACGA 70500

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Db      241 AAGCTTCGCGAGCTAGCGCTCGCGGCGAGGCTTTTCGTGGGGGCTTCTGTCTCAGGATGA 300
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QY      70741 GGCACATGCCGATATCTGACCGGATAGGACAGACAGCGGTGGCGCTGACATAGACTCTCAA 70800
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QY      70801 G 70801
Db      481 G 481

RESULT 5
AF241165      875 bp      mRNA      linear      VRL 02-APR-2001
LOCUS      Cercopithecine herpesvirus 17 glycoprotein R8.1 mRNA, complete cds.
DEFINITION      AF241165.1 GI:13506782
ACCESSION      AF241165.1 GI:13506782
VERSION
KEYWORDS
SOURCE      Cercopithecine herpesvirus 17
ORGANISM      Cercopithecine herpesvirus 17
REFERENCE      1 (bases 1 to 875)
AUTHORS      Lin,S.F., Robinson,D.R., Oh,J., Kung,H.J. and Luciw,P.A.
TITLES      Gammaherpesvirinae: Rhadinovirus.
JOURNAL      (RRV) ORPR8.1
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Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      71557 CTGGACCTTACAGATGGAATAATACGAGCGGTATACAGGACCTACCTCGAAGAGTCCG 71616
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QY      71737 AGAGCGCCTGGGACAGACACGAGGCGCAATCATACAGACCTCCACAGATCAAGCA 71796
Db      301 AGAGCGCCTGGGACAGACACGAGGCGCAATCATACAGACCTCCACAGATCAAGCA 360
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QY      71857 GACTCCGCGGAGTCACAGTCAG 71879
Db      421 GACTCCGCGGAGTCACAGTCAG 443

RESULT 6
EHVU20824      184427 bp      DNA      linear      VRL 02-FEB-1996
LOCUS      Equine herpesvirus 2, complete genome.
DEFINITION      EHVU20824
ACCESSION      020824
VERSION      020824.1 GI:695172
KEYWORDS
SOURCE      Equine herpesvirus 2
ORGANISM      Equine herpesvirus 2
REFERENCE      1 (bases 1 to 184427)
AUTHORS      Telford,E.A., Watson,M.S., Aird,H.C., Perry,J. and Davison,A.J.
TITLES      The DNA sequence of equine herpesvirus 2
JOURNAL      J. Mol. Biol. 249 (3), 520-528 (1995)
MEDLINE      95302501
PUBMED      7783207
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GNVGLGLVYVSGEDFPALOEYIESHMLAKRCGATLLGFPVMDGSAAPMGRA
SRPSFTGATRASIIIPKACLSVRRGGASVFMIGDFRQPRAGGAYASHDSGRILA
SILAAVOTFINAGGRAVLSTQSRLEGTMHAKTAAACVGLKTYTSLPBEVASHL
SHFSPGNASNNRSLISKPLNVEAOVLLTVNTPRNRLLEGVTFEGCRVSLGHL
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SDAGPRSDAREVLLGLIRHPTVCGKNYIKVHRCGASRVAAOCQGVPLDIPVDYEM
VYVPRSGPPSSMEPTWTETPOVDDCFLLHEDGSCVCSALGKNSVFPPTPRAGAK
MAIAESVLSLALARIIEDEVYNLSLAWPLHGAQGEVFTLLTRCKRFEDACVSN
VTSCASSRRAGGDPPEGADIKSFVASAFAYTPCAFWKLTPLDKEARSVILFLPAS
GHAFAFAYVOOVROKQKTYGSPVNSGAYLKLARAVLHRAKLAVSGHDVGIGIM
AALAEVMAAGMRSLDVEVPRLDGDDPFLTSGVPALEPLSSASAAVYLSKRTI
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EGYPEREREPFLATTPRTIINRPMKTRVAVLLRCEPFLAALDALRDFDLAS
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CDS
26436..29873
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SRIFYEATHTSIALALVRYVPGILGLBEOSSHDOYKILKRYICRFPATGHGAD
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29997..32183
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CDPRDYSDAARPRDLYLKTIRGCLRLNDICHTHRGVASDPLSTLVWGSALYASNA
RLVNHLEPRQFVGLGNADLTAGGEAPFENSKYTKNALHGORLREHDSLVHFTRL
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30114..30119
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32195..34819
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MVASRSMKPEFEFVYVSGDITEMSPLTEKNGTEPKILKRPSTOLLNVAVTKGVGL
GQADNARFPRAITGDISLMSKATTENSYCDLILMKFSNAIQOHNSSLFIANDIT
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QPLQIOLDLTHAKLNLJTNAATSPSTPRRRRDLSSVSGGKNNDNKSRES
VAAQVOFAVDNLRKSNIRYVGLSIRAMCREQYASLAWMLKINFTSYWASLTYGAP
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LGPNEETVLSQYEVNCHCEHYFOAGNQQYKKQDYVYVYVNTLNTPIPLTHMITIN
LSLVENIDFVIELEYKSTERKLSNVEDIEMFRERYNTYTONLGRDLDDSDIDHGD
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VVVVYVLEMTRSKTSIYSAPIMLYGVYRAAOEPAPHVASDOJIRNIIIMGHQFOQOR
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35089..38115
/note="ORF 09"

polyA_signal

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Query Match 0.1%; Score 25; DB 1; Length 184427;
Best Local Similarity 100.0%; Pred No. 0.0067;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50042 TCGTACGTTCTATTGAAGCAGT 50066
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Db 81099 TCGTACGTTCTATTGAAGCAGT 81123

RESULT 7
KSU18551 1855 bp DNA linear VRL 24-MAY-1995
LOCUS Kaposi's sarcoma-associated herpes-like virus putative minor capsid protein gene, complete cds, and major capsid protein gene, partial cds.
VERSION U18551
KEYWORDS U18551.1 GI:604505

SOURCE Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8)
ORGANISM Human herpesvirus 8
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 1855)
AUTHORS Chang, Y., Cesarman, E., Pessin, M.S., Lee, F., Culpepper, J., Knowles, D.M. and Moore, P.S.
TITLE Identification of herpesvirus-like DNA sequences in AIDS-associated Kaposi's sarcoma
JOURNAL Science 266 (3192), 1865-1869 (1994)
MEDLINE 95090463
PUBMED 7997879
REFERENCE 2 (bases 1 to 1855)
AUTHORS Chang, Y.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-1994) Yuan Chang, Pathology, Columbia University, 630 W. 168th St., New York, NY 10032, USA
FEATURES
source location/Qualifiers
1. 1855
/organism="Human herpesvirus 8"
/mol_type="genomic DNA"
/strain="KSHV0"
/specific_host="Homo sapiens"
/db_xref="taxon:37296"
/clone="KS5"
/tissue_type="Kaposi's sarcoma lesion in skin"
/clone_lib="lambda FIX II, KSI library from AIDS-KS patient of Y. Chang, P.S. Moore"
1. 608
/note="putative major capsid protein; similar to Saimirine herpesvirus major capsid protein, Swiss-Prot Accession Number Q00999, and EBV major capsid protein (BcLF1), Swiss-Prot Accession Number P03226"
/codon_start=2
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/db_xref="GI:604506"
/translation="TCEIIPPTVTSVAVFQTPSPNPRGRASVSCDAYSNSAERLF

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633. 1550
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1826
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/citation=[1]
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1850
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BASE COUNT 410 a 518 c 481 g 446 t
ORIGIN

Query Match 0.1%; Score 23; DB 1; Length 1855;
Best Local Similarity 100.0%; Pred No. 0.066;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44313 AGTCACGTTCTATTATCT 44335
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Db 1455 AGTCACGTTCTATTATCT 1477

RESULT 8
KSU40377/c 20705 bp DNA linear VRL 16-FEB-1996
LOCUS Kaposi's sarcoma-associated herpes-like virus clone KS5,
DEFINITION ORF20-ORF35 gene region.
ACCESSION U40377
VERSION U40377.1 GI:1136805
KEYWORDS

SOURCE Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8)
ORGANISM Human herpesvirus 8
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 7571 to 9425)
AUTHORS Chang, Y., Cesarman, E., Pessin, M.S., Lee, F., Culpepper, J., Knowles, D.M. and Moore, P.S.
TITLE Identification of herpesvirus-like DNA sequences in AIDS-associated Kaposi's sarcoma
JOURNAL Science 266 (5192), 1865-1869 (1994)
MEDLINE 95090463
PUBMED 7997879
REFERENCE 2 (bases 7571 to 9425)
AUTHORS Moore, P.S. and Chang, Y.
TITLE Detection of herpesvirus-like DNA sequences in Kaposi's sarcoma in patients with and without HIV infection
JOURNAL N. Engl. J. Med. 332 (18), 1181-1185 (1995)
MEDLINE 95214703
PUBMED 7700310
REFERENCE 3 (bases 7571 to 9425)
AUTHORS Cesarman, E., Moore, P.S., Rao, P.H., Inghirami, G., Knowles, D.M. and Chang, Y.
TITLE In vitro establishment and characterization of two acquired immunodeficiency syndrome-related lymphoma cell lines (BC-1 and BC-2) containing Kaposi's sarcoma-associated herpesvirus-like

JOURNAL (KSHV) DNA sequences
MEDLINE Blood 86 (7), 2708-2714 (1995)
95399773
PUBMED 7670109
REFERENCE 4 (bases 1 to 20705)
AUTHORS Moore, P.S., Gao, S.J., Dominguez, G., Cesarman, E., Lungu, O.,
Knowles, D.M., Garber, R., Pellett, P.E., McGeech, D.J., and Chang, Y.
TITLE Primary characterization of a herpesvirus agent associated with
Kaposi's sarcoma
J Virol. 70 (1), 549-558 (1996)
JOURNAL 96099469
MEDLINE 8523568
PUBMED 5 (bases 1 to 20705)
REFERENCE Moore, P.S., Chang, Y., Dominguez, G., and Pellett, P.E.
AUTHORS Direct Submission
TITLE Submitted (08-NOV-1995) Patrick S. Moore, Division of Epidemiology,
JOURNAL Columbia University, 630 W. 168th Street, New York, NY 10032, USA
FEATURES Location/Qualifiers
SOURCE 1. .20705
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/mol_type="genomic DNA"
/db_xref="taxon:37296"
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/note="submitter-supplied organism name synonym=Human
herpesvirus 8 (HHV8); lambda FIX II genomic library clone
from an AIDS Kaposi's sarcoma lesion; Open reading frame
designation follow that of the gene homologs in
herpesvirus saimiri"
complement(3. .86)
CDS /note="ORF35: Homolog to the herpesvirus saimiri1 (HVS)
ORF35, equine herpesvirus 2 (EHV2) ORF35, and Epstein-Barr
virus (EBV) BGLF3.5 gene products; Method: conceptual
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complement(67. .1050)
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supplied by author"
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LLEFGPASFCDCLYKOHCGYGPVLLPGHMYAPKRDLISFYNAHALKTYKFLYGD
SGWAAACRPPEPARIQRYVYSOKMIIASDPTVISHKCLGCHIVQONSIIAGCGTHVG
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746. .1969
exon /note="ORF29a: first ATG located at position 1049"
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CDS /join(1049. .1969,5221. .6363)
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the HVS ORF29, EHV2 ORF29, and EBV BGLF1 gene products.
first ATG located at position 1049; Method: conceptual
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FLPRHGTWIVAIISMLASVENINIGVAAKHVANSVFAEIIKTLGRMPKPN
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GMFOKAKLIEISSVNSDRSTSLNLRNAOKRMNVSYVCADHREDHIDLALV
SCPTCLHPTIYTTIDSIKTTTNLFMEGARDTELMGGAASSNATLKVGDALVTO
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CDS complement(1648. .1653)
/note="ORF3"
complement(2026. .2964)
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EBV BGLF2 gene products; Method: conceptual translation
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/db_xref="GI:1136809"
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ITFCQFLBEASGLRPPIYAPPSBHVFDLRLQELHVSQVRKDLTNCJMGLEFRN
VNPFWLGGSVWLLFLGVDMACFPGVDGMPSLARVAALLTRCDHPCVCHGLGRH
VNVFRGYCSAQSPGLSNICPCIKSCGTNGVTRVGNRNFLGLLFDPIQSRVYALKI
TSHPTRHVENVLGVDDGTILVPSVQTLGLPTNV"
complement(2957. .4321)
CDS /note="ORF32: Homolog to the HVS ORF32, EHV2 ORF32, and
EBV BGLF1 gene products; Method: conceptual translation
supplied by author"
/codon_start=1
/product="gene 32 protein"
/protein_id="AAB08386.1"
/db_xref="GI:1136810"
/translation="MDAHAINERYVGPCHRLAHVLPRTLHHAITLPEEIIESTY
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PDPALTRPLQVLGLLACSGDGRATHMLALEAGVYRGSIDPVPVQKPARTHR
PPVPLSEPNVADVPATWRATNVYSGAPYVCYERGGDEDDMLPIPSPEEPV
PPPGIVEMDLFTNTKODCPVDVPLEACRQGYTLRQRVVAIIPROAEIADAKSH
LEACTVLRGLASASAMTRATSPPLGNAACMVDYLCMBESRPHLGLIELGVNCGCT
GDGMLETLKQPDVQKTVSGSLVACVIVPALEAWLVLPGFAIRARVASKEDLVFIR
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complement(3014. .3019)
CDS /note="ORF32"
complement(3015. .3020)
/note="ORF34, ORF33"
complement(4288. .4962)
/note="ORF31: Homolog to the HVS ORF31, EHV2 ORF31, and
EBV BDLF4 gene products; Method: conceptual translation
supplied by author"
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complement(4357. .4362)
polyA_signal /note="ORF31; ORF30"
CDS complement(4869. .5102)
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BDLF3.5 gene products; Method: conceptual translation
supplied by author"
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5221. .6363
exon /note="ORF29b"
/number=2
complement(5269. .5274)
polyA_signal /note="ORF28"
complement(5335. .5340)
TATA_signal /note="ORF32; ORF31; ORF30"

polyA_signal 6359..6364
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/note="ORF28"
/complement(6982..6987)
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/complement(6983..7855)
/note="ORF27; Homolog to the HVS ORF27, EBV2 ORF27, and
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Query Match 0.1%; Score 23; DB 1; Length 20705;
Best local Similarity 100.0%; Pred. No. 0.088; 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 44313 AGTCGAGTCTATATTATCT 44335
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Db 7971 AGTCGAGTCTATATTATCT 7949

RESULT 9
AY170317 59673 bp DNA linear VRL 24-APR-2003
LOCUS Porcine lymphotropic herpesvirus 2 isolate 568 long unique region,
DEFINITION partial sequence
ACCESSION AY170317 AF940477
VERSION AY170317.1 GI:27452844
KEYWORDS
SOURCE Porcine lymphotropic herpesvirus 2
ORGANISM Porcine lymphotropic herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
REFERENCE
AUTHORS 1 (bases 1 to 59673)
Chmielewicz,B., Goltz,M., Franz,T., Bauer,C., Brema,S.,
Ellerbrok,H., Beckmann,S., Rziha,H.-J., Lahrmann,K.-H., Romero,C.
and Ehlers,B.
TITLE A novel porcine gammaherpesvirus
JOURNAL Virology 308 (2), 317-329 (2003)
MEDLINE 22594013
PUBMED 12706081
REFERENCE 2 (bases 1 to 59673)
Chmielewicz,B., Goltz,M., Rziha,J., Romero,C., Franz,T. and
Ehlers,B.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2002) P24 Xenotransplantation, Robert
Koch-Institut, Nordufer 20, Berlin 13353, Germany
REFERENCE 3 (bases 1 to 59673)
Chmielewicz,B., Goltz,M., Franz,T., Bauer,C., Brema,S.,
Ellerbrok,H., Beckmann,S., Rziha,H.-J., Lahrmann,K.-H., Romero,C.
and Ehlers,B.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-2002) P24 / Xenotransplantation, Robert
Koch-Institut, Nordufer 20, Berlin 13353, Germany
COMMENT On Apr 11, 2003 this sequence version replaced gi:29468328.
FEATURES
Source location/Qualifiers
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/organism="Porcine lymphotropic herpesvirus 2"
/mol_type="genomic DNA"
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rhadinovirus human herpesvirus 8: determinants of its pathogenicity?
J. Virol. 71 (6), 4187-4192 (1997)
MEDLINE 97296220
PUBMED 9151804
REFERENCE 6 (bases 1 to 133661)
AUTHORS Neipel, F., Albrecht, J.-C., Ensser, A., Huang, Y.-Q., Li, J.J.,
Friedman-Kien, A.E. and Fleckenstein, B.
TITLE The genome of human herpesvirus 8 cloned from Kaposi's sarcoma
JOURNAL Unpublished
AUTHORS 7 (bases 1 to 133661)
Neipel, F., Albrecht, J.-C., Ensser, A., Huang, Y.-Q., Li, J.J.,
Friedman-Kien, A.E. and Fleckenstein, B.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1997) Virology, University of Erlangen,
Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen
91054, Germany
REFERENCE 8 (bases 1 to 133661)
AUTHORS Neipel, F., Albrecht, J.-C., Ensser, A., Huang, Y.-Q., Li, J.J.,
Friedman-Kien, A.E. and Fleckenstein, B.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Virology, University of Erlangen,
Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen
91054, Germany
REMARK Sequence update by submitter
COMMENT On Jul 9, 2001 this sequence version replaced gi:2246466.
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RESULT 11
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LOCUS Kaposi's sarcoma-associated herpesvirus long unique region, 80
DEFINITION putative ORF's and kaposin gene, complete cds.
ACCESSION U75698
VERSION U75698.1 GI:2065526
KEYWORDS
SOURCE
ORGANISM
Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8
VIRUSES: dsDNA viruses, no RNA stage: Herpesviridae;
Gammaherpesvirinae: Rhadinovirus.
REFERENCE
1 (bases 47193 to 47522: 133099 to 133729)
Chang, Y., Cesarman, E., Pessin, M.S., Lee, F., Culpepper, J.,
Knowles, D.M. and Moore, P.S.
Identification of herpesvirus-like DNA sequences in AIDS-associated
Kaposi's sarcoma
Science 266 (5192), 1865-1869 (1994)
JOURNAL MEDLINE
95090463
PUBMED 7997879
REFERENCE
2 (bases 35021 to 55726)
Moore, P.S., Gao, S.J., Dominguez, G., Cesarman, E., Lungu, O.,
Knowles, D.M., Garber, R., Pellett, P.E., McGeoch, D.J. and Chang, Y.
Primary characterization of a herpesvirus agent associated with
Kaposi's sarcoma
Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
JOURNAL MEDLINE
96099469
PUBMED 8523568
REFERENCE
3 (bases 28661 to 29741; 117919 to 118101)
Zhong, W., Wang, H., Herndler, B. and Ganem, D.
Restricted expression of Kaposi sarcoma-associated herpesvirus
(human herpesvirus 8) genes in Kaposi sarcoma
Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
JOURNAL MEDLINE
96270595
PUBMED 862871
REFERENCE
4 (bases 122794 to 123567; 123809 to 127297; 129372 to 130400;
130551 to 134441)
Cesarman, E., Nador, R.G., Bai, F., Bohenzky, R.A., Russo, J.J.,
Moore, P.S., Chang, Y. and Knowles, D.M.
Kaposi's sarcoma-associated herpesvirus contains G protein-coupled
receptor and cyclin D homolog which are expressed in Kaposi's
sarcoma and malignant lymphoma
J. Virol. 70 (11), 8218-8223 (1996)
JOURNAL MEDLINE
97048116
PUBMED 8892957
REFERENCE
5 (bases 1 to 137508)
Moore, P.S., Boshoff, C., Weiss, R.A. and Chang, Y.
Molecular mimicry of human cytokine and cytokine response pathway
genes by KSHV
Science 274 (5293), 1739-1744 (1996)
JOURNAL MEDLINE
97094384
PUBMED 8939871
REFERENCE
6 (bases 1 to 137508)
Russo, J.J., Bohenzky, R.A., Chien, M.-C., Chen, J., Yan, M.,

TITLE
Maddalena, D., Parry, J.P., Peruzzi, D., Edelman, I.S., Chang, Y. and
Moore, P.S.
Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
(HHV8)
Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14862-14867 (1996)
JOURNAL MEDLINE
97121480
PUBMED 8962146
REFERENCE
7 (bases 1 to 137508)
Russo, J.J., Bohenzky, R.A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J.P., Peruzzi, D., Edelman, I.S., Chang, Y. and
Moore, P.S.
Direct Submission
Submitted (17-OCT-1996) Dept of Pathology/Genome Center/Division of
Epidemiology, Columbia University, 650 West 168th Street, New York,
NY 10032, USA
8 (bases 1 to 137508)
Russo, J.J., Bohenzky, R.A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J.P., Peruzzi, D., Edelman, I.S., Chang, Y. and
Moore, P.S.
Direct Submission
Submitted (02-MAY-1997) Dept of Pathology/Genome Center/Division of
Epidemiology, Columbia University, 650 West 168th Street, New York,
NY 10032, USA
REMARK
COMMENT
Sequence update by submitter
On May 3, 1997 this sequence version replaced gi:1718251.
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DEFINITION
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ACCESSION
AY037858 AF148640 AF159308 AF227125 AF159309 AF159310
AF227123 AF227124 U45963 U93160 U93909
AY037858.1 GI:18025465
VERSION
AY037858.1
SOURCE
Cercopithecine herpesvirus 15
ORGANISM
Cercopithecine herpesvirus 15
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
1 (bases 1 to 171096)
REFERENCE
1 Franken, M., Deyere, O., Rosenzweig, M., Annis, B., Kieff, E. and
Wang, F.
Comparative analysis identifies conserved tumor necrosis factor
receptor-associated factor 3 binding sites in the human and simian
Epstein-Barr virus oncogene LMP1
J. Virol. 70 (11), 7819-7826 (1996)
MEDLINE
97048062
PUBMED
8892903
REFERENCE
2 (bases 1 to 171096)
Rivallier, P., Quink, C. and Wang, F.
Strong selective pressure for evolution of an Epstein-Barr virus
LMP2 homologue in the rhesus lymphocryptovirus
J. Virol. 73 (10), 8867-8872 (1999)
MEDLINE
99412410
PUBMED
10482645
REFERENCE
3 (bases 1 to 171096)
Jiang, H., Cho, Y.G. and Wang, F.
Structural, functional, and genetic comparisons of Epstein-Barr
virus nuclear antigen 3a, 3b, and 3c homologues encoded by the
rhesus lymphocryptovirus
J. Virol. 74 (13), 5921-5932 (2000)
MEDLINE
20304984
PUBMED
10846073
REFERENCE
4 (bases 1 to 171096)
Rao, P., Jiang, H. and Wang, F.
Cloning of the rhesus lymphocryptovirus viral capsid antigen and
Epstein-Barr virus-encoded small RNA homologues and use in
diagnosis of acute and persistent infections
J. Clin. Microbiol. 38 (9), 3219-3225 (2000)
MEDLINE
20440631
PUBMED
10970361
REFERENCE
5 (bases 1 to 171096)
Rivallier, P., Jiang, H., Cho, Y.G., Quink, C. and Wang, F.
Complete nucleotide sequence of the rhesus lymphocryptovirus:
genetic validation for an Epstein-Barr virus animal model
J. Virol. 76 (1), 421-426 (2002)
MEDLINE
21602573
PUBMED
11739708
REFERENCE
6 (bases 1 to 171096)
Wang, F., Franken, M. and Annis, B.
Direct Submission
Submitted (11-JAN-1996) Medicine, Brigham and Women's Hospital, 181
Longwood Avenue, Boston, MA 02115, USA
JOURNAL
7 (bases 1 to 171096)
Moghaddam, A., Koch, J., Annis, B. and Wang, F.
Direct Submission
Submitted (12-MAR-1997) Medicine, Brigham and Women's Hospital, 181
Longwood Avenue, Boston, MA 02115, USA
REFERENCE
8 (bases 1 to 171096)

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AUTHORS      Moghaddam, A., Annis, B. and Wang, F.
TITLE        Direct Submission
JOURNAL      Submitted (17-MAR-1997) Medicine, Brigham and Women's Hospital, 181
              Longwood Avenue, Boston, MA 02115, USA
REFERENCE    9 (bases 1 to 171096)
AUTHORS      Rivallier, P., Quink, C. and Wang, F.
TITLE        Direct Submission
JOURNAL      Submitted (04-MAY-1999) Medicine, Brigham and Women's Hospital, 181
              Longwood Avenue, Boston, MA 02115, USA
REFERENCE    10 (bases 1 to 171096)
AUTHORS      Jiang, H. and Wang, F.
TITLE        Direct Submission
JOURNAL      Submitted (16-JUN-1999) Medicine, Brigham and Women's Hospital, 181
              Longwood Avenue, Boston, MA 02115, USA
REFERENCE    11 (bases 1 to 171096)
AUTHORS      Rao, P. Y., Jiang, H. and Wang, F.
TITLE        Direct Submission
JOURNAL      Submitted (21-JAN-2000) Medicine, Brigham and Women's Hospital, 181
              Longwood Avenue, Boston, MA 02115, USA
REFERENCE    12 (bases 1 to 171096)
AUTHORS      Rivallier, P., Jiang, H., Cho, Y.-G., Quink, C. and Wang, F.
TITLE        Direct Submission
JOURNAL      Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181
              Longwood Avenue, Boston, MA 02115, USA
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COMMENT       On or before Dec 31, 2001 this sequence version replaced
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Db 108504 GGGGGCTTGTATTAAGGCC 108483

RESULT 13
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LOCUS HHV507799 171823 bp DNA circular VRL 04-APR-2003

DEFINITION Human herpesvirus 4 complete wild type genome.

ACCESSION AJ507799.1 GI:23893576

VERSION AJ507799.1

KEYWORDS complete genome.
Human herpesvirus 4 (Epstein-Barr virus)

SOURCE Human herpesvirus 4

ORGANISM Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1
Arrand, J.R., Rymo, L., Walsh, J.E., Bjorck, E., Lindahl, T. and Griffin, B.E.
Molecular cloning of the complete Epstein-Barr virus genome as a set of overlapping restriction endonuclease fragments
Nucleic Acids Res. 9 (13), 2999-3014 (1981)

JOURNAL MEDLINE 82014887

PUBMED 6269068

REFERENCE 2
Kozak, M.
Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes
Nucleic Acids Res. 9 (20), 5233-5262 (1981)

JOURNAL MEDLINE 82059504

PUBMED 7301588

REFERENCE 3
Deininger, P.L., Bankier, A., Farrell, P., Baer, R. and Barrell, B.
Sequence analysis and in vitro transcription of portions of the Epstein-Barr virus genome
J. Cell. Biochem. 19 (3), 267-274 (1982)

JOURNAL MEDLINE 83109311

PUBMED 6296170

REFERENCE 4
Farrell, P.J., Deininger, P.L., Bankier, A. and Barrell, B.
Homologous upstream sequences near Epstein-Barr virus promoters
Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)

JOURNAL MEDLINE 83169725

PUBMED 6300857

REFERENCE 5
Bankier, A.T., Deininger, P.L., Farrell, P.J. and Barrell, B.G.
Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8 Epstein-Barr virus
Mol. Biol. Med. 1 (1), 21-45 (1983)

JOURNAL MEDLINE 85035713

PUBMED 6092825

REFERENCE 6
Seguin, C., Farrell, P.J. and Barrell, B.G.
DNA sequence and transcription of the BamHI fragment B region of B95-8 Epstein-Barr virus
Mol. Biol. Med. 1 (3), 369-392 (1983)

JOURNAL MEDLINE 85060424

PUBMED 6094953

REFERENCE 7
Jeang, K.T. and Hayward, S.D.
Organization of the Epstein-Barr virus DNA molecule. III. Location of the p3HR-1 deletion junction and characterization of the NotI 12-O-tetradecanoylphorbol-13-acetate-induced mRNA transcript
J. Virol. 48 (1), 135-148 (1983)

JOURNAL MEDLINE 83294686

PUBMED 6310141

REFERENCE 8
Bankier, A.T., Deininger, P.L., Satchwell, S.C., Baer, R., Farrell, P.J. and Barrell, B.G.
DNA sequence analysis of the EcoRI Dhet fragment of B95-8 Epstein-Barr virus containing the terminal repeat sequences
Mol. Biol. Med. 1 (4), 425-445 (1983)

JOURNAL MEDLINE 85060428

PUBMED 6094955

REFERENCE 9
Farrell, P.J., Bankier, A., Seguin, C., Deininger, P. and Barrell, B.G.
Latent and lytic cycle promoters of Epstein-Barr virus
EMBO J. 2 (8), 1331-1338 (1983)

JOURNAL MEDLINE 20331131

PUBMED 10872327

REFERENCE 10
Jones, M.D., Foster, L., Sheedy, T. and Griffin, B.E.
The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion similar to that observed in a non-transforming strain (p3HR-1) of the virus
EMBO J. 3 (4), 813-821 (1984)

JOURNAL MEDLINE 84207939

PUBMED 6327290

REFERENCE 11
Biggin, M., Farrell, P.J. and Barrell, B.G.
Transcription and DNA sequence of the BamHI L fragment of B95-8 Epstein-Barr virus
EMBO J. 3 (5), 1083-1090 (1984)

JOURNAL MEDLINE 84236104

PUBMED 6203743

REFERENCE 12
Vates, J., Warren, N., Reisman, D. and Sugden, B.
A cis-acting element from the Epstein-Barr viral genome that permits stable replication of recombinant plasmids in latently infected cells
Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3806-3810 (1984)

JOURNAL MEDLINE 84222045

PUBMED 6328526

REFERENCE 13
Gibson, T., Stockwell, P., Ginsburg, M. and Barrell, B.
Homology between two EBV early genes and HSV ribonucleotide reductase and 38k genes
Nucleic Acids Res. 12 (12), 5087-5099 (1984)

JOURNAL MEDLINE 84247360

PUBMED 6330697

REFERENCE 14
(bases 1 to 171823)
Baer, R.J., Bankier, A.T., Biggin, M.D., Deininger, P.L., Farrell, P.J., Gibson, T.J., Hatfull, G.F., Hudson, G.S., Satchwell, S.C., Seguin, C., Tuffnell, P.S. and Barrell, B.G.
DNA sequence and expression of the B95-8 Epstein-Barr virus genome
Nature 310 (5974), 207-211 (1984)

JOURNAL MEDLINE 84270667

PUBMED 6087149

REFERENCE 15
Bodrescu, M. and Perricaudet, M.
Clustered alternative splice sites in Epstein-Barr virus RNAs
Nucleic Acids Res. 15 (14), 5887 (1987)

JOURNAL MEDLINE 87289053

PUBMED 3039467

REFERENCE 16
Laux, G., Perricaudet, M. and Farrell, P.J.
A spliced Epstein-Barr virus gene expressed in immortalized lymphocytes is created by circularization of the linear viral genome
EMBO J. 7 (3), 769-774 (1988)

JOURNAL MEDLINE 88283646

PUBMED 2840285

REFERENCE 17
Parker, B.D., Bankier, A., Satchwell, S., Barrell, B. and Farrell, P.J.
Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B95-8 deletion region
Virology 179 (1), 339-346 (1990)

JOURNAL MEDLINE 91021036

PUBMED 2171209

REFERENCE 18
(bases 1 to 171823)
Hatfull, G.F., Barrell, B.G., Quinn, J. and McGeoch, D.
Unpublished

JOURNAL MEDLINE 91021036

PUBMED 2171209

REFERENCE 19
Binne, U.K., Amou, M. and Farrell, P.J.
Induction of Epstein-Barr virus late promoters on small plasmids in the EBV late lytic cycle requires ori lyt

JOURNAL	Unpublished
REFERENCE	20 (bases 1 to 171823)
AUTHORS	Farrell,P.J.
TITLE	Direct Submission
JOURNAL	Submitted (01-AUG-2002) Farrell P., Ludwig Institute for Cancer Research, Imperial College School of Medicine, St. Mary's Campus, Norfolk Place London W2 1PG
COMMENT	Construction: This sequence was assembled from B95-8 EBV [14] and Raj1 EBV [18] with sequence corrections [16, 19]. The number of major internal repeat units has been reduced from 11.6 [14] to a more typical 7.6 and the B95-8 deletion sequences have been restored to give a sequence more representative of wild type EBV. Numbering Like the modified B95-8 sequence[14, 16] accession number V01555, this sequence starts 1 base to the left of the EcoRI site separating EcoRI Duet from EcoRI I (ie the first A of AGAATTC.). Location/Qualifiers 1..171823 /organism="Human herpesvirus 4" /mol_type="genomic DNA" /strain="B95-8" /db_xref="taxon:10376" join(1..139223,15155..171823) /organism="Human herpesvirus 4" /mol_type="genomic DNA" /strain="B95-8" /db_xref="taxon:10376" 139224..151554 /organism="Human herpesvirus 4" /mol_type="genomic DNA" /strain="Raj1" /db_xref="taxon:10376" join(166103..171823,1..1682) /gene="LMP2" join(166103..166458,58..272,360..458,540..788,871..955,1028..1196,1280..1495,1574..1680) /gene="LMP2" /codon_start=1 /product="terminal protein LMP2A" /protein_id="CAD53382.1" /db_xref="GI:23893577" /translacion="MGSLEWPMGACPPSPRGDDPDTGCGNNSQYPSASGSGSNTPIIFPNDEKRSNEPPPEPDPTWGNDRSDYQPLCTOOSLYLGQHGDNDLPPIYS PRDSQSHIYEAGRGSMNPCLFVIAYAFEMAAIAASCFTASVSIVYATGALALS LLDLAAVASSYAAROKRLTFPVLTVAWFPAICLMRIEDPPNSLFLALLAAGAVTWS LOGIVLVMLVTILTAIRRRMRRLTVGGCMLFIACVYLIVDAVLOISFLMGATVVS MTLLLFNFVLHSSPGGLGTIGAILTLAALLLAALSLASIICTLNUTTFILMLMTLV VLTISSCSSCPSLSKILLARFLTAALLLAALSLASIICTLNUTTFILMLMTLV FCMLLIIVAGLITFLIALITEWGSNGNRYPGFEMGLGLTWAGAVMLTYVSNLS MWLAGFLIFLIGFALGVIRCRCYCVCYCLTESESRPPRYHNIV" 58..272 /gene="LMP2" /number=2 join(59..272,360..458,540..788,871..951,1026..1196, 1280..1495,1574..1680) /gene="LMP2" /codon_start=1 /product="terminal protein LMP2B" /protein_id="CAD53383.1"
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LOCUS	

DEFINITION	Epstein-Barr virus (EBV) genome, strain B95-8.
ACCESSION	V01555 J02070 K01729 K01730 V01554 X00498 X00499 X00784
VERSION	V01555.1 GI:59074
KEYWORDS	DNA polymerase; EBNA; genome; ribonucleotide reductase; tandem repeat; terminal repeat.
SOURCE	Human herpesvirus 4 (Epstein-Barr virus)
ORGANISM	Human herpesvirus 4
REFERENCE	1. Vinuses; dsDNA viruses, no RNA stage: Herpesviridae: Gammaherpesvirinae: Lymphocryptovirus.
AUTHORS	1 (bases 1 to 172281)
TITLE	Arrand, J.R., Rymo, L., Walsh, J.E., Bjorck, E., Lindahl, T. and Griffin, B.E.
JOURNAL	Molecular cloning of the complete Epstein-Barr virus genome as a
MEDLINE	set of overlapping restriction endonuclease fragments
PUBMED	Nucleic Acids Res. 9 (13), 2999-3014 (1981)
REFERENCE	2 (bases 1 to 172281)
AUTHORS	Kozak, M.
TITLE	Possible role of flanking nucleotides in recognition of the AUG
JOURNAL	initiator codon by eukaryotic ribosomes
MEDLINE	Nucleic Acids Res. 9 (20), 5233-5262 (1981)
PUBMED	82059504
REFERENCE	7301588
AUTHORS	3 (bases 1 to 172281)
TITLE	Deininger, P.L., Bankier, A., Farrell, P., Baer, R. and Barrell, B.
JOURNAL	Sequence analysis and in vitro transcription of portions of the
MEDLINE	Epstein-Barr virus genome
PUBMED	J. Cell. Biochem. 19 (3), 267-274 (1982)
REFERENCE	6296170
AUTHORS	4 (bases 1 to 172281)
TITLE	Farrell, P.J., Deininger, P.L., Bankier, A. and Barrell, B.
JOURNAL	Homologous upstream sequences near Epstein-Barr virus promoters
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)
PUBMED	83169725
REFERENCE	6300857
AUTHORS	5 (bases 142687 to 159853)
TITLE	Bankier, A.T., Deininger, P.L., Farrell, P.J. and Barrell, B.G.
JOURNAL	Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
MEDLINE	Epstein-Barr virus
PUBMED	Mol. Biol. Med. 1 (1), 21-45 (1983)
REFERENCE	85035713
AUTHORS	6 (bases 112620 to 125316)
TITLE	Seguin, C., Farrell, P.J. and Barrell, B.G.
JOURNAL	DNA sequence and transcription of the BamHI fragment B region of
MEDLINE	B95-8 Epstein-Barr virus
PUBMED	Mol. Biol. Med. 1 (3), 369-392 (1983)
REFERENCE	85060424
AUTHORS	6094953
TITLE	7 (bases 45644 to 52450)
JOURNAL	Jiang, K.T. and Hayward, S.D.
MEDLINE	Organization of the Epstein-Barr virus DNA molecule. III. Location
PUBMED	of the PSHR-1 deletion junction and characterization of the NotI
REFERENCE	repeat units that form part of the template for an abundant
AUTHORS	12-O-tetradecanoylphorbol-13-acetate-induced mRNA transcript
TITLE	J. Virol. 48 (1), 135-148 (1983)
JOURNAL	83294686
MEDLINE	6310141
PUBMED	8 (bases 159853 to 172281)
REFERENCE	Bankier, A.T., Deininger, P.L., Satchwell, S.C., Baer, R., Farrell, P.J.
AUTHORS	and Barrell, B.G.
TITLE	DNA sequence analysis of the EcoRI DheI fragment of B95-8
JOURNAL	Epstein-Barr virus containing the terminal repeat sequences
MEDLINE	Mol. Biol. Med. 1 (4), 425-445 (1983)
PUBMED	6094955
REFERENCE	9 (bases 1 to 172281)
AUTHORS	Farrell, P.J., Bankier, A., Seguin, C., Deininger, P. and Barrell, B.G.
TITLE	Latent and lytic cycle promoters of Epstein-Barr virus
JOURNAL	EMBO J. 2 (8), 1331-1338 (1983)
MEDLINE	20331131

PUBMED 10872327
 10 (bases 45415 to 52824)
 JONES,M.D., Foster,L., Sneezy,T. and Griffin,B.E.
 The EB virus genome in Daudi Burkitt's lymphoma cells has a
 deletion similar to that observed in a non-transforming strain
 (P3HR-1) of the virus
 EMBO J. 3 (4), 813-821 (1984)
 JOURNAL 84207939
 MEDLINE 6327290
 PUBMED 11 (bases 87650 to 92703)
 REFERENCE Biggin,M., Farrell,P.J. and Barrell,B.G.
 JOURNAL Transcription and DNA sequence of the BamHI L fragment of B95-8
 MEDLINE 84236104
 PUBMED 6203743
 REFERENCE 12 (bases 7315 to 9312)
 JOURNAL Yates,J., Warren,N., Reisman,D. and Sugden,B.
 MEDLINE A cis-acting element from the Epstein-Barr viral genome that
 PUBMED permits stable replication of recombinant plasmids in latently
 REFERENCE infected cells
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3806-3810 (1984)
 MEDLINE 6328526
 PUBMED 13 (bases 76089 to 79808)
 REFERENCE Gibson,T., Stockwell,P., Ginsburg,M. and Barrell,B.
 JOURNAL Homology between two EBV early genes and HSV ribonucleotide
 MEDLINE Nucleic Acids Res. 12 (12), 5087-5099 (1984)
 PUBMED 84247360
 REFERENCE 14 (bases 1 to 172281)
 JOURNAL Baer,R.D., Bankier,A.T., Biggin,M.D., Deininger,P.L., Farrell,P.J.,
 MEDLINE Gibson,J.T., Hatfull,G.F., Hudson,G.S., Satchwell,S.C., Seguin,C.,
 PUBMED Tufnell,P.S. and Barrell,B.G.
 REFERENCE DNA sequence and expression of the B95-8 Epstein-Barr virus genome
 JOURNAL Nature 310 (5974), 207-211 (1984)
 MEDLINE 84270667
 PUBMED 15 (bases 1 to 172281)
 REFERENCE Bodescot,M. and Perricaudet,M.
 JOURNAL Clustered alternative splice sites in Epstein-Barr virus RNAs
 MEDLINE Nucleic Acids Res. 15 (14), 5887 (1987)
 PUBMED 87289053
 REFERENCE 16 (bases 1 to 172281)
 JOURNAL Laux,G., Perricaudet,M. and Farrell,P.J.
 MEDLINE A spliced Epstein-Barr virus gene expressed in immortalized
 PUBMED lymphocytes is created by circularization of the linear viral
 REFERENCE genome
 JOURNAL EMBO J. 7 (3), 769-774 (1988)
 MEDLINE 88283646
 PUBMED 2840285
 REFERENCE 17 (bases 1 to 172281)
 JOURNAL Hatfull,G.F., Barrell,B.G., Quinn,J. and McGeoch,D.
 MEDLINE Unpublished
 PUBMED 18 (bases 1 to 172281)
 REFERENCE Farrell,P.J. and Barrell,B.G.
 JOURNAL Direct Submission
 MEDLINE Submitted (05-JUN-1984)
 PUBMED 19 (bases 1 to 172281)
 REFERENCE Farrell,P.J.
 JOURNAL Direct Submission
 MEDLINE Submitted (18-MAR-1988) Farrell P., Ludwig Institute for Cancer
 PUBMED Research, St. Mary's Hospital Medical School, Norfolk Place London
 REFERENCE W2 1PG
 JOURNAL CDS
 MEDLINE Listed under this feature are all known protein coding regions as
 PUBMED well as all the major open reading frames in the sequence. In
 REFERENCE general the term major is taken as the longest frame in a
 JOURNAL particular region taking into account the adjacent longest frames
 MEDLINE and likely transcription signals. Note that on this basis some long
 PUBMED overlapping frames have been excluded and on the other hand some

small frames have been included which might represent exons or
 genes because they occur in a logical combination with other
 features or because of some other experimental data. The reading
 frames are named according to the Bam HI fragment in which they
 start. eg BALF3 is the third leftward frame starting in Bam HI
 fragment A. BORF1 is the first rightward frame in Bam HI fragment
 O. If there is an obvious TATA sequence followed by an in frame Met
 codon that satisfies the rules of Kozak [12] in that there is a
 purine at -3 and/or a G at +4 then the reading frame is numbered
 from the A of the ATG to the base preceding the termination codon.
 If there is no obvious initiation codon or there is a substantial
 reading frame in phase before the ATG then the reading frame is
 numbered from the first base of the first codon.
 SITES OF POLYA signals
 This feature lists all occurrences of the sequence AATAAA which is
 found normally approximately 20 bases upstream of the mRNA
 processing/polyA addition site. The rarely used homolog AATAAG is
 only listed when it is found in a position close to the end of a
 major reading frame.
 SITES OF DONOR and ACCEPT sequences
 This is not a comprehensive listing of all such sequences and only
 the positions of a few have been noted because they occur in
 potentially interesting positions. The number quoted in the table
 is the position of the terminal base in the intron in each case.
 Restriction enzyme SITES.
 Only the positions of the sites Bam HI (BAM) are listed.
 RPT
 This feature is used to define repetitive sequences.
 SITE DEL
 This feature defines deletions in B95-8 with respect to other
 strains such as Raji and also to deletions in other strains such as
 P3HR1 and DAUDI with respect to B95-8.
 SITE HPM
 Denotes sequences with twofold symmetry ie could form hairpin
 loops. This is not a comprehensive list - only a few occurrences
 noted.
 ORGRL
 Denotes the region that encompasses an origin of replication (ori
 P) [13].
 NUMBERING
 The DNA sequence of B95-8 EBV has been revised [19]. The original
 (Baer et al, 1984) base 359 has been deleted so the new sequence
 around that position reads TCAGTCCTT. To avoid renumbering the
 entire sequence, position 1 has been moved 1 base to the left of
 the EcoRI site separating EcoRI Dhet from EcoRI I
 (ie the first A of AGAATTC).
 Location/Qualifiers
 1..172281
 /organism="Human herpesvirus 4"
 /mol_type="genomic DNA"
 /strain="B95-8"
 /db_xref="taxon:10376"
 58..272
 mRNA
 Query Match 0.1%; Score 22; DB 1; Length 172281;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 48982 GGGGGCTTTGTTATTAAAGGCC 49003
 Db 126940 GGGGGCTTTGTTATTAAAGGCC 126919
 RESULT 15
 HS4B958RAJ/c 184113 bp DNA linear VRL 12-APR-1996
 LOCUS HS4B958RAJ Epstein-Barr virus, artifactual joining of B95-8 complete genome
 DEFINITION and the sequences from Raji of the large deletion found in B95-8.
 ACCESSION M80517 M75989
 VERSION M80517.1 GI:330330
 KEYWORDS Human herpesvirus 4 (Epstein-Barr virus)
 SOURCE Human herpesvirus 4
 ORGANISM

Viruses; dsDNA viruses, no RNA stage: Herpesviridae;
 Gammaherpesvirinae: Lymphocryptovirus.
 1 (sites)
 Baer, R.J., Bankier, A.T., Biggin, M.D., Deininger, P.L., Farrell, P.J.,
 Gibson, T.J., Hatfull, G.F., Hudson, G.S., Satchwell, S.C., Seguin, C.,
 Tufnell, P.S., and Bartell, B.G.
 DNA sequence and expression of the B95-8 Epstein-Barr virus genome
 Nature 310 (5974), 207-211 (1984)
 84270667
 MEDLINE
 PUBMED
 6087149
 2 (sites)
 Parker, B.D., Bankier, A., Satchwell, S., Bartell, B. and Farrell, P.J.
 Sequence and transcription of Raji Epstein-Barr virus DNA spanning
 the B95-8 deletion region
 Virology 179 (1), 339-346 (1990)
 91021036
 MEDLINE
 PUBMED
 2171209
 3 (sites)
 Sample, J., Brooks, L., Sample, C., Young, L., Rowe, M., Gregory, C.,
 Rickinson, A. and Kieff, E.
 Restricted Epstein-Barr virus protein expression in Burkitt
 lymphoma is due to a different Epstein-Barr nuclear antigen 1
 transcriptional initiation site
 Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6343-6347 (1991)
 91296817
 MEDLINE
 PUBMED
 1648738
 4 (bases 1 to 184113)
 Jenson, H.B.
 GenBank Curator Program
 Unpublished (1992)
 Original source text: Human herpesvirus 4 DNA.
 The B95-8 genome (V01555) has a large deletion in the right side of
 the genome which has been sequenced in Raji (M35547). These
 sequences have been joined to form an extended and more complete,
 although artifactual, EBV sequence.
 For features, refer to feature tables of V01555 and M35547.
 Location/Qualifiers
 1..184113
 /organism="Human herpesvirus 4"
 /mol_type="genomic DNA"
 /db_xref="taxon:10376"
 1..152008
 /note="B95-8 sequences (corresponds to 1-152,008 of
 V01555)."
 152009..152012
 /note="Overlap of B95-8 and Raji sequences at B95-8
 deletion point (corresponds to 152,009-152,012 in V01555,
 and 1-4 in M35547)."
 153013..163839
 /note="Raj1 sequences (corresponds to 5-11,831 of M35547)."
 163840..163843
 /note="Overlap of B95-8 and Raj1 sequences at B95-8
 deletion point (corresponds to 152,009-152,012 of V01555,
 and 11,832-11,835 of M35547)."
 163844..184113
 /note="B95-8 sequences (corresponds to 152,013-172,282 of
 V01555)."
 BASE COUNT 36002 a 55824 c 54622 g 37665 t
 ORIGIN
 Query Match 0.1%; Score 22; DB 1; Length 184113;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 48982 GGGGCTTGTATTAAAGCC 49003
 Db 126940 GGGGCTTGTATTAAAGCC 126919
 RESULT 16
 AF198100 288539 bp DNA linear VRL 31-MAR-2000
 LOCUS AF198100
 DEFINITION Fowlpox virus, complete genome.

AF198100
 AF198100.1 GI:7271507
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Fowlpox virus
 Viruses; dsDNA viruses, no RNA stage: Poxviridae: Chordopoxvirinae;
 Avipoxvirus.
 1 (bases 1 to 288539)
 Afonso, C.L., Tuijman, E.R., Lu, Z., Zsak, L., Kutish, G.F. and Rock, D.L.
 The genome of fowlpox virus
 J. Virol. 74 (8), 3815-3831 (2000)
 20193820
 MEDLINE
 PUBMED
 10729156
 2 (bases 1 to 288539)
 Afonso, C.L., Tuijman, E.R., Lu, Z., Zsak, L., Kutish, G.F. and Rock, D.L.
 Direct Submission
 Submitted (24-OCT-1999) Microbiology, Plum Island Animal Disease
 Center, U.S. Dept. Agriculture, Agricultural Research Service, P.O.
 Box 848, Greenport, NY 11944-0848, USA
 Location/Qualifiers
 1..288539
 /organism="Fowlpox virus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10261"
 /country="USA: APHIS Center for Veterinary Biologics,
 Ames, Iowa"
 /note="Virulent FPV; Fowlpox Challenge Virus"
 1..9520
 /note="left end"
 complement(1874..2491)
 /gene="FPV001"
 complement(1874..2491)
 /gene="FPV001"
 /note="C-type lectin gene family protein identical to
 FPV260 (vaccinia A40R), similar to Rattus norvegicus
 GB:A021330"
 /codon_start=1
 /product="ORF FPV001"
 /protein_id="AAFA4603.1"
 /db_xref="GI:7271757"
 /translation="MKNNYPREYKREKKFLRDNSEYIIPITCLTSVYITSLFA
 ALFVARDCKRDSFLEDTTATITSSATYTRNLYHCRDMISHTGLSTGER
 VGFNRQIQKCEKLSDMIGKSEEMKALKNTGNDHSRFVNDRAASTPDVNECA
 YGRSVSEVPKVLTPSCSVARLVCKRTDNTSSFFNOYE"
 3367..4035
 /gene="FPV002"
 3367..4035
 /gene="FPV002"
 /note="Identical to FPV259 Fowlpox GB:A06621"
 /codon_start=1
 /product="ORF FPV002 hypothetical protein"
 /protein_id="AAFA4597.1"
 /db_xref="GI:7271751"
 /translation="WIVETINAMLLYPLCLRLCNSVPATCKCVHCLLYPEVCC
 ECMSEITLDSLEHSCCYCCVPLLIIRFRVRVILPTLKATDCIRLPCLVLRCKRT
 ICPPLAKSMCRCEFCPCVFLCLFPCGMILRMHGRGLTVREGEAFSDSDPARGT
 WNDWCEDLCVIMSPCCYVRCIRTCMDPTFKIKFYFIAPASPRMPEBPSLSRK
 VESS"
 complement(4500..4871)
 /gene="FPV003"
 complement(4500..4871)
 /gene="FPV003"
 /note="Identical to FPV258 Fowlpox PIR:C31685 (vaccinia
 A40R), similar to Homo sapiens SW:007108"
 /codon_start=1
 /product="ORF FPV003 C-type lectin gene family protein"
 /protein_id="AAFA4606.1"
 /db_xref="GI:7271760"
 /translation="MKSILITAMLLMDCANSLNCRGPTSYNNKCIAMVNRDKNHKK
 KTVSEASTCLITPFGMLIARSLIDNEKDKKFLSKGMSGLIIRDCKREYCKAV
 TDGKTFGSPCNATYGFYCID"
 5125..5430
 /gene="FPV004"
 gene
 CDS

CDS 5125..5430
/gene="FPV004"
/note="identical to FPV257 Fowlpox GB:A06621"
/codon_start=1
/product="ORF FPV004 hypothetical protein"
/protein_id="AAFA4598.1"
/db_xref="GI:7271752"
/translation="MNDITFTLFCYKNNKRYRGSGRRRGKGTGILLFHPINHRVIGT
SAHQCKTRRIEFKLYAVAPRVSTTRCGRSHAHVRDKSFESFOKVPDHCIAGSGA"
/complement(5221..5589)
/gene="FPV005"
/complement(5221..5589)
/note="FPV005"
/codon_start=1
/product="ORF FPV005 EFC gene family protein"
/protein_id="AAFA4604.1"
/db_xref="GI:7271758"
/translation="MALNLRVRPVRGEGSIRKYLAAASDPLENDHTGCGVAVAIR
ANFECRARIACAAGDTYKIFLEBGEGLITSVRVGSPTADSGVTRKNCVPEFETDS
SCFTLMCTSYNTVYVYME"
5931..7187
/gene="FPV006"
5931..7187
/note="FPV006"
/note="identical to FPV255 Fowlpox SW:P14361 (vaccinia
C10L), similar to SW:P03296"
/codon_start=1
/product="ORF FPV006 C4L/C10L-like gene family protein"
/protein_id="AAFA4599.1"
/db_xref="GI:7271753"
/translation="MEFSGTGNNOLAVHRTETRTSKKELVNLGISTLNDIKNI
CEDSKIPEKRTTELSTDKRSKOIVFNSLNDLKLHLIYDELSTVVDVSVAVE
NVTILMEKGFARHNDPSTVFSKNIICVHLILYLEQETGETVITIDNNTSVKL
KTDHLEDKTIEHESITVESGRVALFDVLLEKTLASANNVGSIEYELKTNLVDRE
NDLOQCYDMVIERMTEDEKESYSLGMSGRICISHHNGSIVRAREKYGSEFDLCI
YVMNEVDELTGDKKHIIMSTIDKKGTGTFIPIDPLVYKELKAISSKEKEKIDRGF
CNSRREYICCSKYFFDLPTDILHEVINSIDIDTKSVGTPTDWTTLTIEVKQTILG
NNSIELENTVKGNTALEEDNEYGCD"
7599..7817
/gene="FPV007"
7599..7817
/gene="FPV007"
/note="identical to FPV254 Fowlpox GB:D00295"
/codon_start=1
/product="ORF FPV007 hypothetical protein"
/protein_id="AAFA4600.1"
/db_xref="GI:7271754"
/translation="MYSVETRIYKIRKNNKTEMILAIYDRNAVIVKKTGISILLRD
NCTRTMLNIIYDTSRNQWMLRVSVL"
7681..8184
/gene="FPV008"
7681..8184
/gene="FPV008"
/note="identical to FPV253 SW:P14370 (vaccinia A40R),
similar to Gallus gallus GB:AB015628"
/codon_start=1
/product="ORF FPV008 C-type lectin gene family protein"
/protein_id="AAFA4607.1"
/db_xref="GI:7271761"
/translation="MPLIKQVSEVSCAIVLGIILIFTLIVVWCKWYAFY
PSKVPDEMIGNSCYFTINETNWNDSKRLCDVMSDLIFEDTILNFSRIRGKG
SYWIDINQNRKIPGINSFSLYEQVNDICLLFDNISIIEMSCIFHERITCAVEDRYTH
WYETWR"
8048..8248
/gene="FPV009"
8048..8248
/gene="FPV009"
/note="identical to FPV252 Fowlpox GB:D00295"
/codon_start=1
/product="ORF FPV009 hypothetical protein"
/protein_id="AAFA4601.1"
/db_xref="GI:7271755"

gene
CDS
/translation="MNKALMIFVYIITRTVLSKCLVYFTKREYVLKAKIDTPIGIPNTC
VRFYSFLNLSIYLVNRSY"
/complement(9123..10190)
/gene="FPV010"
/complement(9123..10190)
/note="Fowlpox SW:P14369, similar to Homo sapiens
GB:AB006423"
/codon_start=1
/product="ORF FPV010 Serpin gene family protein"
/protein_id="AAFA4354.1"
/db_xref="GI:7271508"
/translation="MGSILRLKELVPEKDCISPRGYTTLIMINIMIGCKRETBDKI
KULGIFGWTVPPIPKSEYVEYDQDELINLSIMLIEGPIKRDFTNSYDIFNA
KVVSFTDDTISETINKWELSTGLIKDLSLADIRLAIINVLVYFKSKWKYFPDTE
LTSKHPFKYNGCTDVADIMQIDVAFYKHBDIIRSQVMALEDEYRKYMTIIPDS
VINGIDVDSLNNGKNINIKITSKDDTKEIYLPKPELEDVDLKDILHMGCDL
FKSGELVGISDPTKRLRIGNIRKRSVKVDEYGTAAVSVESTTGGIKKIPYKANVP
EMFLVADVOTKIPLELGRQG"
/complement(10276..11112)
/gene="FPV011"
/complement(10276..11112)
/note="FPV011"
/note="similar to Bos taurus PIR:S32367"
/codon_start=1
/product="ORF FPV011 alpha-SMAP"
/protein_id="AAFA4355.1"
/db_xref="GI:7271509"
/translation="MOKIKRVSPFKNLFGPIETEEAGVSHANLFAVSQIEMEC
AGKAFKSGDMLNKKNSIAAASSVDANAPFKIDSYEAINCLISIAEVTGIGF
YTVARCHNIAIAYENDITLEDKAFEHYNASGYGGEYSNLTSDCMILATISQK
EDFDRAKLTEDOVGNRNTMTLSKTESRQLYALMCTICSDVSRAKSLDKIKDIFP
AKDRKECKFIEKILAACETKNIETFTSAIEBYDHGNTIDEALMSMLTIRATFDE
VA"
/complement(12038..13033)
/gene="FPV012"
/complement(12038..13033)
/note="FPV012"
/note="similar to Homo sapiens SW:001485"
/codon_start=1
/product="ORF FPV012 Ankyrin repeat gene family protein"
/protein_id="AAFA4356.1"
/db_xref="GI:7271510"
/translation="MDTEADGVNNDGYTSLYKETAKNKKVVELLYKCVNPTNRVD
STYPLHIAKTGNIKIRRLIRYGANVDEKNDGYTALLIATCTDITKCNVLDEGA
NPNVNYKGIPLVPLIISYRPTILKLMDRGANCNOIINIQVYITIMEYINLDE
YKIPILINLVPYIIISFKASITVIEGEMRNIAAIAKNSRLLEVALKCSEIAFMTR
GIGDSLEFICILEDIDIDHNSFPAFLDKLIESQSNLRITYGTNNKTIEMERYREL
ICSAVRVNSCNLSINTWCILPLKGNILISKLNNNDIKKLINDAIKVNKKG"
/complement(13708..13890)
/gene="FPV013"
/complement(13708..13890)
Query Match 0.1%; Score 22; DB 1; Length 286539;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 47634 GTACGAGAAATAAAAAATACGA 47655
Db 41456 GTACGAGAAATAAAAAATACGA 41477
RESULT 17
LOCUS HSBHOHU 1242 bp DNA linear VRL 25-JAN-1995
DEFINITION Bovine herpesvirus 1 (clone p95) UL24 homologue gene, complete cds.
ACCESSION L39072
VERSION L39072.1 GI:633954
KEYWORDS
SOURCE Bovine herpesvirus 1
ORGANISM Bovine herpesvirus 1
Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.

REFERENCE 1 (bases 1 to 1242)
AUTHORS Whitbeck,J.C., Lawrence,W.C. and Bello,L.J.
TITLE Characterization of the bovine herpesvirus 1 homolog of the herpes simplex virus 1 UL24 open reading frame
JOURNAL virology 200 (1), 263-270 (1994)
MEDLINE 94174724
PUBMED 8128626
COMMENT Original
FEATURES
source location/Qualifiers
1..1242
/organism="Bovine herpesvirus 1"
/mol_type="genomic DNA"
/strain="Colorado-1"
/db_xref="taxon:10320"
/clone="p95"
92..95
/note="putative"
117..>1149
117..267
/note="putative"
268..1149
/note="ORF initiated by the first ATG codon downstream of the experimentally determined 5' end of a 5.2-kb mRNA transcript synthesized in BHK-1 infected cells.; homologue of HSV1 UL24; putative"
/codon_start=1
/protein_id="AA61544.1"
/db_xref="GI:633955"
/translation="MARDDRARLRAGTGRHFEALACDARAAGAKLPRLAQ LKRFAPPEYKOVGVSVSEFVNLOSRRDCCLRVAFAGARAVCLVELKTCF STVMNTPSKMDQRLGRLQRLDSARLVRLAPPPVLAFLVFSOSGMVLRVT RLPAQRTASNAARLEAIIAGLAEYAFARARRRAGSPRGKRAEQPRRRQCP LPLATGKRAAATAATPRPADGPPAEAGESGSRPVGSGRHAGNSAGCAKDGGAACIG EISALFPAVAGSPRSGV"
BASE COUNT 170 a 430 c 457 g 185 t
ORIGIN
Query Match 0.1%; Score 21; DB 1; Length 1242;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42218 GTGACGGCCTGCCGCCAG 42238
|||||
Db 742 GTGACGGCCTGCCGCCAG 762
RESULT 18
LOCUS ZYU60962 1902 bp DNA linear VRL 13-JUL-1996
DEFINITION Zucchini yellow mosaic polyprotein gene, cytoplasmic inclusion protein region, partial cds.
ACCESSION U60962.1 GI:1418245
VERSION
KEYWORDS
SOURCE Zucchini yellow mosaic virus
ORGANISM Zucchini yellow mosaic virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage: Potyviridae: Potyvirus.
1 (bases 1 to 1902)
Lee,K.C., Wong,S.M., Mahan,I.P.H. and Chng,C.G.
Direct Submission
Submitted (16-JUN-1996) School of Biological Sciences, National University of Singapore, Lower Kent Ridge Road, Singapore 119260, Singapore
FEATURES
source location/Qualifiers
1..1902
/organism="Zucchini yellow mosaic virus"
/mol_type="genomic DNA"
/strain="Singapore isolate"
/db_xref="taxon:12232"
<1..>1902
/note="cytoplasmic inclusion protein region: nucleotide binding motif, helicase function"

/codon_start=1
/product="polyprotein"
/protein_id="AB03777.1"
/db_xref="GI:1418246"
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ORIGIN
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 51263 AGGCAAGTTCCTCGAATTCAC 51283
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Db 165 AGGCAAGTTCCTCGAATTCAC 185
RESULT 19
LOCUS AF014811 9606 bp RNA linear VRL 04-MAY-2001
DEFINITION Zucchini yellow mosaic polyprotein gene, complete cds.
ACCESSION AF014811
VERSION AF014811.2 GI:13940781
KEYWORDS
SOURCE Zucchini yellow mosaic virus
ORGANISM Zucchini yellow mosaic virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage: Potyviridae: Potyvirus.
1 (bases 1 to 9606)
Lee,K.C. and Wong,S.M.
Direct Submission
Submitted (17-JUL-1997) School of Biological Sciences, National University of Singapore, Lower Kent Ridge Road, Singapore 119260, Singapore
2 (bases 1 to 9606)
Lee,K.C. and Wong,S.M.
Direct Submission
Submitted (04-MAY-2001) School of Biological Sciences, National University of Singapore, Lower Kent Ridge Road, Singapore 119260, Singapore
REMARK
COMMENT Sequence update by submitter
On May 4, 2001 this sequence version replaced gi:2462848.
FEATURES
source location/Qualifiers
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Db	
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LOCUS	
DEFINITION	Human herpesvirus 3 ORF49, ORF50, ORF51, ORF52, ORF54, ORF55, ORF56, ORF57, ORF58, ORF59, ORF60, ORF61, ORF62, ORF63, ORF64, ORF65, ORF66, ORF67, and ORF68 genes, complete cds.
ACCESSION	AF206304
VERSION	AF206304.1 GI:7385021
KEYWORDS	.
SOURCE	Human herpesvirus 3
ORGANISM	Human herpesvirus 3 Viruses; dsDNA viruses, no RNA stage: Herpesviridae; Alphaherpesvirinae: Varicellovirus. 1 (bases 1 to 34718) Argaw,T., Cohen,J.I., Klutuch,M., Lekstrom,K., Yoshikawa,T., Asano,Y. and Krause,P.R. Nucleotide sequences that distinguish Oka vaccine from parental Oka and other varicella-zoster virus isolates Unpublished 2 (bases 1 to 34718) Argaw,T., Cohen,J.I., Klutuch,M., Lekstrom,K., Yoshikawa,T., Asano,Y. and Krause,P.R. Direct Submission Submitted (17-NOV-1999) Division of Viral Products, FDA/CBER, 29A/IC16, HNM-457, 29 Lincoln Drive, Bethesda, MD 20892, USA Location/Qualifiers 1. .34718 /organism="Human herpesvirus 3" /mol_type="genomic DNA" /db_xref="taxon:10335" .1258. .1503 /codon_start=1 /product="ORF49" /protein_id="AAFG1650.1" /db_xref="GI:7385022" /translation="MGQSSSGRGIGLCRKRYNELTYCNGETVALNSEFFEDFPDE NVTEADKSTQRPRVIDVPKKRPSSKSHSKCAC" complement(1597..2904) /codon_start=1 /product="ORF50" /protein_id="AAF61651.1" /db_xref="GI:7385023" /translation="MGTOKKGRPSSEKSPYDTTPPEVEALDHQDPLNWRILIQVMMA FTGLAWMLATLFAASESYGIPCFYAAYVDLEFNATLDGVSGRRGGYSAPLVFL EHSVAATPYTTALTAMAAVVLITLAIIHRETKNRVRSSGVAAVYDPDLFWG LSLMLNNAVLLAKQIGVAAVTLYIGHATSVYFTTTYCGCRKKDELFINIKAVANLR QQSVEFYRLAGPTRAVAVVNLMALMACILLVSIMLETLVANHLHTGLMSVASWST FSYLVAIVYLSELVIILAHYIHLIGSELTLVACATLGTAASHSYMDELXDPISVQSPR LIPTTGTTACLAVFSVMMLLIRMAVYVHHROKRSPFYGAVERPVRVGYIKRWK AHSNSRTNPSPGGYGVYENDSTYEFDREDDELLYERNSGWME" 2903. .5410 /codon_start=1 /product="ORF51"

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5515..7830

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complement(7877..8872)

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CDS

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complement(18216..19619)

CDS

Query Match
Best Local Similarity 100.0%; Pred. No. 1; 5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0.1%; Score 21; DB 1; Length 34718;
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61676 CATAGTATGCGTGGTGGCC 61696
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RESULT 21
BHT1UL/c 37000 bp DNA linear VRL 14-AUG-1996
LOCUS Bovine herpesvirus type 1 UL22-35 genes.
DEFINITION 278205
ACCESSION 278205
VERSION 1
KEYWORDS GI:1491620
capsid protein; DNA binding protein; DNA polymerase; envelope
protein; glycoprotein B; glycoprotein H; proteinase; scaffold
protein; tegument protein; thymidine kinase; UL22; UL23; UL24;
UL25; UL26; UL27; UL28; UL29; UL30; UL31; UL32; UL33; UL34;
UL35; UL36.

SOURCE
ORGANISM Bovine herpesvirus 1
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicelloviruses.
1 (bases 24211 to 27636)
Whitbeck,J.C., Bello,L.J., and Lawrence,W.C.
Comparison of the bovine herpesvirus 1 g1 gene and the herpes
simplex virus type 1 gB gene
J. Virol. 62 (9), 3319-3327 (1988)
88300884
2841484

REFERENCE
AUTHORS 2 (bases 24215 to 27793)
Mitra,V., Nelson,R., and Smith,M.
Sequence of a bovine herpesvirus type-1 glycoprotein gene that is
homologous to the herpes simplex gene for the glycoprotein g8
Virology 166 (2), 542-549 (1988)
89020821
2845660

JOURNAL
MEDLINE 3 (bases 33521 to 36452)
PUBMED Meyer,A.L., Petrovskis,E.A., Dufus,W.P., Thomsen,D.R. and
Post,L.E.
Cloning and sequence of an infectious bovine rhinotracheitis virus
(BH-1) gene homologous to glycoprotein H of herpes simplex virus
Biochim. Biophys. Acta 1090 (2), 267-269 (1991)
92031707
1657187

REFERENCE
AUTHORS 4 (bases 32460 to 33539)
Bello,L.J., Whitbeck,J.C., and Lawrence,W.C.
Sequence and transcript analysis of the bovine herpesvirus 1
thymidine kinase locus
Virology 189 (2), 407-414 (1992)
92351539
1322582

JOURNAL
MEDLINE 5 (bases 31487 to 32728)
PUBMED Whitbeck,J.C., Lawrence,W.C., and Bello,L.J.
Characterization of the bovine herpesvirus 1 homolog of the herpes
simplex virus 1 UL24 open reading frame
Virology 200 (1), 263-270 (1994)
94174724
8128626

JOURNAL
MEDLINE 6 (bases 36100 to 37000)
PUBMED Vleck,C., Benes,V., Lu,Z., Kutish,G.F., Paces,V., Rock,D.,
Leitchworth,G.J., and Schwyzer,M.
Nucleotide sequence analysis of a 30-kb region of the bovine
herpesvirus 1 genome which exhibits a colinear gene arrangement
with the UL21 to UL4 genes of herpes simplex virus
Virology 210 (1), 100-108 (1995)
95313343
7793062

REFERENCE
AUTHORS 7 (bases 27788 to 29695)
TITLE Haanes,E.J., Thomsen,D.R., Homa,F.L. and Lowery,D.E.
The bovine herpesvirus 1 maturational proteinase and scaffold
proteins can substitute for the homologous herpes simplex virus
type 1 proteins in the formation of hybrid type B capsids
J. Virol. 69 (11), 7375-7379 (1995)
96013856
7474173

JOURNAL
MEDLINE 8 (bases 1 to 644)
PUBMED Schwyzer,M., Styger,D., Vogt,B., Lowery,D.E., Simard,C.,
LABOISIÈRE,S., Mitra,V., Vleck,C., and Paces,V.
Gene contents in a 31-kb segment at the left genome end of bovine
herpesvirus-1
Vel. Microbiol. (1996) In press
9 (bases 1 to 37000)
Schwyzer,M., Vleck,C., Lowery,D.E., Bello,L.J., Meyer,G., Mitra,V.,
Thiry,E. and Paces,V.
Gene contents in a 37-kb segment centered in the UL part of the
bovine herpesvirus 1 genome
Unpublished
10 (bases 1 to 37000)
Schwyzer,M.
Direct Submission
Submitted (13-AUG-1996) Martin Schwyzer, Institute of Virology,
Faculty of Veterinary, Medicine, University of Zurich,
Winterthurerstr. 266a, Zurich, CH-8057, Switzerland
Location/Qualifiers
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DB 31987 GTGACCGCCGCGCCAG 31967

RESULT 22

LOCUS HSGEND 112930 bp DNA linear VRL 25-OCT-2002
 DEFINITION Salmirine herpesvirus 2 complete genome.
 ACCESSION X64346
 VERSION X64346.1 GI:60320
 KEYWORDS alkaline exonuclease; complement control protein homologue;
 complete genome; cyclin homologue; DHFR gene; dihydrofolate
 reductase; DNA polymerase; dUMPase; G protein-coupled receptor
 homologue; glycoprotein; glycoprotein B; glycoprotein H; helicase;
 HVS R transactivator; IE-G gene; integral membrane protein; major
 capsid protein; major ssDNA-binding protein; mCOP gene;
 ribonucleotide reductase, large subunit; ribonucleotide reductase,
 small subunit; salmirl transformation-associated protein; scCPH
 gene; STP-A11 gene; thymidine kinase; thymidylate synthase; TK
 gene; transport protein; tyrosine-specific protein kinase; uracil
 DNA glucosidase.
 Salmirine herpesvirus 2
 Salmirine herpesvirus 2
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae; Rhadinovirus.
 1 (bases 1 to 112930)
 Albrecht, J.C., Nicholas, J., Bille, D., Cameron, K.R., Biesinger, B.,
 Newman, C., Wiltman, S., Craxton, M.A., Coleman, H., Fleckenstein, B.
 and Honess, R.W.
 Primary structure of the herpesvirus salmirl genome
 J. Virol. 66 (8), 5047-5058 (1992)
 92333688
 1321287
 2 (bases 1 to 112930)
 Albrecht, J.
 Direct Submission
 Submitted (31-JAN-1992) J. Albrecht, Inst. fuer Klinische und
 Molekulare Virologie, Friedrich-Alexander Uni, Loeschgstrasse 7,
 D-8520 Erlangen, FRG

FEATURES

source location/Qualifiers
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ORGANISM	Cercopithecine herpesvirus 7 viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
REFERENCE	1 (bases 1 to 124138)
AUTHORS	Gray,W.L., Starves,H.B., White,M.W. and Mahalingam,R.
TITLE	The DNA sequence of the simian varicella virus genome
JOURNAL	Virology 284 (1), 123-130 (2001)
MEDLINE	21251382
PUBMED	11352673
REFERENCE	2 (bases 1 to 124138)
AUTHORS	Gray,W.L., Starves,H.B., White,M.W., Ashburn,C.V. and Mahalingam,R.
TITLE	Complete Sequence of the Simian Varicella Virus Genome
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 124138)
AUTHORS	Gray,W.L., Starves,H.B., White,M.W., Ashburn,C.V. and Mahalingam,R.
TITLE	Direct Submission
JOURNAL	Submitted (07-JUN-2000) Microbiology/Immunology, University of Arkansas for Medical Sciences, 4301 W. Markham St., Little Rock, AR 72205, USA
REFERENCE	4 (bases 1 to 124138)
AUTHORS	Gray,W.L., Starves,H.B., White,M.W., Ashburn,C.V. and Mahalingam,R.
TITLE	Direct Submission
JOURNAL	Submitted (02-MAR-2001) Microbiology/Immunology, University of Arkansas for Medical Sciences, 4301 W. Markham St., Little Rock, AR 72205, USA
REMARK	Sequence update by submitter
COMMENT	On Mar 2, 2001 this sequence version replaced gi:11036551.
FEATURES	Location/Qualifiers
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Db

RESULT 25
HEVZYXX
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DEFINITION
ACCESSION
VERSION
KEYWORDS
X04370.1 GI:59989
capsid protein; deoxyypyrimidine kinase; DNA polymerase; DNA-binding
protein; durfase; exonuclease; genome; glycoprotein; kinase;
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unidentified reading frame.
SOURCE
ORGANISM
Human herpesvirus 3
Human herpesvirus 3
Viruses; dsDNA viruses, no RNA stage: Herpesviridae;
Alphaherpesvirinae; Varicellovirus.

REFERENCE 1 (bases 1 to 124884)
AUTHORS Davison,A.J. and Scott,J.E.
TITLE The complete DNA sequence of varicella-zoster virus
J. Gen. Virol. 67 (Pt 9), 1759-1816 (1986)
JOURNAL MEDLINE 86306657
PUBMED 3018124
COMMENT Data kindly reviewed (07-SEP-1987) by Davison A.J.
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LYVRATTOEGSMASGCGFPGIKONTSPMELMLYCHELXRPESYKMSRIARALRE
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/db_xref="SWISS-PROT:P09270"
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complement(9477..10667)
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LOCUS      AB097932
DEFINITION      Human herpesvirus 3 ORF62 gene for IE62 transactivator, complete
cvs, strain: The Oka vaccine.
ACCESSION      AB097932
VERSION
KEYWORDS
SOURCE
ORGANISM
HUMAN herpesvirus 3
Human herpesvirus 3
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicelloviruses.
REFERENCE
1 Gomi,Y., Sunamachi,H., Mori,Y., Nagaike,K., Takahashi,M. and
Yamanishi,K.
TITLE
Comparison of the complete DNA sequences of the Oka varicella
vaccine and its parental virus
J. Virol. 76 (22), 11447-11459 (2002)
JOURNAL
MEDLINE
23276345
PUBMED
12388706
REFERENCE
2 (bases 1 to 125078)
Gomi,Y., Sunamachi,H., Nagaike,K., Mori,Y., Takahashi,M. and
Yamanishi,K.

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TITLE      Yamanishi,K.
JOURNAL    Direct Submission
            Submitted (11-DEC-2002) Yasuyuki Gomi, Kanonji Institute, the
            research foundation for microbial diseases of Osaka university,
            research division; 2-9-41 Yahata-cho, Kanonji-city, Kagawa
            768-0062, Japan (E-mail:ygomi@email.biken.or.jp,
            Tel:81-875-25-4171(ex.620), Fax:81-875-25-4843)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61676 CATAGTATGCGTGGCTGCC 61696
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Db 96706 CATAGTATGCGTGGCTGCC 96726

RESULT 27
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LOCUS      AB097932
DEFINITION      Human herpesvirus 3 ORF62 gene for IE62 transactivator, complete
cvs, strain: The Oka parental.
ACCESSION      AB097932
VERSION
KEYWORDS
SOURCE
ORGANISM
HUMAN herpesvirus 3
Human herpesvirus 3
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicelloviruses.
REFERENCE
1 Gomi,Y., Sunamachi,H., Mori,Y., Nagaike,K., Takahashi,M. and
Yamanishi,K.
TITLE
Comparison of the complete DNA sequences of the Oka varicella

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vacine and its parental virus
 JOURNAL J. Virol. 76 (22), 11447-11459 (2002)
 MEDLINE 22276345
 PUBMED 12388706
 REFERENCE 2 (bases 1 to 125125)
 AUTHORS Gomi, Y., Sunamachi, H., Nagaike, K., Mori, Y., Takahashi, M. and Yamashita, K.
 TITLE Direct Submission
 JOURNAL Submitted (11-DEC-2002) Yasuyuki Gomi, Kanonji Institute, the research foundation for microbial diseases of Osaka university, research division; 2-9-41 Yahata-cho, Kanonji-city, Kagawa 768-0062, Japan (E-mail: ygom@email.biken.or.jp, Tel: 81-875-25-4171 (ex 620), Fax: 81-875-25-4843)
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 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 61676 CATAGTATGCTGCGTTCGCC 61696
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 Db 96682 CATAGTATGCTGCGTTCGCC 96702
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 LOCUS Bovine herpesvirus type 1.1 complete genome.
 DEFINITION AJ004801
 ACCESSION AJ004801.1 GI:2653291
 VERSION complete genome.
 KEYWORDS complete genome.
 SOURCE Bovine herpesvirus type 1.1
 ORGANISM Bovine herpesvirus type 1.1
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

REFERENCE
 AUTHORS Wirth, U.V., Fraefel, C., Vogt, B., Vlcek, C., Paces, V. and Schwyzer, M.
 TITLE Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1 are 3' coterminal and encode a putative zinc finger transactivator protein
 JOURNAL J. Virol. 66 (5), 2763-2772 (1992)
 MEDLINE 92219360
 PUBMED 1313901
 REFERENCE 2 (bases 103034 to 111027; 127191 to 135300)
 AUTHORS Schwyzer, M., Vlcek, C., Menekse, O., Fraefel, C. and Paces, V.
 TITLE Promoter, spliced leader, and coding sequence for BICP4, the largest of the immediate-early proteins of bovine herpesvirus 1
 JOURNAL Virology 197 (1), 349-357 (1993)
 MEDLINE 94025583
 PUBMED 8212570
 REFERENCE 3 (bases 111028 to 114234; 123984 to 127190)
 AUTHORS Schwyzer, M., Wirth, U.V., Vogt, B. and Fraefel, C.
 TITLE BICP22 of bovine herpesvirus 1 is encoded by a spliced 1.7 kb RNA which exhibits immediate early and late transcription kinetics
 JOURNAL J. Gen. Virol. 75 (Pt 7), 1703-1711 (1994)
 MEDLINE 94292919
 PUBMED 8021599
 REFERENCE 4 (bases 66900 to 96900)
 AUTHORS Vlcek, C., Benes, V., Lu, Z., Kutish, G.F., Paces, V., Rock, D., Letchworth, G.J. and Schwyzer, M.
 TITLE Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus 1 genome which exhibits a colinear gene arrangement with the UL21 to UL4 genes of herpes simplex virus
 JOURNAL Virology 210 (1), 100-108 (1995)
 MEDLINE 95313343
 PUBMED 7793062
 REFERENCE 5 (bases 1 to 31444)
 AUTHORS Schwyzer, M., Slyger, D., Vogt, B., Lowery, D.E., Simard, C., Labolastiere, S., Mistra, V., Vlcek, C. and Paces, V.
 TITLE Gene contents in a 31-kb segment at the left genome end of bovine herpesvirus-1
 JOURNAL Vet. Microbiol. 53 (1-2), 67-77 (1996)
 MEDLINE 97164286
 PUBMED 9010999
 REFERENCE 6 (bases 1 to 135301)
 AUTHORS Schwyzer, M., Paces, V., Letchworth, G.J., Mistra, V., Buhk, H.J., Lowery, D.E., Simard, C., Bello, L.J., Thiry, E. and Vlcek, C.
 TITLE Complete DNA sequence of bovine herpesvirus 1
 JOURNAL Unpublished
 REFERENCE 7 (bases 30801 to 67800)
 AUTHORS Schwyzer, M., Vlcek, C., Lowery, D.E., Bello, L.J., Meyer, G. and Mistra, V.
 TITLE Gene contents in a 37-kb segment centered in the UL part of the bovine herpesvirus 1 genome: the last gap
 JOURNAL Unpublished
 REFERENCE 8 (bases 96901 to 99695)
 AUTHORS Letchworth, G.J. and Kutish, G.F.
 TITLE DNA sequence of the BHV-1 UL1 to UL3.5 genes
 JOURNAL Unpublished
 REFERENCE 9 (bases 114235 to 122983)
 AUTHORS Goltz, M., Buhk, H.J., Broll, H., Lewin, M., Mankertz, A., Boerner, B., Borchers, K. and Weigelt, W.
 TITLE Nucleotide sequence of the HindIII O and K fragments located in the US region of the bovine herpesvirus 1 genome
 JOURNAL Unpublished
 REFERENCE 10 (bases 121402 to 123983)
 AUTHORS Schwyzer, M.
 TITLE Glycoprotein E and US9 genes of BHV1
 JOURNAL Unpublished
 REFERENCE 11 (bases 1 to 135301)
 AUTHORS Schwyzer, M.
 TITLE Direct Submission
 JOURNAL Submitted (08-SEP-1997) Institute of Virology, Faculty of Veterinary Medicine, University of Zurich, Winterthurerstrasse

266A, Zurich CH-8057, Switzerland
Location/Qualifiers
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466..1280
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VRKRLGADDEPMPAPPGGASGGGGAAGAPARARVRRPARRRRPARRPAPAE
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RLDLMRPVONGFPPAAGVSPMAVLDGADGAPVEGRVWETLMFGRDLYRMEVR
PAAQAARALRLDLVLRANLVDALASDECIYWKFTAKRLRTKDPDPAVAGAVL
ENLRKLAPFLRCYLRGLPSLELCAARLSLATPASYMFWMLARLSRAVSGAE
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complement(3040..4038)
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GSLRMELRSPAAVYVWGANNATLAADAPCRHAAVQHI PGLDGDDELHGRVAVG
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ALAAVGHGPTTKLARLMCELSARRALADFRDLPDPCARPPALPLAEGFARLG
ARIAAGSVGITHPCAAAYPLXIKIMAVVYALFAGLEISLYLRKRRRCCTGACG
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/db_xref="SPTREMBL:O65817"
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NMPRLACLGESBNDVALADARLVFYLGGPGGSAATPRLARLVILQOR
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PGEKTVLIRFYFQABRQADATYDQAVRDCLATYVAAPNPSGLAPPDVSTA
ALANCCRSGLAGAVAGAPVYAATIEDGLAVRCLRETIIDHRSKYADEEFA
LYVLAEGEFNRQITELRAVYITEPDEGALAPRLAGVSRLEKRAVAFERHVA
QFNVOASYEONVAAVVRLPPTAEVARTYRLLAATANGRTICDAAALRAA
LDHLEGOARNGVNLHAGPASAASVGPGLARVAGPAGSPATPACCVSKRA
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RDQYVYRNELFNRLAVNLVLDVDRFLKRLPRGRDGHMRSFRKALAAALAP
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QYSCEDVSDPAGARETGEAGSAGALATTCGCDKMGFRAVAVPAPVYIAGGP
TLKGIARLVQHAVLLEPPAFAMSGRYLRDEFAVYAAVYTHGSLRLPFFGKPDAAVW
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Query Match 0.18; Score 21; DB 1; Length 135301;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 42218 GTGACGGGCGCGGCCGAC 42238
DB 62787 GTGACGGGCGCTGCCGCCAC 62767

RESULT 29
AF049081/c 425 bp DNA linear VRL 02-AUG-1998
LOCUS
DEFINITION Simian foamy virus strain Sfydab, integrase gene, partial cds.
ACCESSION AF049081
VERSION AF049081.1 GI:3377494
KEYWORDS
SOURCE
ORANISM Simian foamy virus
Viruses; Retroid viruses; Retroviridae; Spumavirus.
REFERENCE
1 (bases 1 to 425)
Hemelen,W., Switzer,W.M., Sandstrom,P., Brown,J., Vedapuri,S.,
Schable,C.A., Kahn,A.S., Lerche,N.W., Schweizer,M.,
Neumann-Haefelin,D., Chapman,L.E. and Folks,T.M.
Identification of a human population infected with simian foamy
viruses
Nat. Med. 4 (4), 403-407 (1998)

MEDLINE 98206861
PUBMED 9546784
REFERENCE 2 (bases 1 to 425)
AUTHORS Switzer,W.M.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1998) HIV & Retrovirology Branch, CDC, 1600
Clifton Rd, Atlanta, GA 30333, USA
FEATURES
source
1. 425
/organism="Simian foamy virus"
/mol_type="genomic DNA"
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/cell_type="peripheral blood lymphocytes"
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LOAHNIATGRDSTFLKYTKYMPNLRDVKVIRCKOCVLTQAVLTAPILRPE
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BASE COUNT 132 a 82 c 82 g 129 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 65512 TGGTAGAGGATCAGCTTTA 65531
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Db 129 TGGTAGAGGATCAGCTTTA 110
RESULT 30
LOCUS AY131198 1772 bp mRNA linear VRL 14-SEP-2002
DEFINITION Human herpesvirus 8 ORF45 mRNA, complete cds.
ACCESSION AY131198
VERSION AY131198.1 GI:22857925
KEYWORDS
SOURCE Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
ORGANISM Human herpesvirus 8
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 1772)
AUTHORS Bachinsky,Y.H., Dovrat,S., Moore,P., Chang,Y. and Sarid,R.
TITLE Identification and expression of the Kaposi's sarcoma-associated
herpesvirus-encoded open reading frame 45 protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1772)
AUTHORS Bachinsky,Y.H., Dovrat,S., Moore,P., Chang,Y. and Sarid,R.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2002) Faculty of Life Sciences, Bar-Ilan
University, Ramat-Gan 52900, Israel
FEATURES
source
1. 1772
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ASMGVNSODDGEFSPAGLSPSDEGVALLEPMAATGTCAGYSPASRNSVGTOSPY
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DGEDEGVLSORIGIMDYGOKRROSTASSGSEYVRCOROPNL SRKAVASYIIISG
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PPLCGNGAIVMPWD"
BASE COUNT 411 a 516 c 489 g 356 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 1772;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64741 GTGAACCAATCCAGCCAG 64760
|||||
Db 192 GTGAACCAATCCAGCCAG 173
RESULT 31
HPV59VG
LOCUS HPV59VG 7896 bp DNA linear VRL 10-FEB-1999
DEFINITION Human papilloma virus type 59, complete viral genome.
ACCESSION X77858
VERSION X77858.1 GI:557236
KEYWORDS complete genome.
SOURCE Human papillomavirus type 59
ORGANISM Human papillomavirus type 59
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
REFERENCE 1
AUTHORS Rho,J., Roy-Burman,A., Kim,H., de Villiers,E.M., Matsukura,T. and
Choe,J.
TITLE Nucleotide sequence and phylogenetic classification of human
papillomavirus type 59
JOURNAL Virology 203 (1), 158-161 (1994)
MEDLINE 94303229
PUBMED 8030272
REFERENCE 2 (bases 1 to 7896)
AUTHORS Choe,J.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1994) J. Choe, C/O Hajo Delius, DKFZ - Abt. ATV,
Im Neuenheimer Feld 506, 69120 Heidelberg, FRG
FEATURES
source
1. 7896
/organism="Human papillomavirus type 59"
/mol_type="genomic DNA"
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872. 2806
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TFESDRITGSDMTAIFGVNPVAEFGKTLIQYVLAHIOCLDCAWGVILLRLK
GKNRITVAGSTLHLVPTCLIEPPLKSGVLAALYVYRTGMSNISEYIGEPKI
ORLTIOHGVDSDVPLSEMIOMAFPNLDIESDIAVEVALIADSNMAAFPEKSNQ
AKYLKCAWCMRHKRAQKROKMSOMIKRCKIEBGGMKPIVOPLRQYEFITE
LCAKDFLKGTPKRNCLVLCGPANTGSIKSLHFLGQTVISHVNSHFMLEPIT
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GLYKYEEQVYVYKFIHDAKKGTTDKRWHVNGVYIDCYDSMCSSTQSVSTAGS
EOLSYSPATPEATVYLGPTWNRQTKRPGCGYTOHQSISVSDYDNVRLH
PGNPRHRIPCSNTPLIHLKDKNGKICRLRYRLVHMLFENISSWMHTNGRSK
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/db_xref="GI:557242"
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/db_xref="SPTREMBL:081970"
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LQMTSLGIFLGLIGTSGTSGRTGICPLAGGRTNTVDSAPKPPVIVPVGPTDS
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FTDPSVIEVPTGIEISGNLISPTSGAHGEIPIMOTFETEGLEPISSSTINPA
RVAGPRLYSRANQOVRNADPLRSTFVYDNPAVDITLITFEDPSEVDPDM
DIVLRPALTSRSTYRFRSGORATMFRGOIGARVYFHDSIPRTHADIELO
PLVSSQATDDIYADIADTDEAPSTANTAFITPKSSFOSLSTRASSTFSNVYTP
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KRVYFETDGSMAF"
5606..7132
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CVPAIGHWKRGACKPTTVVQDCCPELEINPTEGDWVDGYGAMDKRLDKNKS
EVDLIDQOSICKYIPDYLOMSADVAGSMFCLEPREGVAFHFNRSCTMDOLPESLY
IKETDIDANSGSYLSPSGSVYTSQSLEFNNPYMLHKQGLNNGICMNOLEFLVY
DTRNRLSYCASTSSIPNVTYTSRKEVAVRVEEDLOFIDOLKITLTTEVMSYI
HNMTTLEDMNNGYMPPTASIVDTYRFPQSAANYCQKTPADPVPQDPYDKLFKFPV
DKERSADLDQEPFLGKFLDQGARPKFTIGPKRAAPAPSTPSPKRVKRRSSKK
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BASE COUNT 2473 a 1457 c 1594 g 2372 t
ORIGIN
Query Match 0.0% Score 20; DB 1; Length 7896;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 58559 CTGGTATTGAAATATT 58578
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Db 3677 CTGGTATTGAAATATT 3696
RESULT 32
AF074966
LOCUS
DEFINITION
AF074966
ACCESSION
AF074966
VERSION
AF074966.1 GI:5106411
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AUTHORS
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JOURNAL
MEDLINE
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REFERENCES
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FEATURES
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/note="isolated from a Tantalus monkey"
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802..2088
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APGSPOMOTIRLAVCOEDPTAKDLOLDLYLCSLSVASLHQOLDLSIEAETRGIT
GYNDIAGPLRVQANNPQOGILRRYQOOLLAARFALPGSAKDSMASTILOGLEPYHT
FVERNALDNGLPREGTPKPIRLASLAYSANNECQALLDARGHTNSPLGMDMLRACA
WTRPDKTIVLVQPKRPQPCRCCKAGHWSKDCQPPRPEHALCQDPTHMKRDC
PRUKPAISDPEDEALLDLDPIDIPKNSIGEV"
2253..2753
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/product="protease"
/protein_id="AAD39694.1"
/db_xref="GI:5106414"
/translation="MTVLPIALFSSNTPLKDTVLGAGGQODHFKLTSLPVLRLP
RTPIVLSCVDTENMNAITGRDALOCOCGLYLPKKGPPVLLPIQVPAVLGHEH
PPEPISQFPLNQNARSRCNTWSGRPMQALSNPTPGGELIYQSOLKPKMEGDSST
CGPLTL"
2990..6643
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/protein_id="AAD39693.1"
/db_xref="GI:5106413"

/translation="MQLAHILQPIQNAFSCQITLQYMDLILASPSHKDLISLVY
ASLISHGLPVSSENKQTPGTLKFGQIISPMLHYDAVPIPIRSNALPPLQGLG
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VQVPLGLVMTLTGTTTVEOSKOQWPLVLAHPHTSQCIPGQALASVLLDK
YTIQYGLCOTIHNIISTOTFDPQIOTSDHPSPILYHSHREKILCAQSELMNTE
LKTAPILAPVKALMPPLSPVITNAACLPISDGSSTRAATYLMKHLISQSPFLP
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PLPLLSKRVVYLHVRSHNTLPDPTRLNALTDLITPVQLSPALHSLHCGQA
ALLOGATTTASNLRSCHACRKNPNQOHMRGHIRGLPNIHMOGDITFEKKN
LYRLHVVDTEGSAISATOKKETSEASISLLOAIYLGKPNYINTNGPAYISODE
LDMCTPLAIRHTTHYVNPSTSGLEVERNGILKTLIYKYPDKPDLPMQNALSLMT
INHLNLTCHCKTMOVLHSPRIQIPETBSLNQTHYVYKLEGLMSROKQQA
LOENAGPALIVYIASSAQMIPMLKRAACPRVQAPPIPKKITTNGKRELTILIF
FOFCELLIGDYSFSCCTLTIGVSSYHSKPCNPQVCSWTLDLALASDAQALPCCPN
LVYSYSHATYSLYLFPMIRKPNNGGGYSASISDCSLKCPYLGQSWTCPTGA
ISSPYWFOQOVNFOEVSRLTINLHFSKGFPELIDAPGYDPIWFLNTEPSQLP
TAPPLPNSINDHILEPISPKSKLTPVOLITQNTYICIDIRASLSTHVIYYP
NVSYPSSPTPLVPSLALPAPHLTPNNMTHCGPQIOAIYSSPCHSLITLPPSLS
PVPLTSGSRRAVPAVYVLSALAMGAMAGGITSMSLASRSLHVEDDISLTO
ALVKNHKLITAOYNAONRGDLTFWEGGLCALOECCFLNTSHVSLDERP
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8274..9028
LTR
BASE COUNT 2087 a 3150 c 1703 g 2088 t
ORIGIN

Query Match 0.0% Score 20; DB 1; Length 9028;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 79649 GGGGCAACCACTGAGC 79668
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4355 GGGGCAACCACTGAGC 4374

RESULT 33
AF083424 108409 bp DNA linear VRL 07-JAN-2000
LOCUS Ateline herpesvirus 3 complete genome.
DEFINITION AF083424
ACCESSION AF083424
VERSION AF083424.1 GI:4019231
KEYWORDS
SOURCE
ORGANISM
Ateline herpesvirus 3
Ateline herpesvirus 3
Virus; dsDNA virus; no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
1 (bases 1 to 108409)
Albrecht, J.C.
TITLE Primary structure of the Herpesvirus ateles genome
JOURNAL J. Virol. 74 (2), 1033-1037 (2000)
MEDLINE 20091363

PUBMED 10623770
REFERENCE 2 (bases 1 to 108409)
AUTHORS Albrecht, J.-C. and Fleckenstein, B.
TITLE Direct Submission
JOURNAL Submitted (11-Aug-1998) Institut fuer klinische und molekulare
Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4,
Erlangen, Bayern 91054, Germany
Location/Qualifiers
1. 108409
/organism="Ateline herpesvirus 3"
/mol_type="genomic DNA"
/strain="73"
/db_xref="taxon:85618"
/complement(join(90..730,1339..1507))
/note="T10; similar to T1P and STP-C of herpesvirus
saimiri C-488"
/codon_start=1
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/product="tlo"
/protein_id="AAC95538.1"
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KNEDPPLLENGPSPKSPGPPGSGNSPPVLMVKNNGDRKQDVSGGNSAPNS
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RSPFNKRNKILVNDGEMNPICIPQDPEPRANLQKOSATSKNGPOITLREAT
EVESQADQGLNHRVERKRLVIGLIGIIVLLILFLMGLFLLMK"
complement(2144..2264)
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/complement(2752..2865)
/product="HAUR 2"
3224..6961
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VYVRHNASPLEPVGKFFRSYSPPTPTSPAEOLTSYSGQLSLQTTTSRELYDI
LKLSMFTPOGKKNADIIERTICTRTITICDINPTMHQHLKLCVPTGLKFE
ILPOKSLNLOAPENARALSTPISDPLNVEGVYVTEGGFTOPNGLVLMALMR
KNSRLGILVIDIYWTWMSSTNILEGLNVEGVYVTEGGFTOPNGLVLMALMR
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QVTSKLAPNSSTKTHNKEVLKQHFNLITSDLIATINININABEALKTACDAGCK
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QATSETEKLKLOVICTLREDOSLVSGHVDSDGLALVEMALISGGGGRVYVQGE
DTLOFLSETPGIVIEVSTKLXYVQVGLNRNVDLPKVCISPFLEAVSONSIDM
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VPHGLISAIAGFQPKLISIDHPQTSINSDIYVPAKFEIYAGSNMOEENIGALK
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ACCESSION AF319782
VERSION AF319782.2 GI:24762296
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
An Epstein-Barr-related herpesvirus from marmoset lymphomas
Proc. Natl. Acad. Sci. U.S.A. 98 (3), 1224-1229 (2001)
21107697
2 (bases 1 to 149696)
Rivallier, P., Cho, Y. G. and Wang, F.
Complete genomic sequence of an Epstein-Barr virus-related
herpesvirus naturally infecting a new world primate: a defining
point in the evolution of oncogenic lymphocryptoviruses

JOURNAL	J. Virol. 76 (23), 12055-12068 (2002)
MEDLINE	22302315
PUBMED	12414947
REFERENCE	3 (bases 1 to 105145)
AUTHORS	Wang, F.
TITLE	Direct Submission
JOURNAL	Submitted (12-Apr-2001) Medicine, Brigham & Women's Hospital, Boston, MA 02115, USA
REFERENCE	4 (bases 1 to 149696)
AUTHORS	Rivallier, P., Cho, Y. and Wang, F.
TITLE	Direct Submission
JOURNAL	Submitted (04-Jun-2002) Medicine, Brigham & Women's Hospital, Harvard Medical School, Channing Laboratory, 181 Longwood Avenue, Boston, MA 02115, USA
REMARK	Sequence update by submitter
COMMENT	On Nov 7, 2002 this sequence version replaced gi:13676640.
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CDS

gene
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Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION  Chimpanzee cytomegalovirus, complete genome.
ACCESSION  AF480884
VERSION    AF480884.1  GI:19881028
KEYWORDS
SOURCE     Chimpanzee cytomegalovirus
ORGANISM   Chimpanzee cytomegalovirus
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REFERENCE  1 (bases 1 to 241087)
           Davidson,A.J., Dolan,A., Akter,P., Addison,C., Dargan,D.J.,
           Alencor,D.J., McGoch,D.J. and Hayward,G.S.
           The human cytomegalovirus genome revisited: comparison with the
           chimpanzee cytomegalovirus genome
           J. Gen. Virol. 84 (Pt 1), 17-28 (2003)

TITLE     Chimpanzee cytomegalovirus genome
JOURNAL   J. Gen. Virol. 84 (Pt 1), 17-28 (2003)
MEDLINE   22421467
PUBMED    12533697
REFERENCE  2 (bases 1 to 241087)
AUTHORS   Davidson,A.J.
TITLE     Direct Submission
JOURNAL   Submitted (05-FEB-2002) MRC Virology Unit, Church Street, Glasgow
           G11 5JR, U.K.

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TTVGRKESENVLHVNSTFONCTRTVWNHPYITTHKKRKNKPHILCRASSGSYKH
NHHKLCLOCTPKNLFLDLVNHSGKIYAECDGQNHAAQGFILVYNAHITNYRVC
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KKRYRLRDVSESEVYRTEPEDH"
9123..10124
/note="R11 family"
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/protein_id="AA00653.1"
/db_xref="GI:19881033"
/translation="MVDHFAITLVLFLTLASGTVSSCHTSHSVSTTVATSSNP
VNTNSADSNSTSTESTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST
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HTARMTKVNTKETDLCLFEPDYISSTPQAGICFCQHWQSMITLYDTTENAGNYRV
HCDGNHHYDKGYRLQVTSNHTGTNRKCKPNDSTYPDHDNKNKETITENEFQMYD
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complement(10256..10432)
/note="contains hydrophobic domain"
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/product="UL2"
/protein_id="AA00654.1"
/db_xref="GI:19881034"
/translation="MRGDAVSLIYEDDLPSFGSPFNASHAYSPFVLGIFVTVV
WYLMWKLIDNPF"
10504..11097
/note="R11 family: contains hydrophobic domain"
/codon_start=1
/product="UL4"
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/db_xref="GI:19881035"
/translation="MRRRGWRGPPGATPFKYLIVLVSWSVYIGIHYGAIDHAYR
RVKSGDNVTLSPFYHLSGNFWYKRNATGTYPVCSVKTITFPVDVAVECKHHMI

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11469..11924
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/db_xref="GI:19881036"
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TSAAGSTGYNNLQORALNSPDPTTSTLPRQALAPPAHSSSGLFEEFYGLAIHA
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/db_xref="GI:19881037"
/translation="MPPRSFGCGGLNKYWCISCLLIVLVYCAPRGPSPHRSVRROT
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TTTSVPTPLILTTTRNTYVGVSPANVTLSSTMTTACNASVANGMEYROYOPLSLA
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13052..13693
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/protein_id="AA00658.1"
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/translation="MAADPTTSLMSGLCNKALMISCLLIVAFLLASSPTTMYVY
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13799..14305
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/db_xref="GI:19881039"
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14327..14860
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SNSWMSVHTVSSLYMCKERESNDAPENFNVDIOENCHEELLLELPTOYTAAYY
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14939..15657
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/db_xref="GI:19881041"
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HKSVAKTGHSFAH"
15758..16468
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RESULT 39
LOCUS MR008421/c 2359 bp RNA linear VRL 26-Apr-2001
DEFINITION Murine rotavirus EC outer capsid protein VP4 gene, complete cds.
ACCESSION U08421
VERSION U08421.1 GI:475678
KEYWORDS
SOURCE Murine rotavirus
ORGANISM Viruses; dsRNA viruses; Reoviridae; Rotavirus; unclassified rotaviruses.
REFERENCE 1 (bases 1 to 2359)
AUTHORS Dunn,S.J., Burns,J.W., Cross,T.L., Vo,P.T., Ward,R.L., Bremont,M. and Greenberg,H.B.
TITLE Comparison of VP4 and VP7 of five murine rotavirus strains
JOURNAL Virology 203 (2), 250-259 (1994)
MEDLINE 94330134
REFERENCE 2 (bases 1 to 2359)
PUBMED 8053149
AUTHORS Dunn,S.J.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1994) Stephen J. Dunn, Stanford University, Medicine/Gastroenterology, 3801 Miranda Avenue, Palo Alto, CA, 94304, USA
FEATURES
source location/Qualifiers
1..2359
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10..2337
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BASE COUNT 710 a 516 c 542 g 591 t
ORIGIN
Query Match 0.0%; Score 19; DB 1; Length 2359;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59664 ACCTATTGTGNAAGC 59682
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Db 595 ACCTATTGTGNAAGC 577
RESULT 40
LOCUS AF329888/c 2689 bp DNA circular VRL 15-MAR-2002
DEFINITION Maize streak virus strain MSV-E isolate MSV-Pat, complete genome.
ACCESSION AF329888
VERSION AF329888.1 GI:14794711
KEYWORDS

SOURCE Maize streak virus
ORGANISM Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
REFERENCE 1 (bases 1 to 2689)
AUTHORS Martin,D.P., Willemet,J.A., Billharz,R., Velders,R., Odhiambo,B., Njuguna,D., James,D. and Rybicki,E.P.
TITLE Sequence diversity and virulence in Zea mays of Maize streak virus isolates
JOURNAL Virology 288 (2), 247-255 (2001)
MEDLINE 21488909
PUBMED 11601896
REFERENCE 2 (bases 1 to 2689)
AUTHORS Martin,D.P., James,D. and Rybicki,E.P.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2000) Microbiology, University of Cape Town, Private Bag, Cape Town, WC 7000, South Africa
FEATURES
source location/Qualifiers
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/country="South Africa"
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/note="conserved nonanucleotide at origin of (+) strand replication"
19..2664
150..455
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150..455
/gene="V1"
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1203..1207
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complement(1217..2520)
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1274..1349
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/gene="C1/C2"
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PYDMATKLOQFYFYSANKLPDIQEEFISHPSPSDDLNESIKMLQPNITQPADBG
SKROSLYIVGPTVTKSTWARSIGLHNQNNVMDSSYNDAIYNIVDDIPFYCPCW
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/note="replication initiator/associated protein ORF4;
possibly involved in cell cycle regulation"
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2633..2661
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Query Match 0.0%; Score 19; DB 1; Length 2689;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69150 AGAAATCCGAATATCATC 69168
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Db 2446 AGAAATCCGAATATCATC 2428

RESULT 41
AF339477 4676 bp ss-RNA linear VRL 02-FEB-2003
LOCUS Babanki virus strain Dakary 251 nonstructural protein 4 gene,
DEFINITION partial cds; and structural polyprotein precursor, gene, complete
cgs.
ACCESSION AF339477
VERSION AF339477.1 GI:28193938
KEYWORDS
SOURCE Babanki virus
ORGANISM Babanki virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Togaviridae;
Alphavirus; WEEV complex.
REFERENCE 1 (bases 1 to 4676)
AUTHORS Kinney,R.M. and Pfeiffer,M.
TITLE Nucleotide sequence analyses of the 26S mRNAs of viruses of the
genus Alphavirus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4676)
AUTHORS Kinney,R.M. and Pfeiffer,M.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2001) Arbovirus Diseases Branch, Centers for
Disease Control and Prevention, P.O. Box 2087, Fort Collins, CO
80522, USA

FEATURES
source Location/Qualifiers
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/organism="Babanki virus"
/mol_type="genomic RNA"
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BASE COUNT
ORIGIN

Query Match 0.0%; Score 19; DB 1; Length 4676;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71673 CCAAGCACCACCGAGC 71691
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Db 844 CCAAGCACCACCGAGC 862

RESULT 42
AY056701/c 6745 bp RNA linear VRL 14-JAN-2002
LOCUS Human poliovirus 1 strain 3788ALB96 polyprotein gene, partial cds.
DEFINITION Human poliovirus 1 strain 3788ALB96 polyprotein gene, partial cds.
ACCESSION AY056701
VERSION AY056701.1 GI:18146568
KEYWORDS
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
VIRUSES: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 6745)
AUTHORS Marturano,J. and Fiore,L.
TITLE Investigation of the presence of recombinant polioviruses in the

hit population in Albania during the 1996 outbreak

JOURNAL
MEDLINE

J. Clin. Microbiol. 40 (1), 316-317 (2002)

21635047
11773144

REFERENCE

2 (bases 1 to 6745)
Marturano, J. and Fiore, L.

Direct Submission

JOURNAL

Submitted (23-SEP-2001) Laboratory of Virology, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome 00161, Italy

FEATURES

Location/Qualifiers

1..6745

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AMVGTGDEALDLTTSAGTYVALGKRRDLNLTOKRDKEMORLDTYGINLPTVY
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mat_peptide

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Best Local Similarity 100.0%; Score 19; DB 1; Length 6745;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB

5362 GGTGATCATGATGTGGCA 5344

RESULT 43

.AY056702/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

21635047

11773144

2 (bases 1 to 6745)

Marturano, J. and Fiore, L.

Direct Submission

Submitted (23-SEP-2001) Laboratory of Virology, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome 00161, Italy

Location/Qualifiers

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/mol_type="genomic RNA"

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 TITLE Investigation of the presence of recombinant polioviruses in the
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 JOURNAL J. Clin. Microbiol. 40 (1), 316-317 (2002)
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QY	85620	CAGCCCATTAAGTCTGGGGCGCAGAAAGGCCGGAAGATTAAGCTGTGATCTGCTGTGCGCG	85679
Db	85620	CAGCCCATTAAGTCTGGGGCGCAGAAAGGCCGGAAGATTAAGCTGTGATCTGCTGTGCGCG	85679
QY	85680	TCGAGTCCATCTTGATACCTTCCCGATACCGTCTCTCTTGATACATTTCGGAACGGATGCC	85739
Db	85680	TCGAGTCCATCTTGATACCTTCCCGATACCGTCTCTCTTGATACATTTCGGAACGGATGCC	85739
QY	85740	GAAAGGGCGTGAAGCAATTCCGCGCCCGAGAGATGGCAAAACCGCATATTGGCGCAACTCAAG	85799
Db	85740	GAAAGGGCGTGAAGCAATTCCGCGCCCGAGAGATGGCAAAACCGCATATTGGCGCAACTCAAG	85799
QY	85800	CGAGCGCCGCACACGCGCGGCACACACCGGACAAAGACATCTCTTCGGATTAACGCAACCTA	85859
Db	85800	CGAGCGCCGCACACGCGCGGCACACACCGGACAAAGACATCTCTTCGGATTAACGCAACCTA	85859
QY	85860	AAGACAGACCCCGTGAAGCAAAATTTGATCGGTAGGGAATTTCTTATCTTCTCTCAAAAGTAC	85919
Db	85860	AAGACAGACCCCGTGAAGCAAAATTTGATCGGTAGGGAATTTCTTATCTTCTCTCAAAAGTAC	85919
QY	85920	TTGCTCTTTCTTACGCGCTCCACAGCGCGCCCTGGCTTGACACAGCTGCTCTTCCA	85979
Db	85920	TTGCTCTTTCTTACGCGCTCCACAGCGCGCCCTGGCTTGACACAGCTGCTCTTCCA	85979
QY	85980	GACGGCAGTGGGATGTCTCTTAACCTACAACTAGGCACTCATAGTGTGACCGTGGGTGGA	86039
Db	85980	GACGGCAGTGGGATGTCTCTTAACCTACAACTAGGCACTCATAGTGTGACCGTGGGTGGA	86039
QY	86040	TAAATCATTAATTTGGGAAACGACGGGGTGTAGCTGCCAACACGACCTGCTCTTTTGGCTCG	86099
Db	86040	TAAATCATTAATTTGGGAAACGACGGGGTGTAGCTGCCAACACGACCTGCTCTTTTGGCTCG	86099
QY	86100	TCTGCCCCAAAACAGGCCCGGGTACAGACGACTATCGGCTTTGAACTCAGCCATTTCTTGG	86159
Db	86100	TCTGCCCCAAAACAGGCCCGGGTACAGACGACTATCGGCTTTGAACTCAGCCATTTCTTGG	86159
QY	86160	AGGGCCATGCCATTAAGAGATGGGCCCTTCTGATTTCCCAAGCGGCATCTGATTCAGTTCG	86219
Db	86160	AGGGCCATGCCATTAAGAGATGGGCCCTTCTGATTTCCCAAGCGGCATCTGATTCAGTTCG	86219
QY	86220	GCAACGTTTAAACCCATGTAAGTTTCAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	86279
Db	86220	GCAACGTTTAAACCCATGTAAGTTTCAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	86279
QY	86280	GCTGTGACAAACATTAAGAAAGTGGACACAGCTGTGGCTTTGGCGCTCTGTCATGTA	86339

Db	86280	GCTGTGAACAAACATAAAGAAAGGAGCGACAGGTGTGGCGTTTGGCGCTCTCTGTACAGTGA	86339
QY	86340	CCCCCGCGGTACATTTACTTCTCTCCATACGGTGCAGGGTATGATACAGATGTGCTTC	86399
Db	86340	CCCCGCGGTAACTTTACTTCTCTCCATACGGTGCAGGGTATGATACAGATGTGCTTC	86399
QY	86400	CGTTGTTCCGACACCGACACCGGCTCCAGACGGTCTCTCCCGCTGTCACTCC	86458
Db	86400	CGTTGTTCCGACACCGACACCGGCTCCAGACGGTCTCTCCCGCTGTCACTCC	86458
QY	86460	CGCGGCAACCGTGTCTGACATCATCTGCACATCATATTGTCACACGTACGAGATTTCAG	86519
Db	86460	CGCGGCAACCGTGTCTGACATCATCTGCACATCATATTGTCACACGTACGAGATTTCAG	86519
QY	86520	GGCAATGGGACATCCCATGTATTTTGGACTAGTATGACGGGCAATGAAATCCAGCC	86579
Db	86520	GGCAATGGGACATCCCATGTATTTTGGACTAGTATGACGGGCAATGAAATCCAGCC	86579
QY	86580	ACACTTCACGGGCGGGACATCTCCTGGATGTGGCATCTCGCAGCTCCTCAATTAAG	86639
Db	86580	ACACTTCACGGGCGGGACATCTCCTGGATGTGGCATCTCGCAGCTCCTCAATTAAG	86639
QY	86640	CAAGAGATCGAAGCCTCTGAGCGGCTGCGAAGCCGAGCTCATAGTAAATTTTCAGATA	86699
Db	86640	CAAGAGATCGAAGCCTCTGAGCGGCTGCGAAGCCGAGCTCATAGTAAATTTTCAGATA	86699
QY	86700	GTGTGTCATATGCCCTCATGTTGGGTTTCCAGTATTTTACACAGATTTCCAGACTCCGT	86759
Db	86700	GTGTGTCATATGCCCTCATGTTGGGTTTCCAGTATTTTACACAGATTTCCAGACTCCGT	86759
QY	86760	CATACACAGATCAAACTCTCTGCGATGTTTTCTCAGGGCCTCGAAATCTGCCCCGTGC	86819
Db	86760	CATACACAGATCAAACTCTCTGCGATGTTTTCTCAGGGCCTCGAAATCTGCCCCGTGC	86819
QY	86820	AAATTCGACGGGAATCACTGGGAGCGGCAAGGCAAGAAACGTAAATGATTTATCGGCACA	86879
Db	86820	AAATTCGACGGGAATCACTGGGAGCGGCAAGGCAAGAAACGTAAATGATTTATCGGCACA	86879
QY	86880	ACACAGGTGTCCGGGAGGTTTGGGATCAGGAAGGCCACATATACGCACACCGAGCGCG	86939
Db	86880	ACACAGGTGTCCGGGAGGTTTGGGATCAGGAAGGCCACATATACGCACACCGAGCGCG	86939
QY	86940	TCCGAAATTTGAACCTCCGACGTTCTCTCCAAGTAAAAAAGATTACTCAACAGCCCC	86999
Db	86940	TCCGAAATTTGAACCTCCGACGTTCTCTCCAAGTAAAAAAGATTACTCAACAGCCCC	86999
QY	87000	TAGCACAAGGTTGGCGCAAGAGTCTCGGAGTCTGTTGATATTCGTTTAAACGGAGAC	87059
Db	87000	TAGCACAAGGTTGGCGCAAGAGTCTCGGAGTCTGTTGATATTCGTTTAAACGGAGAC	87059
QY	87060	TCCTCAGTGGCGCCTTAGCCCTCGGCGCGGTGTCTCTCGAANAACCTCTCTCGAAGCGA	87119
Db	87060	TCCTCAGTGGCGCCTTAGCCCTCGGCGCGGTGTCTCTCGAANAACCTCTCTCGAAGCGA	87119
QY	87120	ACTGCCCATGGAACAGTATGACAACAGTATGTCGGGATGAGGTTACACAGATCGCAGCC	87179
Db	87120	ACTGCCCATGGAACAGTATGACAACAGTATGTCGGGATGAGGTTACACAGATCGCAGCC	87179
QY	87180	CACCGTAACCTCAGGAAGCAATTGAAGAAGTCTGTATCTTTTCCCGAGACGCCGCCGCG	87239
Db	87180	CACCGTAACCTCAGGAAGCAATTGAAGAAGTCTGTATCTTTTCCCGAGAGCCGCCCGCG	87239
QY	87240	CTTGTCTGGGGGTGTACGCTTCCCTCAATATCTGTGTAGATCTTACTGTCAATTAACATCT	87299
Db	87240	CTTGTCTGGGGGTGTACGCTTCCCTCAATATCTGTGTAGATCTTACTGTCAATTAACATCT	87299
QY	87300	AATTTTCTTAAATTTTCGGGCACTGTAAACCGGTTTATACACAGCCACGGCTGTAGACAAA	87359
Db	87300	AATTTTCTTAAATTTTCGGGCACTGTAAACCGGTTTATACACAGCCACGGCTGTAGACAAA	87359
QY	87360	ATGCTCAAAATATCTTGTATTAATCTTCATGACGCGCATGTCTGGTACACGGTTCCAGCG	87419

Db	87360	ATCGTCAAAATATCTGTTTAAATCTTCATCGACGCGACATGTCGAGTCCAGCGGTCACAGG	874119
QY	87420	GACACGATATAGTGTCTTGTCCCTGTCATCATCCATTCCTACTCCGGGGTATCGCTTAGACTC	874719
Db	87420	GACACGATATAGTGTCTTGTCCCTGTCATCATCCATTCCTACTCCGGGGTATCGCTTAGACTC	874719
QY	87480	CACGGCTCGATGAAACCAACTTTTAAATCATATGCGCGTCCGCGATCTCCGATTTCA	875319
Db	87480	CACGGCTCGATGAAACCAACTTTTAAATCATATGCGCGTCCGCGATCTCCGATTTCA	875319
QY	87540	ATACCTTGACCCGACGGGCTCACTTAAATATCCGAGCCCCAGAACCCAGGCTTCGGTA	875919
Db	87540	ATACCTTGACCCGACGGGCTCACTTAAATATCCGAGCCCCAGAACCCAGGCTTCGGTA	875919
QY	87600	ACAAAAGATCTATGATCTGAAGAAGCCCTAATATATGCGCCACGGGAAAAACTGTGA	876519
Db	87600	ACAAAAGATCTATGATCTGAAGAAGCCCTAATATATGCGCCACGGGAAAAACTGTGA	876519
QY	87660	ACAAATGAAAAAATGTTCTCAGAAAAACGAAGAGAGAAAACTGACGACGCAATCTAG	877119
Db	87660	ACAAATGAAAAAATGTTCTCAGAAAAACGAAGAGAGAAAACTGACGACGCAATCTAG	877119
QY	87720	TCAAACCAGAACCTTAAAGGCGGTCACTGACCCATATCTTTCCCTTCCCGACGAGTGG	877719
Db	87720	TCAAACCAGAACCTTAAAGGCGGTCACTGACCCATATCTTTCCCTTCCCGACGAGTGG	877719
QY	87780	GTTTCTCACAATGCCGTGAGCAAAACGAAGACCTACATATATAGACGCTGTGAGAGA	878319
Db	87780	GTTTCTCACAATGCCGTGAGCAAAACGAAGACCTACATATATAGACGCTGTGAGAGA	878319
QY	87840	AAACTTTATTTGCAAGGACACGAGCAAAAGCAGCTGTGACAGGTAATGTGTCACTG	878919
Db	87840	AAACTTTATTTGCAAGGACACGAGCAAAAGCAGCTGTGACAGGTAATGTGTCACTG	878919
QY	87900	GGCGGCATCCCGGACGCCGCCACAGACACTGTGCAAAATTTGAATGACAGGGGAT	879519
Db	87900	GGCGGCATCCCGGACGCCGCCACAGACACTGTGCAAAATTTGAATGACAGGGGAT	879519
QY	87960	TGTGGGACACGGCTCGGCTTCGGAAGTGGGAGCGCCTCTAGGTGGAGAGCAGATAGG	880119
Db	87960	TGTGGGACACGGCTCGGCTTCGGAAGTGGGAGCGCCTCTAGGTGGAGAGCAGATAGG	880119
QY	88020	GGCGGAAATCCGCTTCGGTGGCGGGGGTGTGACACGCACTAGATATTTGGGCGAG	880719
Db	88020	GGCGGAAATCCGCTTCGGTGGCGGGGGTGTGACACGCACTAGATATTTGGGCGAG	880719
QY	88080	CGAAACACGCGCAGAACTCGCGCTGTGTATATATCATCACCGGCTCCAGCGAACTTC	881319
Db	88080	CGAAACACGCGCAGAACTCGCGCTGTGTATATATCATCACCGGCTCCAGCGAACTTC	881319
QY	88140	GTTTACCAGACGAGGCTGGAACGTGACCATATACGAAATGTAAATCCAGACCCGTG	881919
Db	88140	GTTTACCAGACGAGGCTGGAACGTGACCATATACGAAATGTAAATCCAGACCCGTG	881919
QY	88200	TGCGTAATATCATCAACCCGGGTATGATCTCTCCCGACGCACTTAGATCTGTGTG	882519
Db	88200	TGCGTAATATCATCAACCCGGGTATGATCTCTCTCCCGACGCACTTAGATCTGTGTG	882519
QY	88260	GTCGAGGAACATATCTGTGGGTATGCGCAACAGGCGCTGTTCCGCGCAATGCCGCG	883119
Db	88260	GTCGAGGAACATATCTGTGGGTATGCGCAACAGGCGCTGTTCCGCGCAATGCCGCG	883119
QY	88320	ACAAAGCTGTCTTGAAGTGTGCTTTGGCGCGGCAACAGCGCCGTTGGGCGA	883719
Db	88320	ACAAAGCTGTCTTGAAGTGTGCTTTGGCGCGGCAACAGCGCCGTTGGGCGA	883719
QY	88380	CCGAGACTCATATTTCCCAACCAACCGCCCATAGTATTAACCAACAGCGCGTAGCATCA	884319
Db	88380	CCGAGACTCATATTTCCCAACCAACCGCCCATAGTATTAACCAACAGCGCGTAGCATCA	884319
QY	88440	ACACTGTCTCCCGTCCGCTCCACGGCGCCTTGTACTCATTCGCGGACCGAGATACCG	884919
Db	88440	ACACTGTCTCCCGTCCGCTCCACGGCGCCTTGTACTCATTCGCGGACCGAGATACCG	884919

Qy	88500	GAATCTGGCGTTACCTCGTTGGCTACGTCAGAGCATGCCGCGGTGGCATCCGCTTC	88559
Db	88500	GAATCTGGCGTTACCTCGTTGGCTACGTCAGAGCATGCCGCGGTGGCATCCGCTTC	88559
Qy	88560	GTTACAGAGCGGGCAGATGCTACAAAGATCGCAGACAGCGAATAACGGCGCACTGTT	88619
Db	88560	GTTACAGAGCGGGCAGATGCTACAAAGATCGCAGACAGCGAATAACGGCGCACTGTT	88619
Qy	88620	AGCGCGCGGGCGCAGAGTTCCCTCAGTGTGATACATCTTCGAGGCTGACATGTTGGC	88679
Db	88620	AGCGCGCGGGCGCAGAGTTCCCTCAGTGTGATACATCTTCGAGGCTGACATGTTGGC	88679
Qy	88680	TATAGCGCTGGCCAAACAGTTCTTACATTCCTGACGCTCAATCGTGTGTTACCGGTG	88739
Db	88680	TATAGCGCTGGCCAAACAGTTCTTACATTCCTGACGCTCAATCGTGTGTTACCGGTG	88739
Qy	88740	CCGTATGCTTTAAATTTGACAAATAGTCAGATACATGTTTCTCTCATGCTACAGACGC	88799
Db	88740	CCGTATGCTTTAAATTTGACAAATAGTCAGATACATGTTTCTCTCATGCTACAGACGC	88799
Qy	88800	ACCGCGCGCTTTAAATGATTTCCAAAGTAAACGAAACAGAGTCTTTCCATCCATCAGCA	88859
Db	88800	ACCGCGCGCTTTAAATGATTTCCAAAGTAAACGAAACAGAGTCTTTCCATCCATCAGCA	88859
Qy	88860	ATGATCTCAGATGCTTATCATTTATCGCAACATCGAGCAACCATGCCCTCAGGGCAGA	88919
Db	88860	ATGATCTCAGATGCTTATCATTTATCGCAACATCGAGCAACCATGCCCTCAGGGCAGA	88919
Qy	88920	CGCGCGGTTTACCGGATGCAACCTGCCGCTCTCCGCCATCTCTGAGGGTCCGCTGC	88979
Db	88920	CGCGCGGTTTACCGGATGCAACCTGCCGCTCTCCGCCATCTCTGAGGGTCCGCTGC	88979
Qy	88980	ATAAATGCGTTAAATCTATCCCCCGCGTGCAGCTGTACTTAAAGTACACACCTTCG	89039
Db	88980	ATAAATGCGTTAAATCTATCCCCCGCGTGCAGCTGTACTTAAAGTACACACCTTCG	89039
Qy	89040	GCGACAGCGCGTAGGGCTGGCAGGAGCGGACCGCAGCAGCATTTTTCATCTAGCCCG	89099
Db	89040	GCGACAGCGCGTAGGGCTGGCAGGAGCGGACCGCAGCAGCATTTTTCATCTAGCCCG	89099
Qy	89100	CTTACTAGCGGAAATCTGCGGCTCTACAAATCCACCGAGCGCGCGGAATGTACCATAG	89159
Db	89100	CTTACTAGCGGAAATCTGCGGCTCTACAAATCCACCGAGCGCGCGGAATGTACCATAG	89159
Qy	89160	TCAATTCATCTGACAGATCACCAAAAGTGACAGGAGCCTGGGCTTTTACTGAGGCCAG	89219
Db	89160	TCAATTCATCTGACAGATCACCAAAAGTGACAGGAGCCTGGGCTTTTACTGAGGCCAG	89219
Qy	89220	GCGGACCCCAAGGTAAAGAGTGAAGTGTGCTGGGAGACAGTGTCCCGGGAACGGGTG	89279
Db	89220	GCGGACCCCAAGGTAAAGAGTGAAGTGTGCTGGGAGACAGTGTCCCGGGAACGGGTG	89279
Qy	89280	ACCGGCGAGTGTGCGCAGTAGACCCATAACATAGAAATTTGAGATTTGACAGAGATC	89339
Db	89280	ACCGGCGAGTGTGCGCAGTAGACCCATAACATAGAAATTTGAGATTTGACAGAGATC	89339
Qy	89340	GCAACAGCGGTTGGCTGGTCCCTCTGCTGCTGCTCCCTGCGCAGCAACCGTGTGCC	89399
Db	89340	GCAACAGCGGTTGGCTGGTCCCTCTGCTGCTGCTCCCTGCGCAGCAACCGTGTGCC	89399
Qy	89400	TGGTTCTGTTATCCACATATACATCCCGCATTTGCCATGCAAAAACGCCCTCCTCAC	89459
Db	89400	TGGTTCTGTTATCCACATATACATCCCGCATTTGCCATGCAAAAACGCCCTCCTCAC	89459
Qy	89460	ACCGGTTTAAATCTCAGACAGGTTTCTCTGCTCCGCGGTAGCGGCCATCCAACT	89519
Db	89460	ACCGGTTTAAATCTCAGACAGGTTTCTCTGCTCCGCGGTAGCGGCCATCCAACT	89519
Qy	89520	GAGGTTTGAAGCAGATCTTATAGCTGTGCCATAGAAACCTGTGACCGCGGTTGG	89579
Db	89520	GAGGTTTGAAGCAGATCTTATAGCTGTGCCATAGAAACCTGTGACCGCGGTTGG	89579

Qy	89580	GCTCTTGGCGCTTATGCAATGTACCCCTCTACGGTCTTGAGAGTGTGTTCCGCTACA	89639
Db	89580	GCTCTTGGCGCTTATGCAATGTACCCCTCTACGGTCTTGAGAGTGTGTTCCGCTACA	89639
Qy	89640	GCGACCCAAAATATAAACTGATACGTAGCGCCAAAATGGAGTATCTGGTCTGGAT	89699
Db	89640	GCGACCCAAAATATAAACTGATACGTAGCGCCAAAATGGAGTATCTGGTCTGGAT	89699
Qy	89700	GCGGTGTGCAACCGTGTGCCAACCTGGCGGCGCTGGCATTTACAGACCGCGCACCGT	89759
Db	89700	GCGGTGTGCAACCGTGTGCCAACCTGGCGGCGCTGGCATTTACAGACCGCGCACCGT	89759
Qy	89760	CAGCCTCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	89819
Db	89760	CAGCCTCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	89819
Qy	89820	CCGCTCTAAGTATTTAGGACGGTCTCCGAATACATATCTAAGATGACAGCATACACA	89879
Db	89820	CCGCTCTAAGTATTTAGGACGGTCTCCGAATACATATCTAAGATGACAGCATACACA	89879
Qy	89880	GCGGATCAGCGGCGGCTCTCAAGTAAATAATCTTTCGCGCAAAACGCGTGTGTTG	89939
Db	89880	GCGGATCAGCGGCGGCTCTCAAGTAAATAATCTTTCGCGCAAAACGCGTGTGTTG	89939
Qy	89940	CCCGGCGATGCTCTGTTCAAACCCAGCGTTTCCGAGACACCCCTTAGCAGTCTTTC	89999
Db	89940	CCCGGCGATGCTCTGTTCAAACCCAGCGTTTCCGAGACACCCCTTAGCAGTCTTTC	89999
Qy	90000	GCGCTCCGACAGTGTGCTGGCGTCCACATTTCAATTCCTATCCAGGACATACGCA	90059
Db	90000	GCGCTCCGACAGTGTGCTGGCGTCCACATTTCAATTCCTATCCAGGACATACGCA	90059
Qy	90060	CCACAGTTCGATCCCATCTACATCTGCGGTCATGATATCTTAAGCTCTCTTTCCT	90119
Db	90060	CCACAGTTCGATCCCATCTACATCTGCGGTCATGATATCTTAAGCTCTCTTTCCT	90119
Qy	90120	CGTCGACACAACAGTGTGGGAAAAGTTCGCTCCAAATTTGAAAATTAATCCATC	90179
Db	90120	CGTCGACACAACAGTGTGGGAAAAGTTCGCTCCAAATTTGAAAATTAATCCATC	90179
Qy	90180	TTGCGAGTATTTGAGTATTTCTATCTGCGGTCATTTGAACTTGGTCCAGCAAACT	90239
Db	90180	TTGCGAGTATTTGAGTATTTCTATCTGCGGTCATTTGAACTTGGTCCAGCAAACT	90239
Qy	90240	AACTCAAAAGCCCTCACACACTCCCTTAAAGTGTAGTGAATTTATGCTCACTTATAG	90299
Db	90240	AACTCAAAAGCCCTCACACACTCCCTTAAAGTGTAGTGAATTTATGCTCACTTATAG	90299
Qy	90300	GTCGACGTGTACGTATATGCCCGGTGAAAACCTGCACTTCCTATAAATTTCCCAAA	90359
Db	90300	GTCGACGTGTACGTATATGCCCGGTGAAAACCTGCACTTCCTATAAATTTCCCAAA	90359
Qy	90360	GCGTTTGGGTCGCTCACCTTAACCTAGAGCATTAACAGGTTTCATAGTGTCCGGGT	90419
Db	90360	GCGTTTGGGTCGCTCACCTTAACCTAGAGCATTAACAGGTTTCATAGTGTCCGGGT	90419
Qy	90420	TTGCGCACTCCCGCAGCGGAGAGAAAGCAAGGTTTCAATTTAAAGGGACCAAGTGC	90479
Db	90420	TTGCGCACTCCCGCAGCGGAGAGAAAGCAAGGTTTCAATTTAAAGGGACCAAGTGC	90479
Qy	90480	AACTTTATTTAAGAGAGAAAAAACACACCGCATCAGAGGTTTCCGAGGACACACCCC	90539
Db	90480	AACTTTATTTAAGAGAGAAAAAACACACCGCATCAGAGGTTTCCGAGGACACACCCC	90539
Qy	90540	CAAGACTATTTCTTGGCAGATTTCCGGCAGCCTGTAGTTTCTGATTTATTTGTAATTC	90599
Db	90540	CAAGACTATTTCTTGGCAGATTTCCGGCAGCCTGTAGTTTCTGATTTATTTGTAATTC	90599
Qy	90600	GATTCACATGCGCCCAACATATGATCAATTAATAAACGTTAAACACACACTGTGGGAA	90659
Db	90600	GATTCACATGCGCCCAACATATGATCAATTAATAAACGTTAAACACACACTGTGGGAA	90659
Qy	90660	CAAAATATGCTTCTGGCCCAAGACGTGCGTGAAGCTGACAGCAGCAGCGCTGCTAA	90719

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Oy 91740 AGTCAGGTACAGGCTTCTCGAGGAGGAGGAGTCAAGAAACCCCTCGGGATGGGAC 91799
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Oy 91800 CTTCGAGAGATTTGCCCGGAGGAGGATTAATTCGGTCCGCTCGATCTAATTAATAGCA 91859
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Oy 91920 TCTCATTTGGCGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 91979
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Oy 91980 ATGCGGCGACACGAGACTTAATCACTACATGATGATGATGATGATGATGATGATGATGAT 92039
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D 98760 GCGCGACAGATATGACGAGACCATGCTCTACAGCCCGGATTTGCCGCGAGTTCA 98819
QY 98820 AAACAAACGATATCGATCCCTTGGAGGAGGCTCCGAAACAGCTCCAAAAAATGAT 98879
D 98820 AAACAAACGATATCGATCCCTTGGAGGAGGCTCCGAAACAGCTCCAAAAAATGAT 98879
QY 98880 CGCTATTCCAAATAGATGAGTCTTACAGAGTCTTACAGAGTCTTCAAAAAATGAT 98939
D 98880 CGCTATTCCAAATAGATGAGTCTTACAGAGTCTTACAGAGTCTTCAAAAAATGAT 98939
QY 98940 CTATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 98999
D 98940 CTATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 98999
QY 99000 ATTCTCGGAGTCTTTTACAACTGCTGCACTGCTTACAGAAATTTTGGTGCATAC 99059
D 99000 ATTCTCGGAGTCTTTTACAACTGCTGCACTGCTTACAGAAATTTTGGTGCATAC 99059
QY 99060 GACAGGTGATACCGGAAGCAGCTGCCACAAAGATTTTCAATAGTGTCTTACTTTC 99119
D 99060 GACAGGTGATACCGGAAGCAGCTGCCACAAAGATTTTCAATAGTGTGTACTTTC 99119
QY 99120 AAAACATTCATATGACGAGGCTTCAATCAACATCATGACCTTTGTAGACACCTGA 99179
D 99120 AAAACATTCATATGACGAGGCTTCAATCAACATCATGACCTTTGTAGACACCTGA 99179
QY 99180 AAAAGGATACCCCGATATGAGCTGCTGCTTACAGGAGGCGGCTTTTAAACATGA 99239
D 99180 AAAAGGATACCCCGATATGAGCTGCTGCTTACAGGAGGCGGCTTTTAAACATGA 99239
QY 99240 AACTACTGTAGATTAACGCTAGACACGCTGATTCCAACGGAAGAGGCAACCA 99299
D 99240 AACTACTGTAGATTAACGCTAGACACGCTGATTCCAACGGAAGAGGCAACCA 99299
QY 99300 TCGTGTGAGGATGTTGTATTCAAATTCACGATTCGCTGCTGCAAGAGTCTTAAAG 99359
D 99300 TCGTGTGAGGATGTTGTATTCAAATTCACGATTCGCTGCTGCAAGAGTCTTAAAG 99359
QY 99360 AAGCGTTATGCGGTTTAACTCAACGTCGGAAGAGTGAAGAGAGAGAGAGAGAG 99419
D 99360 AAGCGTTATGCGGTTTAACTCAACGTCGGAAGAGTGAAGAGAGAGAGAGAGAG 99419
QY 99420 TGCACACCTCACGTACATGCAAAAAGATCGCGGAGACAGAAATATGACACACACTTC 99479

Db	99420	TGCAACACCTGCAGTACATGCAAAAAGATGCGCGACACGAAATATGACACCACTTC	99479
QY	99480	CATCCGTGTTTACGAAATACACGAGGGAATATTGCAGTGTTTTAAAGCTTTAAACGTC	99539
Db	99480	CATCCGTGTTTACGAAATACACGAGGGAATATTGCAGTGTTTTAAAGCTTTAAACGTC	99539
QY	99540	TCATGTTAACGTTACGGAGACGTGGTGTACTGACTGACGGCACTGTTGGATTCCTAT	99599
Db	99540	TCATGTTAACGTTACGGAGACGTGGTGTACTGACTGACGGCACTGTTGGATTCCTAT	99599
QY	99600	ATCAACCCCCCTTAATACCGATACCATGTCACAAAAATTTTAACTTTAACGACAAAA	99659
Db	99600	ATCAACCCCCCTTAATACCGATACCATGTCACAAAAATTTTAACTTTAACGACAAAA	99659
QY	99660	CGGACACAAACGACGACATCTTAANGAGCTGCACAGCCCGGACACAAAGACCTCTAT	99719
Db	99660	CGGACACAAACGACGACATCTTAANGAGCTGCACAGCCCGGACACAAAGACCTCTAT	99719
QY	99720	CGCGTGAANAACGAAAGTAGACAGTCGACTGTCAAAAAACAAAGTTGAGCTGCTTCAAAAAC	99779
Db	99720	CGCGTGAANAACGAAAGTAGACAGTCGACTGTCAAAAAACAAAGTTGAGCTTCAAAAAC	99779
QY	99780	TGTACGACGACTTTGGGACCCGCTCCACAAACATTAACCCACCTTATTAACTTGAAT	99839
Db	99780	TGTACGACGACTTTGGGACCCGCTCCACAAACATTAACCCACCTTATTAACTTGAAT	99839
QY	99840	ATTCCGGTAAATTATACGAAACACAAAGTCCGTAGATTGGACACATATTAACCTGCTGA	99899
Db	99840	ATTCCGGTAAATTATACGAAACACAAAGTCCGTAGATTGGACACATATTAACCTGCTGA	99899
QY	99900	CATACACGCGACCCGACGATCGTTAAATTCACCCCGGTTTAAACAGGAGCCTAGATC	99959
Db	99900	CATACACGCGACCCGACGATCGTTAAATTCACCCCGGTTTAAACAGGAGCCTAGATC	99959
QY	99960	GCATCTTTGCAAGATTAAGAGATGGAATTCGCCCAATTTTTGCAATTTAAATTAATAGAGS	100019
Db	99960	GCATCTTTGCAAGATTAAGAGATGGAATTCGCCCAATTTTTGCAATTTAAATTAATAGAGS	100019
QY	100020	GGGTGGCAACGACGACACGAGCGACTGCAAGTTTCGACAAATACGCGCGCTCGACAGTGT	100079
Db	100020	GGGTGGCAACGACGACACGAGCGACTGCAAGTTTCGACAAATACGCGCGCTCGACAGTGT	100079
QY	100080	TAAAGCAACTGCGTTATCTACCTTCGCACAAAGTTATTCTCAATAGAGTCCCCGCTGACGG	100139
Db	100080	TAAAGCAACTGCGTTATCTACCTTCGCACAAAGTTATTCTCAATAGAGTCCCCGCTGACGG	100139
QY	100140	ACACTTAACGACCTCGACGACGTTTAAAGGCAAGGGGCGAGTGGACTTATCTAGAG	100199
Db	100140	ACACTTAACGACCTCGACGACGTTTAAAGGCAAGGGGCGAGTGGACTTATCTAGAG	100199
QY	100200	GGTCCGGGACGCTCGGCTATTAACCAATATGCCCACTGCACACATACCACGCTTATCA	100259
Db	100200	GGTCCGGGACGCTCGGCTATTAACCAATATGCCCACTGCACACATACCACGCTTATCA	100259
QY	100260	AGACCAACGAGTGGACCCGGGCACTCTTCAATCTGAGGATGACTTTGGACTATTTGGAC	100319
Db	100260	AGACCAACGAGTGGACCCGGGCACTCTTCAATCTGAGGATGACTTTGGACTATTTGGAC	100319
QY	100320	TTGACGCGGCGCATCCGCGCAACCTTTCATCGCAATCCCTAAATATGATCTTAACCGGAAATT	100379
Db	100320	TTGACGCGGCGCATCCGCGCAACCTTTCATCGCAATCCCTAAATATGATCTTAACCGGAAATT	100379
QY	100380	ACGCCGGGACCGTTCAATCTTCTGTATTATGCGGGACAAAGCCGGGGCCGCTAATTA	100439
Db	100380	ACGCCGGGACCGTTCAATCTTCTGTATTATGCGGGACAAAGCCGGGGCCGCTAATTA	100439
QY	100440	TCAAAAACAAAAGCTTTTACGTTCGATCCCATGCGCTACCCCAAGTAAATAGTC	100499
Db	100440	TCAAAAACAAAAGCTTTTACGTTCGATCCCATGCGCTACCCCAAGTAAATAGTC	100499
QY	100500	CGGACACGTAATCAAGTTCGACAGCCGACCGCATTAAGTACGTTGACCGCCAG	100559

Db	100500	CGGACACAGTAATCAATTGCTGTGACAGACCCACCGCCACTACTAGAGTACGTGTACCGCCAG	100553
QY	100560	ACAGGAAATACACTGGCAGATTTTCTATACATATATGCCCCAGGAAATATGTCAATCCAGAGC	100619
Db	100560	ACAGGAAATACACTGGCAGATTTTCTATACATATATGCCCCAGGAAATATGTCAATCCAGAGC	100619
QY	100620	ACTACATCCACAACCGCTATATAGAACTATTAAGCTTCCCAAGATGACAGGCCCGGCACATAG	100679
Db	100620	ACTACATCCACAACCGCTATATAGAACTATTAAGCTTCCCAAGATGACAGGCCCGGCACATAG	100679
QY	100680	ATATATCCACCGGCATATAGACCGGTGTGCACCATGTGAACATATCCCAACCCCGCGCGATGCG	100739
Db	100680	ATATATCCACCGGCATATAGACCGGTGTGCACCATGTGAACATATCCCAACCCCGCGCGATGCG	100739
QY	100740	CGGATGTGACGTCAAAATATATCCAACTCGACAGCGGTGGCGAGAACACACACGACGACGT	100799
Db	100740	CGGATGTGACGTCAAAATATATCCAACTCGACAGCGGTGGCGAGAACACACACGACGACGT	100799
QY	100800	CGAGCGCCAAACCCCCACCGGAGCGCTATCCGGTTTACGGGGGCGGAAACACGACAA	100859
Db	100800	CGAGCGCCAAACCCCCACCGGAGCGCTATCCGGTTTACGGGGGCGGAAACACGACAA	100859
QY	100860	GCTACCCAAACCCCGGAAACCAACGACGCGGACAAACCTTAACTCCCGCTCCAGCGC	100919
Db	100860	GCTACCCAAACCCCGGAAACCAACGACGCGGACAAACCTTAACTCCCGCTCCAGCGC	100919
QY	100920	AAACGCGCTGTGACACACCCCGGAATTCCAAAACAACACTGTGAGGACGCTACTTCTTTCAG	100979
Db	100920	AAACGCGCTGTGACACACCCCGGAATTCCAAAACAACACTGTGAGGACGCTACTTCTTTCAG	100979
QY	100980	AACGTGTGCGATTCAGGGGTCCGAAACGCAAGCTTTCAGCTTCAGCCGATATTCGATTC	101039
Db	100980	AACGTGTGCGATTCAGGGGTCCGAAACGCAAGCTTTCAGCTTCAGCCGATATTCGATTC	101039
QY	101040	CCGAGCAACCGTCGTGTGACGAGAAAGGGGCCCCAGTATGAGCGCGTACACAGCATGTGCA	101099
Db	101040	CCGAGCAACCGTCGTGTGACGAGAAAGGGGCCCCAGTATGAGCGCGTACACAGCATGTGCA	101099
QY	101100	TATCCGCCGAGGTGATCTGGATGAGCAGCAGATATCTCTCTATATTCACCGTCGCGCA	101159
Db	101100	TATCCGCCGAGGTGATCTGGATGAGCAGCAGATATCTCTCTATATTCACCGTCGCGCA	101159
QY	101160	CTCCATCGTTTACGACGAGTGTTCGACAGGCCCCCATATGAGGCCGGAGTTTACATFAGAAAG	101219
Db	101160	CTCCATCGTTTACGACGAGTGTTCGACAGGCCCCCATATGAGGCCGGAGTTTACATFAGAAAG	101219
QY	101220	ACGCGACAGAGGACAGATGAGCGCGCTTCTTGAACAGATCGCTCGAGACGCGGAAACGC	101279
Db	101220	ACGCGACAGAGGACAGATGAGCGCGCTTCTTGAACAGATCGCTCGAGACGCGGAAACGC	101279
QY	101280	CGTTCCTCTGCTTCGACGACCTTATATAGGAGCCAGACATTTTCTTCCCTTGATAAAAAAA	101339
Db	101280	CGTTCCTCTGCTTCGACGACCTTATATAGGAGCCAGACATTTTCTTCCCTTGATAAAAAAA	101339
QY	101340	TAGAACAGTTAATCAAGTACGAAAGCGCCCTCGAGACACTGTGCCAAACATCTCGGACAAAC	101399
Db	101340	TAGAACAGTTAATCAAGTACGAAAGCGCCCTCGAGACACTGTGCCAAACATCTCGGACAAAC	101399
QY	101400	AAAAAGGAGCGACCGCTCCGAGAAAGCGCGCCCTCCAGCGAGTGTGACAAAAATATATGATTA	101459
Db	101400	AAAAAGGAGCGACCGCTCCGAGAAAGCGCGCCCTCCAGCGAGTGTGACAAAAATATATGATTA	101459
QY	101460	ATATCATATCTTGAACACGCTATATTAACAGAGCGGACCGGAGACCGTCCGCGTGA	101519
Db	101460	ATATCATATCTTGAACACGCTATATTAACAGAGCGGACCGGAGACCGTCCGCGTGA	101519
QY	101520	AAAAAGTCTTCAATTTTTCATCTCTGTGGGGAAGAAAACTCAACATACCAATTAAGGAGAG	101579
Db	101520	AAAAAGTCTTCAATTTTTCATCTCTGTGGGGAAGAAAACTCAACATACCAATTAAGGAGAG	101579
QY	101580	CCAAGCAGGTCTTAGAACCTGATCTGCAACTGATACCGTTACATACGCGTATACGAGGAG	101639
Db	101580	CCAAGCAGGTCTTAGAACCTGATCTGCAACTGATACCGTTACATACGCGTATACGAGGAG	101639

QY	101640	GAATAATCAACAGGGGGCGTTTCAAAAAACACCTAAACAATAAATCAACCGGTGTCTGG	101699
Db	101640	GAATAATCAACAGGGGGCGTTTCAAAAAACACCTAAACAATAAATCAACCGGTGTCTGG	101699
QY	101700	CGTCAATGAGGGCCACGCACGAGATGGGCATAAAAAAAGTGGCGTTCGCTTCAAGCTGG	101759
Db	101700	CGTCAATGAGGGCCACGCACGAGATGGGCATAAAAAAAGTGGCGTTCGCTTCAAGCTGG	101759
QY	101760	AAGGCTCACAGATTTTCGTCACGACGAAAGCAAAATATCACTCCGGGGCGTGAAGGAACAGA	101819
Db	101760	AAGGCTCACAGATTTTCGTCACGACGAAAGCAAAATATCACTCCGGGGCGTGAAGGAACAGA	101819
QY	101820	TCGCCAACCCACTGAGTCCAGGGCTTTTAAAGCGGTACTCCGGCAGCAGAGTAAAAATATC	101879
Db	101820	TCGCCAACCCACTGAGTCCAGGGCTTTTAAAGCGGTACTCCGGCAGCAGAGTAAAAATATC	101879
QY	101880	TACGGGATATAAATTCAGAACCCATAAACAGCATGAGCAGGGCAACAAGAAATTCCAAC	101939
Db	101880	TACGGGATATAAATTCAGAACCCATAAACAGCATGAGCAGGGCAACAAGAAATTCCAAC	101939
QY	101940	AGGAAGAACTGTTTTTATGTCAGCATGCTCACAGCCCTGGACAGGTTCCAAACCCCTCCGA	101999
Db	101940	AGGAAGAACTGTTTTTATGTCAGCATGCTCACAGCCCTGGACAGGTTCCAAACCCCTCCGA	101999
QY	102000	AAAGCGCATTTTCCAAATGAGATCTTTCCGCACCGTAAAAACGGAATTATGTCGACACC	102059
Db	102000	AAAGCGCATTTTCCAAATGAGATCTTTCCGCACCGTAAAAACGGAATTATGTCGACACC	102059
QY	102060	TGGCGTCATTAACCAACAGGTTAACCGAGGACCGCAACCGCAACCCCAACATTTACCTGG	102119
Db	102060	TGGCGTCATTAACCAACAGGTTAACCGAGGACCGCAACCGCAACCCCAACATTTACCTGG	102119
QY	102120	AGACCCCGCCCGACCAAGAAAGCAGCATTTACCAACATTTCCAAATTTTATCCTCAGCTGG	102179
Db	102120	AGACCCCGCCCGACCAAGAAAGCAGCATTTACCAACATTTCCAAATTTTATCCTCAGCTGG	102179
QY	102180	CAAAATATCATATCCACGTTAAAAATTCCTTAAGTACGCGAATAAACGACATGCAATTAAAG	102239
Db	102180	CAAAATATCATATCCACGTTAAAAATTCCTTAAGTACGCGAATAAACGACATGCAATTAAAG	102239
QY	102240	TAACGCCATGAGCAACGTACAGAGCGTCAAGCTTTGACTCGGAGGCGAGTTAAGCAACA	102299
Db	102240	TAACGCCATGAGCAACGTACAGAGCGTCAAGCTTTGACTCGGAGGCGAGTTAAGCAACA	102299
QY	102300	TCCTTAATTTAGAGTGGCCATACGAACCCGTGCGCAACCGGTTCAAGAACTGCCCTCTGG	102359
Db	102300	TCCTTAATTTAGAGTGGCCATACGAACCCGTGCGCAACCGGTTCAAGAACTGCCCTCTGG	102359
QY	102360	CGCGGGCGAAAGCAAAATGGAATCGTAAACAAAATGGAAGAAACCAACAGGCTCTGG	102419
Db	102360	CGCGGGCGAAAGCAAAATGGAATCGTAAACAAAATGGAAGAAACCAACAGGCTCTGG	102419
QY	102420	ACCAAAATCTGGGAGACCGCCGAACGTTACTTGACACATAATACCGCAATCTCCGAGATG	102479
Db	102420	ACCAAAATCTGGGAGACCGCCGAACGTTACTTGACACATAATACCGCAATCTCCGAGATG	102479
QY	102480	AGAACCCGGTCCGGCCATGTCATACGGAATACTGGAGACCTTAATTACAAACGCAAGCGG	102539
Db	102480	AGAACCCGGTCCGGCCATGTCATACGGAATACTGGAGACCTTAATTACAAACGCAAGCGG	102539
QY	102540	CCCTGATTAAGGCGATTCTGGAACCAAGCGGTTGAAAAAATCTAAGGGCGGCTATCCAGACC	102599
Db	102540	CCCTGATTAAGGCGATTCTGGAACCAAGCGGTTGAAAAAATCTAAGGGCGGCTATCCAGACC	102599
QY	102600	TGGCATCATCGGAGTCTGTTCAATAATATGCTGCTAAACCAACAGCGGGCTCGATTAAACATAT	102659
Db	102600	TGGCATCATCGGAGTCTGTTCAATAATATGCTGCTAAACCAACAGCGGGCTCGATTAAACATAT	102659
QY	102660	CAGACAAATCTGGCCAAAGATCGACGGCATCTGACCAACAAACACAGTTTTCTTTCAAAAG	102719
Db	102660	CAGACAAATCTGGCCAAAGATCGACGGCATCTGACCAACAAACACAGTTTTCTTTCAAAAG	102719

QY	102720	CCACTGTTAGCAAAACGCTCCAAACGCTGGGAGGCAACGCTTAATACGCAATCGTATGAAG	102779
Db	102720	CCACTGTTAGCAAAACGCTCCAAACGCTGGGAGGCAACGCTTAATACGCAATCGTATGAAG	102779
QY	102760	CGCTAAATAAAGGAGCCCTCTCCCTCAACAAGCGCGTCTCCCGGGTTCAAAACA	102839
Db	102760	CGCTAAATAAAGGAGCCCTCTCCCTCAACAAGCGCGTCTCCCGGGTTCAAAACA	102839
QY	102840	TACTGGGACACGCGTCCGTTCCAGATCACGAGACGCTGACGCGAATCTTTCCGGCGTGG	102899
Db	102840	TACTGGGACACGCGTCCGTTCCAGATCACGAGACGCTGACGCGAATCTTTCCGGCGTGG	102899
QY	102900	CCAGCGCACAAAAAGAAATCCGTCGGCATGATTCAGATAGTGGACGCGATACCGGTC	102959
Db	102900	CCAGCGCACAAAAAGAAATCCGTCGGCATGATTCAGATAGTGGACGCGATACCGGTC	102959
QY	102960	ACCTAAACGAGCTGAAGCTCGTAACCTACCAATCCGCTGTGCACAAAGCCACACGGCGCA	103019
Db	102960	ACCTAAACGAGCTGAAGCTCGTAACCTACCAATCCGCTGTGCACAAAGCCACACGGCGCA	103019
QY	103020	AACTGTTAATGATTAATTAACCCGTGACCTCAAGAGGCGGAGGTGTCTCAGAAACGGTCC	103079
Db	103020	AACTGTTAATGATTAATTAACCCGTGACCTCAAGAGGCGGAGGTGTCTCAGAAACGGTCC	103079
QY	103080	TGGAACAACGGTGGCAAGAAAAGTGTAAAGTTTCAACCGTGCAGCTCCAAAGAAATCG	103139
Db	103080	TGGAACAACGGTGGCAAGAAAAGTGTAAAGTTTCAACCGTGCAGCTCCAAAGAAATCG	103139
QY	103140	AAGACTTTTTCACGTCGCGCACCGTTCAGCAAAAGCCCGAATAATTCGAGAAAAACACTTAC	103199
Db	103140	AAGACTTTTTCACGTCGCGCACCGTTCAGCAAAAGCCCGAATAATTCGAGAAAAACACTTAC	103199
QY	103200	GGACCGCTGATCAACCAATTCAACGGCCACAGACGACCGCGCTCCGAGGGCCACCGCGCTTC	103259
Db	103200	GGACCGCTGATCAACCAATTCAACGGCCACAGACGACCGCGCTCCGAGGGCCACCGCGCTTC	103259
QY	103260	CCATGGACTACACGCGCGACGCCCAATCCACGCCACAGCGCCGTTTCTACGGCTACCGCGG	103319
Db	103260	CCATGGACTACACGCGCGACGCCCAATCCACGCCACAGCGCCGTTTCTACGGCTACCGCGG	103319
QY	103320	AAAAAGGAAAGGCCCATGGAATTAATAATCAACAGCGCTTCAGGATTTCAACTTCAACC	103379
Db	103320	AAAAAGGAAAGGCCCATGGAATTAATAATCAACAGCGCTTCAGGATTTCAACTTCAACC	103379
QY	103380	TCATGACAGCTTCGGATTGGCAAGAGATGGATTCAGAAATCTCAAGACACGGCTCGTCCC	103439
Db	103380	TCATGACAGCTTCGGATTGGCAAGAGATGGATTCAGAAATCTCAAGACACGGCTCGTCCC	103439
QY	103440	TTCTGTGTAACGGTTGGACCAAAAGCTGTGTCTTCAATGAGAGCATCTCAAAACCCCTGG	103499
Db	103440	TTCTGTGTAACGGTTGGACCAAAAGCTGTGTCTTCAATGAGAGCATCTCAAAACCCCTGG	103499
QY	103500	ACGATATCTCAACGAGAAAGTGGGATCTCTCTTCCAAAGCGGCCCGGCTTCAGACCCC	103559
Db	103500	ACGATATCTCAACGAGAAAGTGGGATCTCTCTTCCAAAGCGGCCCGGCTTCAGACCCC	103559
QY	103560	CAGCGTTTGACGTGCGCGCCCTATCAAAACGCGGTAACCGCTTTCITAAAAACCATAG	103619
Db	103560	CAGCGTTTGACGTGCGCGCCCTATCAAAACGCGGTAACCGCTTTCITAAAAACCATAG	103619
QY	103620	GCCTGCCCATGGTGGCGCAACCTGGCGGACAAATCATCAACCAATGCCAAACGTTCAGTC	103679
Db	103620	GCCTGCCCATGGTGGCGCAACCTGGCGGACAAATCATCAACCAATGCCAAACGTTCAGTC	103679
QY	103680	ACGGGTCGAATCCGACAGACCTTCAACAGGCCACGCTGGGAACAAGTTTGAACGACCGG	103739
Db	103680	ACGGGTCGAATCCGACAGACCTTCAACAGGCCACGCTGGGAACAAGTTTGAACGACCGG	103739
QY	103740	CGGCGGAATACGTGTGAATACTCTCTGACATGCAAGTGCCTTCACAGCACACGGAATGG	103799
Db	103740	CGGCGGAATACGTGTGAATACTCTCTGACATGCAAGTGCCTTCACAGCACACGGAATGG	103799
QY	103800	CCGTAAAGTCGAGGCGCGCGGCTACAGGACGCAATCAACTGCCCGGCCCAACGTCGTGA	103859

Db	103800	CCGTAAAGATCGAAGGCGCGGCTACAGGACGCAATCACTACGCGCGCAACGTGTGA	103859	Db	104880	CGACCGTCGATCCGGAAAAACCACTCACGTCCCGCGACAGGAGAGCCCTCTGCACC	104939
Qy	103860	CTCCCCCGAAACCAACCTAGAAAGCCGCCAAGAACCTAATAACGGCAACTGACGCCCTAA	103919	Qy	104940	GCCAGATCACTACTCAAAAGTCTAGAGGCGTGTGTTCAATATGTTCCACACGCTAA	104999
Db	103860	CTCCCCCGAAACCAACCTAGAAAGCCGCCAAGAACCTAATAACGGCAACTGACGCCCTAA	103919	Db	104940	GCCAGATCACTACTCAAAAGTCTAGAGGCGTGTGTTCAATATGTTCCACACGCTAA	104999
Qy	103920	CCGTGAGAGACTTCTCCAGATTTCTTAAAAAGCTCAATCTTTACACAGACAGCGACTCA	103979	Qy	105000	CCCCGGTTCCGAGCGCCCGGCTGTGAAATATGGCAACGAGGCGACCGCGGGGAGAGG	105059
Db	103920	CCGTGAGAGACTTCTCCAGATTTCTTAAAAAGCTCAATCTTTACACAGACAGCGACTCA	103979	Db	105000	CCCCGGTTCCGAGCGCCCGGCTGTGAAATATGGCAACGAGGCGACCGCGGGGAGAGG	105059
Qy	103980	TTGGCTCCAGAGACGGAATTTGACAACTAGAGCCGACATCTCGCGGCGCGAAGCGC	104039	Qy	105060	CCGCAACGTTGATGAGACAGACAGTGGCCGACATGCGTACAGCGTCCAAAGCTTTCG	105119
Db	103980	TTGGCTCCAGAGACGGAATTTGACAACTAGAGCCGACATCTCGCGGCGCGAAGCGC	104039	Db	105060	CCGCAACGTTGATGAGACAGACAGTGGCCGACATGCGTACAGCGTCCAAAGCTTTCG	105119
Qy	104040	TCGCGCAATCCACCCGCGAGAGATCGAGGCAAGATGGCAACCGCTATCACGCAACTCT	104099	Qy	105120	ACACGTACGACACACACACCGCGCCACGAAACCGGAGAGCGGCAATTTAAACATTTCTGG	105179
Db	104040	TCGCGCAATCCACCCGCGAGAGATCGAGGCAAGATGGCAACCGCTATCACGCAACTCT	104099	Db	105120	ACACGTACGACACACACACCGCGCCACGAAACCGGAGAGCGGCAATTTAAACATTTCTGG	105179
Qy	104100	TACCCCGGCGCCCTCGCAATATCATGAGACCGTTGACCTTATCAAAACCTATAGACT	104159	Qy	105180	CGATGTGCGTTTACGCAAAATCATGAGGGCGCTAGACAGACCGCTGACGCTCCGAAGT	105239
Db	104100	TACCCCGGCGCCCTCGCAATATCATGAGACCGTTGACCTTATCAAAACCTATAGACT	104159	Db	105180	CGATGTGCGTTTACGCAAAATCATGAGGGCGCTAGACAGACCGCTGACGCTCCGAAGT	105239
Qy	104160	TTTTAGTTCAACGGGTATACGCAAAATCTGAGCAAGAGCGCTTACGACAGCCATAG	104219	Qy	105240	TACGAGACACCGCGCTCATTTTCCAGAAAGATGCTTCTAACACCCAGGAAATGCACAA	105299
Db	104160	TTTTAGTTCAACGGGTATACGCAAAATCTGAGCAAGAGCGCTTACGACAGCCATAG	104219	Db	105240	TACGAGACACCGCGCTCATTTTCCAGAAAGATGCTTCTAACACCCAGGAAATGCACAA	105299
Qy	104220	CGGAGTTGCGGTGGAATCGCGCAAAAATCCGTAATGGTCTACAGTCAACAAACG	104279	Qy	105300	CAGTGTACCGCCCATGTGGCCACCCCTGGCGGCGCAATCTTACGATTTAAATCTCTACT	105359
Db	104220	CGGAGTTGCGGTGGAATCGCGCAAAAATCCGTAATGGTCTACAGTCAACAAACG	104279	Db	105300	CAGTGTACCGCCCATGTGGCCACCCCTGGCGGCGCAATCTTACGATTTAAATCTCTACT	105359
Qy	104280	AAACCCACAGTTAAACGTACTGCTGAGCGAGGTGAAAAACAGAGCACCGTCCGCGAC	104339	Qy	105360	CGGAAGCCCTAGACTAATGATGCTGTTCTCCCTAATGTTCCAGGCGCTGCGGACCC	105419
Db	104280	AAACCCACAGTTAAACGTACTGCTGAGCGAGGTGAAAAACAGAGCACCGTCCGCGAC	104339	Db	105360	CGGAAGCCCTAGACTAATGATGCTGTTCTCCCTAATGTTCCAGGCGCTGCGGACCC	105419
Qy	104340	GTCCTACAGATTTGGAAGTGTGCGGAAAAACACGAGACGACTTAAAGGTGCTGAAGCAG	104399	Qy	105420	TAAAGCTAGAGGCCAGGCTCAAAAAAGGCGCCACATTAACACCCCGCTCAGTTGAGATGCT	105479
Db	104340	GTCCTACAGATTTGGAAGTGTGCGGAAAAACACGAGACGACTTAAAGGTGCTGAAGCAG	104399	Db	105420	TAAAGCTAGAGGCCAGGCTCAAAAAAGGCGCCACATTAACACCCCGCTCAGTTGAGATGCT	105479
Qy	104400	CGCTAGACGAACCTCGGCCCTCAGGGTAAAGGCGGAAAAACAACCGTAGACGCGTGA	104459	Qy	105480	TTGCCAAAACAGAGCAATTCGTAATTTCCGCGCCCAATGAGAGTCAAGCAAGGCGCA	105539
Db	104400	CGCTAGACGAACCTCGGCCCTCAGGGTAAAGGCGGAAAAACAACCGTAGACGCGTGA	104459	Db	105480	TTGCCAAAACAGAGCAATTCGTAATTTCCGCGCCCAATGAGAGTCAAGCAAGGCGCA	105539
Qy	104460	AAACAAAAGTGAAGGCAATAGATTCCTGCTGCGGCCACGAGGAGCGGCAAGCAAAAT	104519	Qy	105540	AGAGCTGTGGGGAGACAGCGGCTTTGGCAAAATGTGGATTAACATCAACGCAAGGCGCA	105599
Db	104460	AAACAAAAGTGAAGGCAATAGATTCCTGCTGCGGCCACGAGGAGCGGCAAGCAAAAT	104519	Db	105540	AGAGCTGTGGGGAGACAGCGGCTTTGGCAAAATGTGGATTAACATCAACGCAAGGCGCA	105599
Qy	104520	CATCGAGACTTGAAGCATCGGACACAGGCGGTGGACACATCACCGTCCGCGATTAG	104579	Qy	105600	GGGTGGCGGCGCTCACTGCGGGGCTCACAGAGATAGACGGCGTGTGTTGGACCAACTGT	105659
Db	104520	CATCGAGACTTGAAGCATCGGACACAGGCGGTGGACACATCACCGTCCGCGATTAG	104579	Db	105600	GGGTGGCGGCGCTCACTGCGGGGCTCACAGAGATAGACGGCGTGTGTTGGACCAACTGT	105659
Qy	104580	GAAAGCTTCGAGATCAATGCGGGGAAGCGCAAAATTTCTCAGAGAGCGCACTACCCG	104639	Qy	105660	GGTCCACATTTAAACCCCATGACAGCGGCTCAGAGACAGCTACCACTGATGCGAGA	105719
Db	104580	GAAAGCTTCGAGATCAATGCGGGGAAGCGCAAAATTTCTCAGAGAGCGCACTACCCG	104639	Db	105660	GGTCCACATTTAAACCCCATGACAGCGGCTCAGAGACAGCTACCACTGATGCGAGA	105719
Qy	104640	AAAGGTTCTGAGACATAGGCAAAACATCAGAGACCTTACAGCGCTTAAGTAACTAAA	104699	Qy	105720	CCCTACACTGACCACTTTGGCCCGGCGGCTCAACGCGGAGGAGAGAAAGACACACG	105779
Db	104640	AAAGGTTCTGAGACATAGGCAAAACATCAGAGACCTTACAGCGCTTAAGTAACTAAA	104699	Db	105720	CCCTACACTGACCACTTTGGCCCGGCGGCTCAACGCGGAGGAGAGAAAGACACACG	105779
Qy	104700	AACAGTTCTGAGAGATTTTAAACCAACCCAGCTTAAGCTTTTAAAGCTTCCGCTAT	104759	Qy	105780	AGCACCCGCGCTACGAGTACGAGACAGCGGCGCTACTGCACTCGGGTCAATGACAGA	105839
Db	104700	AACAGTTCTGAGAGATTTTAAACCAACCCAGCTTAAGCTTTTAAAGCTTCCGCTAT	104759	Db	105780	AGCACCCGCGCTACGAGTACGAGACAGCGGCGCTACTGCACTCGGGTCAATGACAGA	105839
Qy	104760	CCCAAAACATTAACGAAAAAGCTTCGCGCGCGCGCGAGTGGTGGGCAACATGA	104819	Qy	105840	CGCGGCTCCAGGCTTCAAAACACACCGGATATCCGCTTTGAGGCGGCTCGGAGCAATGG	105899
Db	104760	CCCAAAACATTAACGAAAAAGCTTCGCGCGCGCGCGAGTGGTGGGCAACATGA	104819	Db	105840	CGCGGCTCCAGGCTTCAAAACACACCGGATATCCGCTTTGAGGCGGCTCGGAGCAATGG	105899
Qy	104820	CCAATACACCTTACAGTGGCGGAGACCGCGCCCACTTTACAAAGTGAATAAAGCGCTAC	104879	Qy	105900	TGTTTACAGTACCGCATGCAATATTTTGGGGGCGACGCCCAAGGCGCTTGGCCAGGGGC	105959
Db	104820	CCAATACACCTTACAGTGGCGGAGACCGCGCCCACTTTACAAAGTGAATAAAGCGCTAC	104879	Db	105900	TGTTTACAGTACCGCATGCAATATTTTGGGGGCGACGCCCAAGGCGCTTGGCCAGGGGC	105959
Qy	104880	CGACCGTGCATCCGAAAAACCAACTCAGTCCGCGGCGCAGGAGAGACCCCTCTGCACC	104939	Qy	105960	GGCGGCGATGGGGTCTCTACACCACTCTGGAATGCGTCCCGACGCTCGACGCCCTTCA	106019
Db	104880	CGACCGTGCATCCGAAAAACCAACTCAGTCCGCGGCGCAGGAGAGACCCCTCTGCACC	104939	Db	105960	GGCGGCGATGGGGTCTCTACACCACTCTGGAATGCGTCCCGACGCTCGACGCCCTTCA	106019

QY	106020	AAAGCCTGTATTAACGACCCCGCAAAACCCGTGGCCATTGAAAGCTACCCGATCCCTCC	106079
Db	106020	AAAGCCTGTATTAACGACCCCGCAAAACCCGTGGCCATTGAAAGCTACCCGATCCCTCC	106079
QY	106080	ACCCGACGACGACGACAGGTCTTCTGAGACAGGACAGTGGCTATCCCTACCGATGCA	106139
Db	106080	ACCCGACGACGACGACAGGTCTTCTGAGACAGGACAGTGGCTATCCCTACCGATGCA	106139
QY	106140	CACACACGAAAGCCCGGTGTGACCTCCCGGCTTGTGGTGCATAGAACCCGAAA	106139
Db	106140	CACACACGAAAGCCCGGTGTGACCTCCCGGCTTGTGGTGCATAGAACCCGAAA	106139
QY	106200	ACCTCGTAACGCGCAAGTACTCCAGTGGGGGCGCTCAAAATTTGAGAGAGCGCGTTT	106259
Db	106200	ACCTCGTAACGCGCAAGTACTCCAGTGGGGGCGCTCAAAATTTGAGAGAGCGCGTTT	106259
QY	106260	ACGTGATGCCCGGACCATACCCCCAGACTGGCCAAAAGCTGTGGTAACTAACA	106319
Db	106260	ACGTGATGCCCGGACCATACCCCCAGACTGGCCAAAAGCTGTGGTAACTAACA	106319
QY	106320	CGTCCGTGAGCGCTCAGCGACAGAGATGTAACTTACTAGCGCTATCCGAG	106379
Db	106320	CGTCCGTGAGCGCTCAGCGACAGAGATGTAACTTACTAGCGCTATCCGAG	106379
QY	106380	AACACGGAACCGTGCAGGAGGATATCTTCGACGCGCTCCGACAAAAGTACACCG	106439
Db	106380	AACACGGAACCGTGCAGGAGGATATCTTCGACGCGCTCCGACAAAAGTACACCG	106439
QY	106440	AACAAACCGCAATCTCTCCGGCATGGGAAAAGGATTAACGATTAATAGCAGAAAGAAA	106499
Db	106440	AACAAACCGCAATCTCTCCGGCATGGGAAAAGGATTAACGATTAATAGCAGAAAGAAA	106499
QY	106500	CGGCCAAAACCTCATTAATTCCTGCGCTCTCTAAAGGGGGAGAGATCCACGGTGG	106559
Db	106500	CGGCCAAAACCTCATTAATTCCTGCGCTCTCTAAAGGGGGAGAGATCCACGGTGG	106559
QY	106560	AAACGACGACCCACATTCACAAAGGCGCAAGCGTCGACACAGCAACAGCAACGTAAC	106619
Db	106560	AAACGACGACCCACATTCACAAAGGCGCAAGCGTCGACACAGCAACAGCAACGTAAC	106619
QY	106620	AGCCCGGTCAAAATTTACTTACACGCGCTCAAGTAAACACCGTCAACCGGCTCAGGCT	106679
Db	106620	AGCCCGGTCAAAATTTACTTACACGCGCTCAAGTAAACACCGTCAACCGGCTCAGGCT	106679
QY	106680	CATCTTCACGCGGAAAATTCACAGCAACGCGTGGCTGACATTAATATCCAAACGTCG	106739
Db	106680	CATCTTCACGCGGAAAATTCACAGCAACGCGTGGCTGACATTAATATCCAAACGTCG	106739
QY	106740	AAACGCGCATATTAACAGCAGCGCTCCGGCCAGGTCAACGAAAGGAAATCTT	106799
Db	106740	AAACGCGCATATTAACAGCAGCGCTCCGGCCAGGTCAACGAAAGGAAATCTT	106799
QY	106800	GGACGATTAACCCCGAGTGTCAACGCAACCGCCAAACCGCGGAGTGA	106859
Db	106800	GGACGATTAACCCCGAGTGTCAACGCAACCGCCAAACCGCGGAGTGA	106859
QY	106860	CTCGCAACGAGGGAACCAACGAGTCCCGCAAGTTACCGATTAATCCACCGGCTA	106919
Db	106860	CTCGCAACGAGGGAACCAACGAGTCCCGCAAGTTACCGATTAATCCACCGGCTA	106919
QY	106920	GGGTCTTTATAGGAGCGCGTCCAAACTCTCGCAGCCGTCGAAAGAGCAGCGGCCA	106979
Db	106920	GGGTCTTTATAGGAGCGCGTCCAAACTCTCGCAGCCGTCGAAAGAGCAGCGGCCA	106979
QY	106980	CACCGACGACATCATGTGCAAAATAGATCGGCAAAATATCGCGAGAGTGGCTCGCC	107039
Db	106980	CACCGACGACATCATGTGCAAAATAGATCGGCAAAATATCGCGAGAGTGGCTCGCC	107039
QY	107040	GCACCCACACCTCGAAGAGGGGCGCAAGGAGCTCAACGTAACACTCCAACGAGGCAC	107099
Db	107040	GCACCCACACCTCGAAGAGGGGCGCAAGGAGCTCAACGTAACACTCCAACGAGGCAC	107099

QY	107100	ACATAACGTCCTCTTAGCGCAAGGTCAAAAACAGTACAGGGCGCGAAATCCGGCC	107159
Db	107100	ACATAACGTCCTCTTAGCGCAAGGTCAAAAACAGTACAGGGCGCGAAATCCGGCC	107159
QY	107160	TTTAAACAGCACTCTCCAGCGGCCCGCCACCAACCGCATTCAAACCCCGCATTCATACA	107219
Db	107160	TTTAAACAGCACTCTCCAGCGGCCCGCCACCAACCGCATTCAAACCCCGCATTCATACA	107219
QY	107220	CGCTCCCGAAGAGGAGCGGCGGTGCTTACGACGAAATCGAGGTGGAATCGACCCAA	107279
Db	107220	CGCTCCCGAAGAGGAGCGGCGGTGCTTACGACGAAATCGAGGTGGAATCGACCCAA	107279
QY	107280	CCGAGAGGATTAACGATCGCCCAAAAACAAAGATGTCTCAAGGGCCGAAACCGAG	107339
Db	107280	CCGAGAGGATTAACGATCGCCCAAAAACAAAGATGTCTCAAGGGCCGAAACCGAG	107339
QY	107340	ACTCCAGGTGACCGCGCGCTGGTTCACACATAGAGATTCACTGCACTGGAACACCC	107399
Db	107340	ACTCCAGGTGACCGCGCGCTGGTTCACACATAGAGATTCACTGCACTGGAACACCC	107399
QY	107400	AAATTCGCAAAATTAATACATCACTACCGCTCCCACTCCAGAGTACCCCAATCCCTC	107459
Db	107400	AAATTCGCAAAATTAATACATCACTACCGCTCCCACTCCAGAGTACCCCAATCCCTC	107459
QY	107460	CCACTAACATCTGATATACCCCTATCCACGTCAACATCAACAGAAATACACAG	107519
Db	107460	CCACTAACATCTGATATACCCCTATCCACGTCAACATCAACAGAAATACACAG	107519
QY	107520	CCAAAGATGTGTTAAATGCGATTAATCAAAACGTACGAAACAACTTCAAGCGCTG	107579
Db	107520	CCAAAGATGTGTTAAATGCGATTAATCAAAACGTACGAAACAACTTCAAGCGCTG	107579
QY	107580	ACGCTCATCGAGGCGATTCGCCAAGATAAGTTTATATCTGTAACGGCCCATCTCA	107639
Db	107580	ACGCTCATCGAGGCGATTCGCCAAGATAAGTTTATATCTGTAACGGCCCATCTCA	107639
QY	107640	CTTGCTTTTATTTTGAAGCAGCGCTTGTGTCCAGATAGTTCGCTGAGTGA	107699
Db	107640	CTTGCTTTTATTTTGAAGCAGCGCTTGTGTCCAGATAGTTCGCTGAGTGA	107699
QY	107700	TAAAGAGTGGACCTATGCGCAAGAGCGCACGCTCCCGGGTCCCGGCGCACCGGCG	107759
Db	107700	TAAAGAGTGGACCTATGCGCAAGAGCGCACGCTCCCGGGTCCCGGCGCACCGGCG	107759
QY	107760	GGGGCCCATGAGCATATCAATGAATGGGGCCCGCTGAGATCTGATTAAGCTATTTGA	107819
Db	107760	GGGGCCCATGAGCATATCAATGAATGGGGCCCGCTGAGATCTGATTAAGCTATTTGA	107819
QY	107820	CCGAGGAGTGGAGGCGCACCGGGCAACGCTCGGGGGCGCGAGCCGAGCCGCAAAAC	107879
Db	107820	CCGAGGAGTGGAGGCGCACCGGGCAACGCTCGGGGGCGCGAGCCGAGCCGCAAAAC	107879
QY	107880	GCCCGAGATTAAGTAACTACGTCCTTTTGGCCGCAAGGCCCGCGAGTGTCTTGGC	107939
Db	107880	GCCCGAGATTAAGTAACTACGTCCTTTTGGCCGCAAGGCCCGCGAGTGTCTTGGC	107939
QY	107940	CAGAAATTCATCTCTCTTTGCAATATGATGTGATGATGTTGGCGCTTAAACAC	107999
Db	107940	CAGAAATTCATCTCTCTTTGCAATATGATGTGATGATGTTGGCGCTTAAACAC	107999
QY	108000	CAGATATTAATAGTTTGGCATGAGTGGCGTGGGGGAGACATGCACTGGGGAGTT	108059
Db	108000	CAGATATTAATAGTTTGGCATGAGTGGCGTGGGGGAGACATGCACTGGGGAGTT	108059
QY	108060	GTTTCATCTCGGCAACAGCGGGTATTTGGGTAATCTGCTCAAGCGCTCCGTAACGAT	108119
Db	108060	GTTTCATCTCGGCAACAGCGGGTATTTGGGTAATCTGCTCAAGCGCTCCGTAACGAT	108119
QY	108120	TGGCTCTTAACCGCAAGAGCAATCTTTTAACTTATTAACCTTCCACAGAG	108179
Db	108120	TGGCTCTTAACCGCAAGAGCAATCTTTTAACTTATTAACCTTCCACAGAG	108179
QY	108180	AGGAGGATTAAGACGAGTCAATAAACAGCTCGGCGCACAGCAATCTTAAATAG	108239

Db	108180	AGGACGATATGACGAGGCTCAATAAACAAGCTGGCCACACGCAAAATGCTTTATAGG	108239
Qy	108240	CCGGTCGGCAGTCCGGGACGCCAAACAGGGGACAGACGACGCTTAACGAGGGATTCCG	108299
Db	108240	CCGGTCGGCAGTCCGGGACGCCAAACAGGGGACAGACGACGCTTAACGAGGGATTCCG	108299
Qy	108300	TCTCTAGTGCATGTGCCCGCTGTGTGGCAGACAGCACCGTAAATAGGAGTCTCAACA	108359
Db	108300	TCTCTAGTGCATGTGCCCGCTGTGTGGCAGACAGCACCGTAAATAGGAGTCTCAACA	108359
Qy	108360	CACGATCTCGAATAGAGATATACCCGATGTGCGATTCGCCCAATTAAGAGCAAT	108419
Db	108360	CACGATCTCGAATAGAGATATACCCGATGTGCGATTCGCCCAATTAAGAGCAAT	108419
Qy	108420	ACGCGCCCGGTGTAGCAGATCGAAAGCTGCTCTCTTTTGGTCGACGTGAANAAC	108479
Db	108420	ACGCGCCCGGTGTAGCAGATCGAAAGCTGCTCTCTTTTGGTCGACGTGAANAAC	108479
Qy	108480	ACGTTGTGGGTGGGAAATTTACGTTTCAATTTACCCCGTCCGAATTTCAACAGTAA	108539
Db	108480	ACGTTGTGGGTGGGAAATTTACGTTTCAATTTACCCCGTCCGAATTTCAACAGTAA	108539
Qy	108540	CCGCACTGAGGACACACACACCTCGGAGCTGGCAGGTCCTCTCCAGTACGCTCCG	108599
Db	108540	CCGCACTGAGGACACACACACCTCGGAGCTGGCAGGTCCTCTCCAGTACGCTCCG	108599
Qy	108600	GCCACACCTGGGACCAACAGGTAGAGATACAGGAAACAGTACGTTATACCCCAAT	108659
Db	108600	GCCACACCTGGGACCAACAGGTAGAGATACAGGAAACAGTACGTTATACCCCAAT	108659
Qy	108660	ACTTTTACCCAGGTCCGGGATATCTCCGTCGTGTCGACATCCCTCATAGGCAACA	108719
Db	108660	ACTTTTACCCAGGTCCGGGATATCTCCGTCGTGTCGACATCCCTCATAGGCAACA	108719
Qy	108720	ACACGGGACATGCTCAGCAGGAGCCCTTAAGCTCAGCTCTCAGAGGCGTTAAACGG	108779
Db	108720	ACACGGGACATGCTCAGCAGGAGCCCTTAAGCTCAGCTCTCAGAGGCGTTAAACGG	108779
Qy	108780	TTGCGCGACGGGAGCGGTGCGGCCAGTTCTCGCAGCGAGGCCAGAAATCCCGCTCGAA	108839
Db	108780	TTGCGCGACGGGAGCGGTGCGGCCAGTTCTCGCAGCGAGGCCAGAAATCCCGCTCGAA	108839
Qy	108840	GGGCGCGGAGACACTCATTCAGTTAGTCCCAAGCTGGAAGTGAAGTGAAGGAAACGTTT	108899
Db	108840	GGGCGCGGAGACACTCATTCAGTTAGTCCCAAGCTGGAAGTGAAGTGAAGGAAACGTTT	108899
Qy	108900	AACTGCATCGAGACACAACCGCCCGCTTCATTTCTCCGAAACGGGACAGATCAAC	108959
Db	108900	AACTGCATCGAGACACAACCGCCCGCTTCATTTCTCCGAAACGGGACAGATCAAC	108959
Qy	108960	GCGTCTGTGGCAAAACAGGTAAACAGGGGAAACCGCTGGCAGATTAAGGTTTGCAC	109019
Db	108960	GCGTCTGTGGCAAAACAGGTAAACAGGGGAAACCGCTGGCAGATTAAGGTTTGCAC	109019
Qy	109020	ACGAGACAACCGCCCTGAAAGACACAACAAGATACCTGAGACACGCGCTCTGGGA	109079
Db	109020	ACGAGACAACCGCCCTGAAAGACACAACAAGATACCTGAGACACGCGCTCTGGGA	109079
Qy	109080	ACGCGCGTTAACTTAACTTCTGCTGCTGGGACAGCCACGCGCTCAGATACACTC	109139
Db	109080	ACGCGCGTTAACTTAACTTCTGCTGCTGGGACAGCCACGCGCTCAGATACACTC	109139
Qy	109140	AGCACCCACGCGTACGCTTACACAACCGCGCATATGCTGACGCGCATCTCAG	109199
Db	109140	AGCACCCACGCGTACGCTTACACAACCGCGCATATGCTGACGCGCATCTCAG	109199
Qy	109200	TGCGCGTTTAAAGTGGGTATTCGCGCTCCAGCGGATAGCAATCTCTTACAGGCGCTC	109259
Db	109200	TGCGCGTTTAAAGTGGGTATTCGCGCTCCAGCGGATAGCAATCTCTTACAGGCGCTC	109259
Qy	109260	TGAAGATGGGGAGAAATTAAGTCAAGCCATTGTGGGGTCTGCTCCAGCA	109319
Db	109260	TGAAGATGGGGAGAAATTAAGTCAAGCCATTGTGGGGTCTGCTCCAGCA	109319
Db	109260	TGAAGATGGGGAGAAATTAAGTCAAGCCATTGTGGGGTCTGCTCCAGCA	109319
Qy	109320	CCGAGCCCGTACGACAAAACACACAGTACATTCGGGGCATATGCCATTAAGCTATA	109379
Db	109320	CCGAGCCCGTACGACAAAACACACAGTACATTCGGGGCATATGCCATTAAGCTATA	109379
Qy	109380	GAGGCGCGGAGATCTTAAGCCCGGAGAACCATCATCAGCAACGATTTGGGCAAGTAA	109439
Db	109380	GAGGCGCGGAGATCTTAAGCCCGGAGAACCATCATCAGCAACGATTTGGGCAAGTAA	109439
Qy	109440	CCGCGCCCATGACAGGAGCTTCGCTTACAGCAGGTTAAGCAACGGCCGAGGCAATC	109499
Db	109440	CCGCGCCCATGACAGGAGCTTCGCTTACAGCAGGTTAAGCAACGGCCGAGGCAATC	109499
Qy	109500	CCCAATTTGATACGATTAATTTGTTAATTTGATATTCGCGCACGCTCTCGCGCCCAAT	109559
Db	109500	CCCAATTTGATACGATTAATTTGTTAATTTGATATTCGCGCACGCTCTCGCGCCCAAT	109559
Qy	109560	ATCCTTCAACTCCGACCCCGAAGGGCGGACGAGGCCGCTTCGCTCAACGCAACGAG	109619
Db	109560	ATCCTTCAACTCCGACCCCGAAGGGCGGACGAGGCCGCTTCGCTCAACGCAACGAG	109619
Qy	109620	GCCGTCGAGTACCCGTCAGGCAAAAACGTTCTTAAGAGGTTTAAACGTTTAC	109679
Db	109620	GCCGTCGAGTACCCGTCAGGCAAAAACGTTCTTAAGAGGTTTAAACGTTTAC	109679
Qy	109680	GCTCTTGGAGTACAGACCAAAACGTTAAACCTGTGCTGCTCCGTAAGTACGTCG	109739
Db	109680	GCTCTTGGAGTACAGACCAAAACGTTAAACCTGTGCTGCTCCGTAAGTACGTCG	109739
Qy	109740	GCATATGACCATGGAGCGTAAAGCTTAAGTCTCCGAGAAACACAGACGCTTAA	109799
Db	109740	GCATATGACCATGGAGCGTAAAGCTTAAGTCTCCGAGAAACACAGACGCTTAA	109799
Qy	109800	TTTCAATAAATCGTCTGGCCAGGACACGAGCAGTCTCTCAAGATACAGTCCGA	109859
Db	109800	TTTCAATAAATCGTCTGGCCAGGACACGAGCAGTCTCTCAAGATACAGTCCGA	109859
Qy	109860	ATTATATAGGACAGTTTTCCTCAACATGGGCATCGGCTCAGTGGCTTACACAAAAACA	109919
Db	109860	ATTATATAGGACAGTTTTCCTCAACATGGGCATCGGCTCAGTGGCTTACACAAAAACA	109919
Qy	109920	TTTCAAGCGTGGGCAAAACGTTGTATATTAATTAACAAACAGGGGAGGAGGATAGG	109979
Db	109920	TTTCAAGCGTGGGCAAAACGTTGTATATTAATTAACAAACAGGGGAGGAGGATAGG	109979
Qy	109980	CAGTCTCTAGTTTGTGAGCCAAACTATATACAAACTCGAGATATAGACGACAGC	110039
Db	109980	CAGTCTCTAGTTTGTGAGCCAAACTATATATACAAACTCGAGATATAGACGACAGC	110039
Qy	110040	GTCGTGCAAGGCGCAGGTGTCACACGGGAGCCGCCGCTTTAGCGTATAGGGAGCCCC	110099
Db	110040	GTCGTGCAAGGCGCAGGTGTCACACGGGAGCCGCCGCTTTAGCGTATAGGGAGCCCC	110099
Qy	110100	GTCCTGACACCTCTCAAGTCCAGGAGATTCACAGGAGTCCAGATTAAGAGCACTAA	110159
Db	110100	GTCCTGACACCTCTCAAGTCCAGGAGATTCACAGGAGTCCAGATTAAGAGCACTAA	110159
Qy	110160	ATCCGACAGCTCGTCAACTAAACGTTTCCGGAACCTCATCGTTAAAGATCTTTAGGT	110219
Db	110160	ATCCGACAGCTCGTCAACTAAACGTTTCCGGAACCTCATCGTTAAAGATCTTTAGGT	110219
Qy	110220	GCTGTGCGTGGCTCCCGTAAAAACCGGCTCGTGTATACGATTTGTAAATGACTGTTT	110279
Db	110220	GCTGTGCGTGGCTCCCGTAAAAACCGGCTCGTGTATACGATTTGTAAATGACTGTTT	110279
Qy	110280	TACGCGCTTAACTTGGGCTCAGAGCATGAGTCAAGTACAGTACGAGTACGCGGCTG	110339
Db	110280	TACGCGCTTAACTTGGGCTCAGAGCATGAGTCAAGTACAGTACGAGTACGCGGCTG	110339
Qy	110340	AGCAGATGACAGAGAAAGTTTAAATACTGACAGTAAATGCGGTTGAGCGCTGGA	110399
Db	110340	AGCAGATGACAGAGAAAGTTTAAATACTGACAGTAAATGCGGTTGAGCGCTGGA	110399

QY	110400	ATATATGTTGGGAACATATATTTTCATGTCTATCGGGGACAGAGGACTCGAACGCCAATTA	110459
Db	110400	ATATATGTTGGGAACATATATTTTCATGTCTATCGGGGACAGAGGACTCGAACGCCAATTA	110459
QY	110460	ATCGCACCGGAACATACAGTGTGACAGAGGTAAAGATGCTCACGGCCGGTACCGGCTTA	110519
Db	110460	ATCGCACCGGAACATACAGTGTGACAGAGGTAAAGATGCTCACGGCCGGTACCGGCTTA	110519
QY	110520	CACGGGACCAGGCACCCCTTCCAAATATTTTACGCTTTAAAAACGGGGCCCCCTTAAGTCGT	110579
Db	110520	CACGGGACCAGGCACCCCTTCCAAATATTTTACGCTTTAAAAACGGGGCCCCCTTAAGTCGT	110579
QY	110580	CCAACTCAGCTTAAAAAATCTCTACCCATTATGTGTGTCCTCGGTGACACTGTGAGACCTCA	110639
Db	110580	CCAACTCAGCTTAAAAAATCTCTACCCATTATGTGTGTCCTCGGTGACACTGTGAGACCTCA	110639
QY	110640	TGAGACACTGGGCCCTCTCGGGGGGACCTGTGAAACAATCTTCCTCCCGGAGACCCGG	110699
Db	110640	TGAGACACTGGGCCCTCTCGGGGGGACCTGTGAAACAATCTTCCTCCCGGAGACCCGG	110699
QY	110700	ACGGAGCTTTTAAACAGCCCGGATTTAATTCACACTCAGAGACTCTCTAACACCCGCCCTCAT	110759
Db	110700	ACGGAGCTTTTAAACAGCCCGGATTTAATTCACACTCAGAGACTCTCTAACACCCGCCCTCAT	110759
QY	110760	CGTGGAGGGTGTGTAGCCCTCTCTGTTCATCTCTGTGTCGGACATTTCCACCCCGGACTCTT	110819
Db	110760	CGTGGAGGGTGTGTAGCCCTCTCTGTTCATCTCTGTGTCGGACATTTCCACCCCGGACTCTT	110819
QY	110820	TCTTGAAGACTACGAGGCTGTGTGCTCAGCTACCTGACCTATACGGCCCCCGCATCATGAGACG	110879
Db	110820	TCTTGAAGACTACGAGGCTGTGTGCTCAGCTACCTGACCTATACGGCCCCCGCATCATGAGACG	110879
QY	110880	CTACCCCTATGGTGGCTGCGACACTTTTGGAACTAACGACAGTACTTCCCGCAATGGG	110939
Db	110880	CTACCCCTATGGTGGCTGCGACACTTTTGGAACTAACGACAGTACTTCCCGCAATGGG	110939
QY	110940	TGAAGATATGGGCATATACACCGGCCAAAGCATCTCGGAATCGACGCTCAGCTGCAT	110999
Db	110940	TGAAGATATGGGCATATACACCGGCCAAAGCATCTCGGAATCGACGCTCAGCTGCAT	110999
QY	111000	TCTTGGCAACCGCGTGTTCGACCCATCGACAGAAACAAATATCTCACATCTCATTT	111059
Db	111000	TCTTGGCAACCGCGTGTTCGACCCATCGACAGAAACAAATATCTCACATCTCATTT	111059
QY	111060	TAAATTTTTTACAAACCGAGTTTATTTAGGGGCATGTTAGAAGGCACGATTTCCGGGATCGT	111119
Db	111060	TAAATTTTTTACAAACCGAGTTTATTTAGGGGCATGTTAGAAGGCACGATTTCCGGGATCGT	111119
QY	111120	TCTGTTTTAAACGTCGTGGCGCGGACAGAAAGAGACCAACAACCTACCGTGGCGT	111179
Db	111120	TCTGTTTTAAACGTCGTGGCGCGGACAGAAAGAGACCAACAACCTACCGTGGCGT	111179
QY	111180	GTTTGTCCGTTGGCGCGGAAATCATCACCAACCGGGATTAACGCTATACCCGAGACTG	111239
Db	111180	GTTTGTCCGTTGGCGCGGAAATCATCACCAACCGGGATTAACGCTATACCCGAGACTG	111239
QY	111240	AAGAGGCGTTCAATCTCAGAAACGCGGAGAAAGCCACGCTCTCGGCGTCTTTTCGG	111299
Db	111240	AAGAGGCGTTCAATCTCAGAAACGCGGAGAAAGCCACGCTCTCGGCGTCTTTTCGG	111299
QY	111300	CAAGCTGGGGAGAAATCCAGCTTCTTGCTCGGACACAAACAGAGAGATATACCATTTAC	111359
Db	111300	CAAGCTGGGGAGAAATCCAGCTTCTTGCTCGGACACAAACAGAGAGATATACCATTTAC	111359
QY	111360	AACCTCGCGCTTCCCAACCCGAGAAAGTGTGACCAATTCACAGGGCCCCCTGCTATGC	111419
Db	111360	AACCTCGCGCTTCCCAACCCGAGAAAGTGTGACCAATTCACAGGGCCCCCTGCTATGC	111419
QY	111420	ACCCAGCGTCAACCTAAAAACAAAAACACACGCGCATCATATCGTTTATGCGAGT	111479
Db	111420	ACCCAGCGTCAACCTAAAAACAAAAACACACGCGCATCATATCGTTTATGCGAGT	111479

QY	111480	GCTCTGGCGGACACACC	GGAGCGCCGGTCTGAAA	ATCTCGCTCCGACATTTCTGG	111539	
Db	111480	GCTCTGGCGGACACACC	GGAGCGCCGGTCTGAAA	ATCTCGCTCCGACATTTCTGG	111539	
QY	111540	AAACATGGAAAAACAACG	TTAAGCTGTCAATTCGCA	TAATCTCTAATACGATCCGG	111599	
Db	111540	AAACATGGAAAAACAACG	TTAAGCTGTCAATTCGCA	TAATCTCTAATACGATCCGG	111599	
QY	111600	ACTCACTGTCAACAGCTG	CGCGAGAACATCTCGCGG	CTAATTTAAACGGTGTGGCAC	111659	
Db	111600	ACTCACTGTCAACAGCTG	CGCGAGAACATCTCGCGG	CTAATTTAAACGGTGTGGCAC	111659	
QY	111660	AAGAAATCCACAAGCAT	TTTTTTTTTTGGACCGG	TGTGCTCTGGAACACTCTGC	111719	
Db	111660	AAGAAATCCACAAGCAT	TTTTTTTTTTGGACCGG	TGTGCTCTGGAACACTCTGC	111719	
QY	111720	GTCGGCGGGTTTATTTA	ATGAGCCCACTCCGGA	AGATTAAGAGCTCAAAAGCT	GTGTC	111779
Db	111720	GTCGGCGGGTTTATTTA	ATGAGCCCACTCCGGA	AGATTAAGAGCTCAAAAGCT	GTGTC	111779
QY	111780	TGGCAACCGGAGAGTT	CTCTAGACTGCAACAG	ATATTTAGCTGCGAGACTT	ACAGACC	111839
Db	111780	TGGCAACCGGAGAGTT	CTCTAGACTGCAACAG	ATATTTAGCTGCGAGACTT	ACAGACC	111839
QY	111840	TGGCGGCTCTCTTTA	AGGGGCTCAACTGCGC	CAAAATGCGCAAAAC	CAGCTGTGAGA	111899
Db	111840	TGGCGGCTCTCTTTA	AGGGGCTCAACTGCGC	CAAAATGCGCAAAAC	CAGCTGTGAGA	111899
QY	111900	TAAATCGGTAACGTG	GAATTTCAATGCGCTG	ACACAACTCAAACTACCC	ATCCGCTTC	111959
Db	111900	TAAATCGGTAACGTG	GAATTTCAATGCGCTG	ACACAACTCAAACTACCC	ATCCGCTTC	111959
QY	111960	AAACCTCCAACTAT	TACATTTAATCTTCA	GAAGCGCAGCAGACAA	TGCGCAAAACAGCCCA	112019
Db	111960	AAACCTCCAACTAT	TACATTTAATCTTCA	GAAGCGCAGCAGACAA	TGCGCAAAACAGCCCA	112019
QY	112020	GAAATGATTTGCGCT	GAGCGCGGTACGAC	CTAAGCGTCAAGCGAC	CGGAGCGGCCCC	112079
Db	112020	GAAATGATTTGCGCT	GAGCGCGGTACGAC	CTAAGCGTCAAGCGAC	CGGAGCGGCCCC	112079
QY	112080	ACTCCACGGGACCGG	ATCCAGGACGGAGCG	AGCTGCAAAAGCGAA	ATATGCACTGGAAAA	112139
Db	112080	ACTCCACGGGACCGG	ATCCAGGACGGAGCG	AGCTGCAAAAGCGAA	ATATGCACTGGAAAA	112139
QY	112140	AGTTAGTTTCAGACA	CGCAGTTTTTTTTCT	GCCCTAAAGCGCGC	CAAGAGCTGGGGATGG	112199
Db	112140	AGTTAGTTTCAGACA	CGCAGTTTTTTTTCT	GCCCTAAAGCGCGC	CAAGAGCTGGGGATGG	112199
QY	112200	ACTTTTAAAGAGAA	TGGGGACCCCGATAT	GCACTCAAAAGTCCG	TATATGTTCCGCTTAA	112259
Db	112200	ACTTTTAAAGAGAA	TGGGGACCCCGATAT	GCACTCAAAAGTCCG	TATATGTTCCGCTTAA	112259
QY	112260	ACCTAAAAACCAT	TCGCCCCGGGTGGT	GTCTCTATCATATTCG	GACACTCGTCAAA	112319
Db	112260	ACCTAAAAACCAT	TCGCCCCGGGTGGT	GTCTCTATCATATTCG	GACACTCGTCAAA	112319
QY	112320	ACATGGGGTTCAAC	TGTTCTGTGTGAC	AGCCCAACTCAGAG	TGAGGGTGTCTGTGGACG	112379
Db	112320	ACATGGGGTTCAAC	TGTTCTGTGTGAC	AGCCCAACTCAGAG	TGAGGGTGTCTGTGGACG	112379
QY	112380	CAACGCGCTCGG	CGAAGATTCGCGC	AGAGAAAAACAG	CAAGTGTTCAGTGGCGTTAA	112439
Db	112380	CAACGCGCTCGG	CGAAGATTCGCGC	AGAGAAAAACAG	CAAGTGTTCAGTGGCGTTAA	112439
QY	112440	CCTTTTACCAACAC	CGCCGAAAAAGGT	CTGCACACAAGGG	CTTTTACGTGTCTCTCA	112499
Db	112440	CCTTTTACCAACAC	CGCCGAAAAAGGT	CTGCACACAAGGG	CTTTTACGTGTCTCTCA	112499
QY	112500	GCCACTCCATGGA	AGTCGTTAGAAAAAG	CTTACAGCAACCCG	GGTGTCTACAGCCACAC	112559
Db	112500	GCCACTCCATGGA	AGTCGTTAGAAAAAG	CTTACAGCAACCCG	GGTGTCTACAGCCACAC	112559
QY	112560	TAGTCTCTAAAAAC	CTTTGGCCACGAT	CTTTTACATTTTAC	AGATGCAATGCCGATGAGA	112619

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Db 112620 GACTCGACCTCTGGGGGCTTTCCACACTAGAGACCTACACCTGGGGGAAACAGTCTGC 112679
Qy 112680 GACTCATTTAGCAACCTTCCAAATTTATGACATTAAGGCTGATCAACCAACGCT 112739
Db 112680 GACTCATTTAGCAACCTTCCAAATTTATGACATTAAGGCTGATCAACCAACGCT 112739
Qy 112740 ACATTAATGAAGTTTAACCTCGCCGACGGACACCGCAACCGTGAGCGTTCTGTACAA 112799
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QY	117000	AACGGATGTAAATTAATTCAAACCTATATAATTCCACCCTGTTAGGGGATCCACGT	117059
Db	117000	AACGGATGTAAATTAATTCAAACCTATATAAAATTCACCCTGTTAGGGGATCCACGT	117059
QY	117060	GTACCTGAATTAATACGGGATACAGAGCTGTAGCTTGGTAATGGGATACCAAGCTGGAGTG	117119
Db	117060	GTACCTGAATTAATACGGGATACAGAGCTGTAGCTTGGTAATGGGATACCAAGCTGGAGTG	117119
QY	117120	ACTCATACCATTGGATTAATATCCAGGGATACAGCTGTAGCTGGTAACGGGTACAG	117179
Db	117120	ACTCATACCATTGGATTAATATCCAGGGATACAGCTGTAGCTGGTAACGGGTACAG	117179
QY	117180	GCTGAGTGACTCATACCATGGGATTAATACAGGGATACAGGCTGTAGCTGGTAT	117239
Db	117180	GCTGAGTGACTCATACCATGGGATTAATACAGGGATACAGGCTGTAGCTGGTAT	117239
QY	117240	GGGTACACAGGCTGGAGTGACTATACCATGGGATTAATATACAGGGATACAGGCTGTAG	117299
Db	117240	GGGTACACAGGCTGGAGTGACTATACCATGGGATTAATATACAGGGATACAGGCTGTAG	117299
QY	117300	TTCGGTATGGGTACCAAGGCTGGAGTACTCATACCATGGGATTAATATCCAGGGATACA	117359
Db	117300	TTCGGTATATGGGTACCAAGGCTGGAGTACTCATACCATGGGATTAATATCCAGGGATACA	117359
QY	117360	GGCTGTAGGTTGCGTAATTTAAATCAACTATATAATTTTACCCTGGTGGGGAATCCCGTT	117419
Db	117360	GGCTGTAGGTTGCGTAATTTAAATCAACTATATAATTTTACCCTGGTGGGGAATCCCGTT	117419
QY	117420	TGTACTGAATTAATATAGGAATACAGGCTGTAGAAATCGTATATGGAAACCAAGGCTGTAG	117479
Db	117420	TGTACTGAATTAATATAGGAATACAGGCTGTAGAAATCGTATATGGAAACCAAGGCTGTAG	117479
QY	117480	GACTAGGCTGGGATGACTCATATCCATGGAATTCATTAACAAGGAAATATATAAGAAATA	117539
Db	117480	GACTAGGCTGGGATGACTCATATCCATGGAATTCATTAACAAGGAAATATATAAGAAATA	117539
QY	117540	TATATATATATATAGGGAAGCTGTGAACCAAAACCCAAATCGCGGATTTGGCTGTTTGG	117599
Db	117540	TATATATATATATAGGGAAGCTGTGAACCAAAACCCAAATCGCGGATTTGGCTGTTTGG	117599
QY	117600	CCAACACAGAGGAATTCCTCGATGTGACAGCGGACTGCGGCATATGTTTCGAGCAAT	117659
Db	117600	CCAACACAGAGGAATTCCTCGATGTGACAGCGGACTGCGGCATATGTTTCGAGCAAT	117659
QY	117660	TTTGATTTACAGAAAGCGCGGCAATTCGCAACCGGAATCTCGGACGAGCAAGCAAAAGATA	117719
Db	117660	TTTGATTTACAGAAAGCGCGGCAATTCGCAACCGGAATCTCGGACGAGCAAGCAAAAGATA	117719
QY	117720	GACGGCCGCGGCGACCAATGGCCGCCGGGTAGTTGATTTGAGCGGCTTGGCCGCGCAA	117779
Db	117720	GACGGCCGCGGCGACCAATGGCCGCCGGGTAGTTGATTTGAGCGGCTTGGCCGCGCAA	117779
QY	117780	TGGGAAAGTCCCTTCGCGGCGGCCCTTATCCCTGGCTTAAAGGATTAACGCCCTATAA	117839
Db	117780	TGGGAAAGTCCCTTCGCGGCGGCCCTTATCCCTGGCTTAAAGGATTAACGCCCTATAA	117839
QY	117840	CATGCGTGGCGGTGACACCGCGCGCAAAACCCCGCGCGCGGTTCGGCTGACCTCGCC	117899
Db	117840	CATGCGTGGCGGTGACACCGCGCGCGCAAAACCCCGCGCGCGGTTCGGCTGACCTCGCC	117899
QY	117900	GCGACCCCGCGGCTCATATGGGCAACATATGGGTGATGGGACACGCGGCAACATTATTC	117959
Db	117900	GCGACCCCGCGGCTCATATGGGCAACATATGGGTGATGGGACACGCGGCAACATTATTC	117959
QY	117960	GCTGACCGCGGAGACACCCCGCGCAAAAGACGGGCGATGGGTACGCCGCGGACATAC	118019
Db	117960	GCTGACCGCGGAGACACCCCGCGCAAAAGACGGGCGATGGGTACGCCGCGGACATAC	118019
QY	118020	GAAACATTTTCAATATACCCCAAGTCGACCCCGCGGCGCAAAATCTGGGGCCCATATGTTGG	118079

Db	118020	GAAGACATTTTTCATTAACCCCGAGTGCAGCCCGCGGCCCAAAATCTG66GCGCATGTGTGC	118079
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VERSION AF210726.1 GI:7329990
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ORGANISM Macaca mulatta rhadinovirus 26-95
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
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REFERENCE 1 (bases 1 to 130733)
AUTHORS Alexander, L., Denekamp, L., Knapp, A., Auerbach, M.R., Damanla, B. and
Desrosters, R.C.
TITLE The primary sequence of rhesus monkey rhadinovirus isolate 26-95:
sequence similarities to Kaposi's sarcoma-associated herpesvirus
and rhesus monkey rhadinovirus isolate 17577
JOURNAL J. Virol. 74 (7), 3388-3398 (2000)
MEDLINE 20173730
PUBMED 10708456
REFERENCE 2 (bases 1 to 130733)
AUTHORS Alexander, L., Denekamp, L.M., Knapp, A., Auerbach, M., Czajak, S.,
Damanla, B. and Desrosters, R.C.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1999) Microbiology, New England Regional Primate
Research Center, One Pinehill Dr, Southborough, MA 01772, USA

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QY	81780	TCTCGCTATTTCCATACGAGACGAGTATGCAAGTTACTTTGTTCCACGGGACCCGGCAACGG	81839
Db	79786	TCTCGCTATTTCCATACGAGACGAGTATGCAAGTTACTTTGTTCCACGGGACCCGGCAACGG	79825
QY	81840	TCTTGTCTCATTTCTCCCAAAACCAATCCGGGTACTGCGCCGATTCGACCCGGGCAACA	81899
Db	79826	TCTTGTCTCATTTCTCCCAAAACCAATCCGGGTACTGCGCCGATTCGACCCGGGCAACA	79885
QY	81900	GCGAGGCCCTGATATGCACTCAGCGCGCGCATTCGCGGATATGGAGGCTTGACGGATC	81959
Db	79886	GCGAGGCCCTGATATGCACTCAGCGCGCGCATTCGCGGATATGGAGGCTTGACGGATC	79945
QY	81960	AGCTCTCAAGACAATAATGAAACCCCTTGCCTTACAGCGCACAGTTCATTAATGTATCTAAAT	82019
Db	79946	AGCTCTCAAGACAATAATGAAACCCCTTGCCTTACAGCGCACAGTTCATTAATGTATCTAAAT	80005
QY	82020	GACGAGTCATATGTGCCCTTAACATATGCGTAAGACTACTCAAACTGTGCTTAAGGGAGA	82079
Db	80006	GACGAGTCATATGTGCCCTTAACATATGCGTAAGACTACTCAAACTGTGCTTAAGGGAGA	80065
QY	82080	GTGACAAACACCTGGCACTCAATTAATAATTTGAGTTCGGGCAATGACCGGTCCCTCCCTC	82139
Db	80066	GTGACAAACACCTGGCACTCAATTAATAATTTGAGTTCGGGCAATGACCGGTCCCTCCCTC	80125
QY	82140	TGTGTAGTATTAAACCCCATATGCGCACATATTCAAGAACAAACCACTCCAGATTACAACAA	82199
Db	80126	TGTGTAGTATTAAACCCCATATGCGCACATATTCAAGAA--CAAACTCCAGATTACAACAA	80183
QY	82200	ACTTTATTACAGATAGAAAGGCGCTCAGCGGCTCAAAAACCGGTGCGGCGCACAGGTTAA	82259
Db	80184	ACTTTATT--CAGATAGAAAGGCGCTCAGCGGCTCAAAAACCGGTGCGGCGCACAGGTTAA	80242
QY	82260	CATTAAACATTATAGCGGGGAGACAAGCCCGGCACACACACTCTGTGGCACAGCTGAATTATT	82319
Db	80243	CATTAAACATTATAGCGGGGAGACAAGCCCGGCACACACACTCTGTGGCACAGCTGAATTATT	80302
QY	82320	AGCGGTACAGTCTTTTGCACCTCGCGCTCGGGTGTAGATACGCCCAAAATATAGTTAA	82379
Db	80303	AGCGGTACAGTCTTTTGCACCTCGCGCTCGGGTGTAGATACGCCCAAAATATAGTTAA	80362
QY	82380	ACACAAGCTTGTGAAGGCGCGCTCCGTCCGGAGATGTTTGGCCATGGCTGTCTATATAG	82439
Db	80363	ACACAAGCTTGTGAAGGCGCGCTCCGTCCGGAGATGTTTGGCCATGGCTGTCTATATAG	80422
QY	82440	TCAACCAAGTTAAATGACAGACAGCGGTTGGGCGACAGACAGGACCGCAACCGCCCCGTA	82499
Db	80423	TCAACCAAGTTAAATGACAGACAGCGGTTGGGCGACAGACAGGACCGCAACCGCCCCGTA	80482
QY	82500	GATTTGCAGGTTCCCTTGAACGAAAGCGCAGGGGAATCCCAACACATCTAATGTAAATGGCCG	82559
Db	80483	GATTTGCAGGTTCCCTTGAACGAAAGCGCAGGGGAATCCCAACACATCTAATGTAAATGGCCG	80542
QY	82560	GAGGGGTGCGCCCAAAAGCGCAACCCGGCGCAAAAAGATCTTTATTCAGAGAAAGCGCAAGCC	82619

Db 80543 GAGGGTCGGCCCAAAACGCAACCCGGCCAAAAGTCTTTATCCAGGAAGCGCAACGCC 80602
OY 82620 TCGGCTGAAAGCTCTGCTAAGTGGAGCTTGGAAATCCGGAACAGAGTGCCTGCTGGAGATC 82679
Db 80603 TCGGCTGAAAGCTCTGCTAAGTGGAGCTTGGAAATCCGGAACAGAGTGCCTGCTGGAGATC 80662
OY 82680 GGTGGCGGCGCATATGTGCCCTTGAGGGCGACGTTGGCAATGGAGACACAGGATGCCG 82739
Db 80663 GGTGGCGGCGCATATGTGCCCTTGAGGGCGACGTTGGCAATGGAGAGCGACAGGATGCCG 80722
OY 82740 TTGGAGGATTCAGTCCACACTTCACCACTGTGTGCCCAATATGTAATAACATTAATAGCT 82799
Db 80723 TTGGAGGATTCAGTCCACACTTCACCACTGTGTGCCCAATATGTAATAACATTAATAGCT 80782
OY 82800 AACATCCAACTGTTTACACCCCGGCTCCACGCGACAGTGTATCCGAACACCGCGCGCA 82859
Db 80783 AACATCCAACTGTTTACACCCCGGCTCCACGCGACAGTGTATCCGAACACCGCGCGCA 80842
OY 82860 AACGGAACAACTTATTCACGGCTCTCTGGCGACACCCCGGTATACATAGCAGTAGTCCG 82919
Db 80843 AACGGAACAACTTATTCACGGCTCTCTGGCGACACCCCGGTATACATAGCAGTAGTCCG 80902
OY 82920 GAGGCGTGTATCGCAACAGACACAGCCTCAGGATATGTAAGGGAATGATTCGG 82979
Db 80903 GAGGCGTGTATCGCAACAGACACAGCCTCAGGATATGTAAGGGAATGATTCGG 80962
OY 82980 CATCTGTCCGATATGAGATCGAAGGTTGTCTTATGTTAGACAGTCCGACACAGGTTTGA 83039
Db 80963 CATCTGTCCGATATGAGATCGAAGGTTGTCTTATGTTAGACAGTCCGACACAGGTTTGA 81022
OY 83040 CATCTGTCCGATATGAGATCGAAGGTTTGTTCATCTTATGAGCGTTATATTCCTCCGA 83099
Db 81023 CATCTGTCCGATATGAGATCGAAGGTTTGTTCATCTTATGAGCGTTATATTCCTCCGA 81082
OY 83100 GCGCGGTGCAAGATGCGCTGATCGACAGTAGTCAATATAATGTTTTTTCGCGCTCC 83159
Db 81083 GCGCGGTGCAAGATGCGCTGATCGACAGTAGTCAATATAATGTTTTTTCGCGCTCC 81142
OY 83160 TCGACTCTCTGCTCCCTCTGTCTGTGTATTCACAGGATCGGATTAAGTTCTTTCTCTCG 83219
Db 81143 TCGACTCTCTGCTCCCTCTGTCTGTGTATTCACAGGATCGGATTAAGTTCTTTCTCTCG 81202
OY 83220 TCAACCCACCGAATCCGGGATGAGAGCCTGTCTGACAGATTTCCACCGAGCATCTCTGA 83279
Db 81203 TCAACCCACCGAATCCGGGATGAGAGCCTGTCTGACAGATTTCCACCGAGCATCTCTGA 81262
OY 83280 AAGCTGATGATGTTGGTCACTGAGACCGGCGCTCCATATCTCGCGCGGTGACAGCGCA 83339
Db 81263 AAGCTGATGATGTTGGTCACTGAGACCGGCGCTCCATATCTCGCGCGGTGACAGCGCA 81322
OY 83340 TCGCAAACTTGTCCAAAGTTACCTCTGACAAAGACAGCTGCAACCTCAGACAGACTAGCGG 83399
Db 81323 TCGCAAACTTGTCCAAAGTTACCTCTGACAAAGACAGCTGCAACCTCAGACAGACTAGCGG 81382
OY 83400 TCGCAAAAGGGAACCTGTGTGTAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 83459
Db 81383 TCGCAAAAGGGAACCTGT 81442
OY 83460 GTCTGTACACTCTGTGGGCGGGAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 83519
Db 81443 GTCTGTACACTCTGTGGGCGGGAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 81502
OY 83520 GTCTGTACACTCTGTGGGCGGGAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 83579
Db 81503 GTCTGTACACTCTGTGGGCGGGAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 81562
OY 83580 GGGGCAACAGGCTGT 83639
Db 81563 GGGGCAACAGGCTGT 81622
OY 83640 GTCCCGAGAGGCGGCAAGCTTCTCATGAAGCCATGAAGTTAAATTTCTGTGTGTGTGT 83699

Db 81623 GTCCCGAGACGGGCGCAAGCTTCTCATGAAGCCATGAAGTTAAATTTCTGTGTGTGTGT 81682
OY 83700 AGAGGAACATGACCTCTCTGT 83759
Db 81683 AGAGGAACATGACCTCTCTGT 81742
OY 83760 GGGTTTCCCTGT 83819
Db 81743 GGGTTTCCCTGT 81802
OY 83820 CCTGTGTATACGAGACAGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 83879
Db 81803 CCTGTGTATACGAGACAGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 81862
OY 83880 CACGATCTGAGATGGAACACAGACAGTGAACCCGCTGCATAGAAACACAGATGACCG 83939
Db 81863 CACGATCTGAGATGGAACACAGACAGTGAACCCGCTGCATAGAAACACAGATGACCG 81922
OY 83940 GATGGGGAACCGGGCGGATGCAACGAACACCTCTCCGATCTTGGAGAGTGTATCCA 83999
Db 81923 GATGGGGAACCGGGCGGATGCAACGAACACCTCTCCGATCTTGGAGAGTGTATCCA 81982
OY 84000 GTGCGGAACGCGCAAAATATAACACCTGATTTCTCAACCGCAAAACGCGCAATTTGAT 84059
Db 81983 GTGCGGAACGCGCAAAATATAACACCTGATTTCTCAACCGCAAAACGCGCAATTTGAT 82042
OY 84060 GAGGACGCGGCTCTCTGGACCCGAGACAGATGTGTCTGGGCGTACGCTGATCTTCGTCG 84119
Db 82043 GAGGACGCGGCTCTCTGGACCCGAGACAGATGTGTCTGGGCGTACGCTGATCTTCGTCG 82102
OY 84120 GAGGACGCAACGTGGGCAAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 84179
Db 82103 GAGGACGCAACGTGGGCAAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 82162
OY 84180 ACACCTGTCTCAAAATATTTATATATCCCTTCAGAGTTCATCAAGATACAGCATAC 84239
Db 82163 ACACCTGTCTCAAAATATTTATATATCCCTTCAGAGTTCATCAAGATACAGCATAC 82222
OY 84240 ATCCAGATATCAATCAAGGTTTATCCCGGAAGGCGTCCAGCGCGACCGTCTCCGCA 84299
Db 82223 ATCCAGATATCAATCAAGGTTTATCCCGGAAGGCGTCCAGCGCGACCGTCTCCGCA 82282
OY 84300 CGACCCCATGTCTCACTTCTTGAATCCAGATTCCTCCCTCAAAACCCCTCAAAATATCGTC 84359
Db 82283 CGACCCCATGTCTCACTTCTTGAATCCAGATTCCTCCCTCAAAACCCCTCAAAATATCGTC 82342
OY 84360 TCTTACACTCTAGCAGAGTTTCCATCTAGCCCAACCTGACAGACCTCTCTCCAGCAGTAG 84419
Db 82343 TCTTACACTCTAGCAGAGTTTCCATCTAGCCCAACCTGACAGACCTCTCTCCAGCAGTAG 82402
OY 84420 CGACAAAGGCTGAGGATTCAGCTGCGCCCTTCTTCCAGACAGCTTAAGCTTTTCTTC- 84478
Db 82403 CGACAAAGGCTGAGGATTCAGCTGCGCCCTTCTTCCAGACAGCTTAAGCTTTTCTTC- 82462
OY 84479 CCTCATCGCAACAGTGTAGGTGTGAATAGTTTTCGTTGAGATGAGTGAAGGTCACAG 84538
Db 82463 CCTCATCGCAACAGTGTAGGTGTGAATAGTTTTCGTTGAGATGAGTGAAGGTCACAG 82522
OY 84539 ATCTAGATGAGCTGTAGTGTAGATCTGATTCGATTCGATTCGATTCGATTCGATTCGAT 84598
Db 82523 ATCTAGATGAGCTGTAGTGTAGATCTGATTCGATTCGATTCGATTCGATTCGATTCGAT 82582
OY 84599 GCGCGGATACGAGTACTTTTCCCTGATGATATTTTGAAGGCTCTATCTCTCAAAAC 84658
Db 82583 GCGCGGATACGAGTACTTTTCCCTGATGATATTTTGAAGGCTCTATCTCTCAAAAC 82642
OY 84659 GTGCACTGGCTTGAAGACAGCTCATTTTCGCCACTTCCTCATTTTAAACCATATAT 84718
Db 82643 GTGCACTGGCTTGAAGACAGCTCATTTTTCGCCACTTCCTCATTTTAAACCATATAT 82702
OY 84719 GTTCTGTGTCTACGTTTGTGACGTCACCTGCAACAGACAGGTTGATGATCCGAGTTTC 84778
Db 82703 GTTCTGTGTCTACGTTTGTGACGTCACCTGCAACAGACAGGTTGATGATCCGAGTTTC 82762

QY	84779	GCCTCTCAGTGCCTTGACAAACACTGGCCACAGATTAAAGATGAGCAAAAGCCATAG	84838
Db	82763	GCTTCCTCAGTGCCTTGACAAACACTGGCCACAGATTAAAGATGAGCAAAAGCCATAG	82822
QY	84839	CTTTCGATTTCAGTCAACCGGACAGTGGTGGACATTGAAAGATTGGCCACACAT	84898
Db	82823	CTTTCGATTTCAGTCAACCGGACAGTGGTGGACATTGAAAGATTGGCCACACAT	82882
QY	84899	TCAGCTGTGCATCTACMACCCCGACCAATATGGACGTCGACATTCCCTATCAACACTA	84958
Db	82883	TCAGCTGTGCATCTACMACCCCGACCAATATGGACGTCGACATTCCCTATCAACACTA	82942
QY	84959	GTACAGAAAAACGAAACCAACAGCCAGGTGACATTTCCAGGTTAAGAAATTTATTAA	85018
Db	82943	GTACAGAAAAACGAAACCAACAGCCAGGTGACATTTCCAGGTTAAGAAATTTATTAA	83002
QY	85019	GCCGCGCAATCCATCTAACAAAAACAGCAAAATGTTTATCAAGGTGCGCTATAGATTTCGT	85078
Db	83003	GCCGCGCAATCCATCTAACAAAAACAGCAAAATGTTTATCAAGGTGCTATAGATTTCGT	83062
QY	85079	TTGATTAAACAATATAGATAGTGGAGCCTCCAGAGTTTCGCTCCGCCACGGAAACA	85138
Db	83063	TTGATTAAACAATATAGATAGTGGAGCCTCCAGAGTTTCGCTCCGCCACGGAAACA	83122
QY	85139	ACCCGAAACCCAGAGTTTACAAAGGCGGGGGGGACCCGTTGCGCGGGGAGGGGA	85198
Db	83123	ACCCGAAACCCAGAGTTTACAAAGGCGGGGGGGACCCGTTGCGCGGGGAGGGGA	83182
QY	85199	CCTGGCCATATCAAGCAAAATACGATCAGTGTCAATATGGCCACACGTGCATCCGGTGA	85258
Db	83183	CCTGGCCATATCAAGCAAAATACGATCAGTGTCAATATGGCCACACGTGCATCCGGTGA	83242
QY	85259	GGCAGATATGGGCAAACTGTACGGTTCCACGGTATTTCCCTGAACACACAGTTTAGAC	85318
Db	83243	GGCAGATATGGGCAAACTGTACGGTTCCACGGTATTTCCCTGAACACACAGTTTAGAC	83302
QY	85319	CCCAGTAATCGTGAACTAATTTCCCTGCTGGTGTGTCAGAAATATATTCATCCACAG	85378
Db	83303	CCCAGTAATCGTGAACTAATTTCCCTGCTGGTGTGTCAGAAATATATTCATCCACAG	83362
QY	85379	CCATTTCAAAGCGCTCTCGAGTCTCTGACACACACAGCACTACGTGCTTGATGATCGG	85438
Db	83363	CCATTTCAAAGCGCTCTCGAGTCTCTGACACACACAGCACTACGTGCTTGATGATCGG	83422
QY	85439	AGGAAACACAGCGCTGAAAGGGGTCCATTCACAAACACACAGGTGTCGCCGCTTATTTGT	85498
Db	83423	AGGAAACACAGCGCTGAAAGGGGTCCATTCACAAACACACAGGTGTCGCCGCTTATTTGT	83482
QY	85499	TGCTTTTGAAGATAGCCTGATTCCTGCCCCGGTGGCTGTCAACAGCTACGCCGCAATTG	85558
Db	83483	TGCTTTTGAAGATAGCCTGATTCCTGCCCCGGTGGCTGTCAACAGCTACGCCGCAATTG	83542
QY	85559	CCCCTACTAATTAATCTTTTATGCAATGACCCCAATGGATGGCGGGCAGATGGGGCAGC	85618
Db	83543	CCCCTACTAATTAATCTTTTATGCAATGACCCCAATGGATGGCGGGCAGATGGGGCAGC	83602
QY	85619	ACACGCCATTAAGTCTGGCGGCGGAGAGGCCGGAAGATACGCTGATCGTCTGCTGCGC	85678
Db	83603	ACACGCCATTAAGTCTGGCGGCGGAGAGGCCGGAAGATACGCTGATCGTCTGCTGCGC	83662
QY	85679	GTCGTGTCAATCTTGATAGACCTTCCCGATACCGTCTCTGTGATCATCTTAGGAGGGTCC	85738
Db	83663	GTCGTGTCAATCTTGATAGACCTTCCCGATACCGTCTCTGTGATCATCTTAGGAGGGTCC	83722
QY	85739	CGAAAGGCGGTGAAGCATTCCTCCGGCCGAGCATGGCAAAACCGCATTTTGCGAATCAAG	85798
Db	83723	CGAAAGGCGGTGAAGCATTCCTCCGGCCGAGCATGGCAAAACCGCATTTTGCGAATCAAG	83782
QY	85799	GGGAGGCGGCACACCGCGGGGACACACCGGACAAACATCTCTTGCGATGAAGCAACT	85858
Db	83783	GGGAGGCGGCACACCGCGGGGACACACCGGACAAACATCTCTTGCGATGAAGCAACT	83842

QY	85859	AAAGACCAAGCGCGCTGACAGCGAAATTGATGCGTGAAGGAATTCTTATCTTCTCTCAAAAGTA	85918
Db	83843	AAAGACCAAGCGCGCTGACAGCGAAATTGATGCGTGAAGGAATTCTTATCTTCTCTCAAAAGTA	839020
QY	85919	CTTCTCTCTTCTTACGGCTCTCCAGACAGGGCCCCCTGGCTTGACACAGCCTGCTCTCTCC	85978
Db	83903	CTTCTCTCTTCTTACGGCTCTCCAGACAGGGCCCCCTGGCTTGACACAGCCTGCTCTCTCC	83966
QY	85979	AGACGGCAGTGGGATGTGTCTTAACATCACAGTAGGAGATCATATAGTGTGACCGCGCGGTG	86038
Db	83963	AGACGGCAGTGGGATGTGTCTTAACATCACAGTAGGAGATCATATAGTGTGACCGCGCGGTG	84022
QY	86039	ATAATCATTAATGGGAAACACGCGTGTGACTGCCAACACAGCCTGCTCTTTGGCTC	86098
Db	84023	ATAATCATTAATGGGAAACACGCGTGTGACTGCCAACACAGCCTGCTCTTTGGCTC	84082
QY	86099	GTCAGGCCAAACAGCGCGGGGTACAGACCATATGGGCTTTGCAAGTCAGGCATTTCTCT	86158
Db	84083	GTCAGGCCAAACAGCGCGGGGTACAGACCATATGGGCTTTGCAAGTCAGGCATTTCTCT	8412
QY	86159	GAGGGCCATGCGCATTAACAGAAATGGGCGCCCTCTTCGATATCCCAAGCGCCATGTTCTAGTC	86218
Db	84143	GAGGGCCATGCGCATTAACAGAAATGGGCGCCCTCTTCGATATCCCAAGCGCCATGTTCTAGTC	842020
QY	86219	GGCAACGTTTAAACCATGTAAAGTTCAGTTCAATTTAAATTAAGACACAACTCGGCCCA	86278
Db	84203	GGCAACGTTTAAACCATGTAAAGTTCAGTTCAATTTAAATTAAGACACAACTCGGCCCA	84262
QY	86279	TGCTGTGACAAACCTTAAGAAAGTGGGACACAGTGTGC - GCTTGGCGGCTCTGTGCAGATG	86337
Db	84263	TGCTGTGACAAACCTTAAGAAAGTGGGACACAGTGTGTGGCGGCTCTGTGCAGATG	84322
QY	86338	AAACCCGCGGGTAACATTTACTTCCTCCATACGAGGTGGAGGGGTAGATTACAGATGAGCTT	86397
Db	84323	AAACCCGCGGGTAACATTTACTTCCTCCATACGAGGTGGAGGGGTAGATTACAGATGAGCTT	84388
QY	86398	CCCGTGTTCGGAAGCACGACACCCGCTCGAGAGGTCCTCGTCCCGCGTGCATCT	86457
Db	84383	CCCGTGTTCGGAAGCACGACACCCGCTCGAGAGGTCCTCGTCCCGCGTGCATCT	84424
QY	86458	CCCCGGGACCGTGTGCTGACATCATCTGACACATCATATTGACACAGTAAAGCAAGTTTC	86517
Db	84443	CCCCGGGACCGTGTGCTGACATCATCTGACACATCATATTGACACAGTAAAGCAAGTTTC	84502
QY	86518	AGGGCAATGGGAGATCCCATGTAATTTTTCGACATGAGTAACGGGCAATGAATAATCCAC	86577
Db	84503	AGGGCAATGGGAGATCCCATGTAATTTTTCGACATGAGTAAGACGGGCAATGAATAATCCAC	84566
QY	86578	GCACAGTCACGCGGCGGAGCATCTCTGAGATTGGCGATCTCGCCACAGTCCCTCAAAATTA	86637
Db	84563	GCACAGTCACGCGGCGGAGCATCTCTGAGATTGGCGATCTCGCCACAGTCCCTCAAAATTA	84622
QY	86638	TGCAAGAGATTCGAACGCGCTGGAGCGGCTGGGAAGGCCGACAGCTCATATGTAATTTTCAGAA	86697
Db	84623	TGCAAGAGATTCGAACGCGCTGGAGCGGCTGGGAAGGCCGACAGCTCATATGTAATTTTCAGAA	84682
QY	86698	TAGTTGGGCAATGCCGTCATGTGTGCGGCTTCTCCAGGTTTTCACACAGATTCACAGACTCC	86757
Db	84683	TAGTTGGGCAATGCCGTCATGTGTGCGGCTTCTCCAGGTTTTCACACAGATTCACAGACTCC	84742
QY	86758	GTCATTAACACAGATCAAAACCTCTCTCGCATGTTTTCGACAGGCGCTGCAAAATCTGCCCTG	86812
Db	84743	GTCATTAACACAGATCAAAACCTCTCTCGCATGTTTTCGACAGGCGCTGCAAAATCTGCCCTG	84802
QY	86818	GCAAACTCGCAGGGAATCAACTGGGAGACGCGACAGAAACGTCATATGGAATATTCGCA	86877
Db	84803	GCAAACTCGCAGGGAATCAACTGGGAGACGCGACAGAAACGTCATATGGAATATTCGCA	84862
QY	86878	CAACACAGGTGTCCGGGAGCTTTGGGTGATTCAGAAAGGCCACATATTAGCGCACACCCGAGCGG	86937
Db	84863	CAACACAGGTGTCCGGGAGCTTTGGGTGATTCAGAAAGGCCACATATTAGCGCACACCCGAGCGG	84922
QY	86938	GCTGCGAAAATTTTCAACTCCGAGCTTCTCTCCAAAGTAATAAAAAAGATACCTTCACAGCG	86997

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Db 84923 GCTCGAATTTGAACTCGACGTTCTCCAAAGTAAAAAGATCTCAACAGCC 84982
86998 CCTACACAGTTTGGCGACAGAGATCTGAGTCTGTTGGATTTCCGTTTAAACGAG 87057
84983 CCTAGACAGGTTGGCGAAGAGTCTGAGTCTGTTGGATTTCCGTTTAAACGAG 85042
87058 ACTTCAGTGGGCGCTTAGCCCTGGCGCCGCTGTCTCTCGAANAACATCTCTGACG 87117
85043 ACTTCAGTGGGCGCTTAGCCCTGGCGCCGCTGTCTCTCGAANAACATCTCTGACG 85102
87118 CAACGCGCATGTAACAGTATGCAACGATGTGTGGGATGAGGTATACAGATGCGAG 87177
85103 CAACGCGCATGTAACAGTATGCAACGATGTGTGGGATGAGGTATACAGATGCGAG 85162
87178 CCCACGTAACCTCGAAGAAAGCAATTTGAAAGAGTCTGTATCTTTCCCGACAGAGCGCCCG 87237
85163 CCCACGTAACCTCGAAGAAAGCAATTTGAAAGAGTCTGTATCTTTCCCGACAGAGCGCCCG 85222
87238 GCGTTGCTGGGCGGTCTAGCTCCCTCAAAATACGTGTGAGATCTCACTGCATATACATC 87297
85223 GCGTTGCTGGGCGGTCTAGCTCCCTCAAAATACGTGTGAGATCTCACTGCATATACATC 85282
87298 CTAATTTCTTAATTTCTGGGATGTGAACCGGTTTGAACACGCGACGCGCTGAGCA 87357
85283 CTAATTTCTTAATTTCTGGGATGTGAACCGGTTTGAACACGCGACGCGCTGAGCA 85342
87358 AAATGCTCAATATCTTGTATATCTTCATCATGACGCACTGTGGTGACCGGTTCCAC 87417
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87418 GGGACAGATATAGTGTCTGTCGTCGTCATCCCATTCACGCGGGGATAGCTTAGAC 87477
85403 GGGACAGATATAGTGTCTGTCGTCGTCATCCCATTCACGCGGGGATAGCTTAGAC 85462
87478 TCACAGGCTCGATGACCAACCTTTTAATCATATGCGTCCGCACTCGGCTAT 87537
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87718 AGTCAACCCAGACCTAAAGGCGCTACCTGACCCATATCTTCCCTCCGAGGAGTG 87777
85703 AGTCAACCCAGACCTAAAGGCGCTACCTGACCCATATCTTCCCTCCGAGGAGTG 85762
87778 CGGTTTCACATGCGCGTGAAGAAACGAAAGCTACACATATATAGACAGTGTGAAG 87837
85763 CGGTTTCACATGCGCGTGAAGAAACGAAAGCTACACATATATAGACAGTGTGAAG 85822
87838 GAAACTTTATTTGACGAGACAGGCAAAAGCAAGCTGTGCAAGCAATGTGTGAC 87897
85823 GAAACTTTATTTGACGAGACAGGCAAAAGCAAGCTGTGCAAGCAATGTGTGAC 85882
87898 TGGGCGGATCCCGCAGCGCCGACAGACACTGTGCAAAATTTGAATGAGAGGGG 87957
85883 TGGGCGGATCCCGCAGCGCCGACAGACACTGTGCAAAATTTGAATGAGAGGGG 85942
87958 ATTGGGACACAGGCTCGCTTCCGAGATGGAGACGCTCCTAGTGGAGAGACGATAG 88017
85943 ATTGGGACACAGGCTCGCTTCCGAGATGGAGAGGCTCCTAGTGGAGAGACGATAG 86002
88018 GCGGCTGGAATCGGCTCGGATGGGGGCTGACCGGACCTGAGATATTTGGGCG 88077
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Db 86003 GCGGCTGGAATCGGCTTCGCTGTGTGGGCGGTGCTGACACCGCACCTGAGATTTGGCG 86062
88078 AGCGAAACACGCGAGAACTCGCGGTTGTTAATATATTCACCGGCTCCAGCAACCT 88137
86063 AGCGAAACACGCGAGAACTCGCGGTTGTTAATATATTCACCGGCTCCAGCAACCT 86122
88138 CCGTTACCGACAGAGAGCTGGAACGTGACCCATATACGAATGTAAATCCACAGCCG 88197
86123 CCGTTACCGACAGAGAGCTGGAACGTGACCCATATACGAATGTAAATCCACAGCCG 86182
88198 TCTGCTAATATATCAACCGGCTGATCTCTTCCGAGCAGCTTTAGATGCTGTC 88257
86183 TCTGCTAATATATCAACCGGCTGATCTCTTCCGAGCAGCTTTAGATGCTGTC 86242
88258 TGGTAGGAACATATCTGTGGGTATGCGGCAACAGGCGCTGTCCGCGGAATGCC 88317
86243 TGGTAGGAACATATCTGTGGGTATGCGGCAACAGGCGCTGTCCGCGGAATGCC 86302
88318 GCACAACGCTGTCTTGGAGTGTGGCTTTGGCGCGGCGACAGGCGGAACCGCTTGGG 88377
86303 GCACAACGCTGTCTTGGAGTGTGGCTTTGGCGCGGCGACAGGCGGAACCGCTTGGG 86362
88378 GACCGACCTCCATGTTCCCAACACGCGCCATAGTAATAACACAGCGCTAGCATC 88437
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88438 CAACACTGCTCCCGCTCGCTCCACAGCGCGCTTCTGTACTCCATCCGCGACGAGATC 88497
86423 CAACACTGCTCCCGCTCGCTCCACAGCGCGCTTCTGTACTCCATCCGCGACGAGATC 86482
88498 GGGATGCGGGGTTACCTCGTGGGTAGCTGACGTACAGAGATGCGCGGTTGCAATCCG 88557
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88738 TGCCGATGCGCTTTAATTTGACAAATAGTCCAGATCATGTTTCTCATCGTCAAGAG 88797
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86843 CAATGCAATTCAGAGTGTATATCATATATGCAACAATGAGCAACATGCGCTCGAGGCA 86902
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86903 GACGCGCGGTTTACCGGATGACCGCTCGCTTCCGCAATCTGAGAGGTCGCGTC 86962
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86963 GCATAACTGCTTAAAAATCATCCCGCGGTGACCTGTACTTACAGTCAACCTT 87022
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89098 CGCCTACTAGAGGAAATCTGGGCTTACAAATCCACGAGCGCGGCAATGTGACATG 89157
87083 CGCCTACTAGAGGAAATCTGGGCTTACAAATCCACGAGCGCGGCAATGTGACATG 87142
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Db	87143	AGTCAATTATCTGTGACAATATCACCAAATGTACAGAGGACCTGGGGTCTTTTACTGGACC	87202
OY	89218	AGGGCACCCCCCAAGGTAAAGAAGTGCTCGTTGGCGGAACAAGTGTGGCCGGGAACGGG	89277
Db	87203	AGGGCCACCCCCAAGGTAAAGAAGTGCTCGTTGGCGGAACAAGTGTGGCCGGGAACGGG	87262
OY	89278	TGACCGGGGCGAGTCTGCGCGAGTAGACCATTAACATAGAAGATTGAGATTTGACAGAGA	89337
Db	87263	TGACCGGGGCGAGTCTGCGCGAGTAGACCATTAACATAGAAGATTGAGATTTGACAGAGA	87322
OY	89338	TGCGACAGCCCCGTTGGTGGCGGTGCCCTGTGGTGTCCCTGGGCGACGGAACCGTGTG	89397
Db	87323	TGCGACAGCCCCGTTGGTGGCGGTGCCCTGTGGTGTCCCTGGGCGACGGAACCGTGTG	87382
OY	89398	CCTGTGTTCTGTATTCCACATACATATCCCGAGCTCATTTGCCATGCAAAAAGACGCCCTCTC	89457
Db	87383	CCTGTGTTCTGTATTCCACATACATATCCCGAGCTCATTTGCCATGCAAAAAGACGCCCTCTC	87442
OY	89458	ACACCCGTTTATATCTCACACACGGTTTTCTCTGTCTCCGGCTTACGGCCCATCCAA	89517
Db	87443	ACACCCGTTTATATCTCACACACGGTTTTCTCTGTCTCCGGCTTACGGCCCATCCAA	87502
OY	89518	CTGAGGTTTGGAAAGCACATCTTATAGCTGTGCCATATGAAGAACACTGCTGACCCGGTTT	89577
Db	87503	CTGAGGTTTGGAAAGCACATCTTATAGCTGTGCCATATGAAGAACACTGCTGACCCGGTTT	87562
OY	89578	GGGGTCTTGGCGCTTATGCANTGTACCCCTCTACGGTCTGGGACGTGTGTTCCGTAC	89637
Db	87563	GGGGTCTTGGCGCTTATGCANTGTACCCCTCTACGGTCTGGGACGTGTGTTCCGTAC	87622
OY	89638	CAGGACCCCAAAATATAAAAACTGTATAGTGACCGSCCAAAATGAGATGATGGTCTGG	89697
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OY	89698	ATGGGTGTGTGCACACGCTGCCAACCCTGGCGGGCTGGCATATAGGACCGCGCCGAC	89757
Db	87683	ATGGGTGTGTGCACACGCTGCCAACCCTGGCGGGCTGGCATATAGGACCGCGCCGAC	87742
OY	89758	GTCACGCTCCGCCGGAGACGGGAGAGBAGGAGGGGCTCCCTGGCTCAAGCCCATGGACGA	89817
Db	87743	GTCACGCTCCGCCGGAGACGGGAGAGBAGGAGGGGCTCCCTGGCTCAAGCCCATGGACGA	87802
OY	89818	GGCGGCTCTTAAGTAAATTTAGACGGTCTCCGATACATATGAGATGCAGGACATAACA	89877
Db	87803	GGCGGCTCTTAAGTAAATTTAGACGGTCTCCGATACATATGAGATGCAGGACATAACA	87862
OY	89878	CAGCGGATCCAGGCGGGGTCTCAAGTAAAAAAATCTTCTCCGCCAAAACGCGTTGTGT	89937
Db	87863	CAGCGGATCCAGGCGGGGTCTCAAGTAAAAAAATCTTCTCCGCCAAAACGCGTTGTGT	87922
OY	89938	TGCGCGGGGATTCGTCGCTGTCAAAACCAGGTTTTCCGAAGACACOCCTTAGACGCTTTT	89997
Db	87923	TGCGCGGGGATTCGTCGCTGTCAAAACCAGGTTTTCCGAAGACACOCCTTAGACGCTTTT	87982
OY	89998	CCGGCACTCCAGACAGTTGTGTGTGGCGTCCACATTCACAGATCCCTATCCAGGCAATACG	90057
Db	87983	CCGGCACTCCAGACAGTTGTGTGTGGCGTCCACATTCACAGATCCCTATCCAGGCAATACG	88042
OY	90058	AACCAACGTTGCATATGCATCTATACCTGGGTGCATGATATCTTAAGCTCTCTTTTC	90117
Db	88043	AACCAACGTTGCATATGCATCTATACCTGGGTGCATGATATCTTAAGCTCTCTTTTC	88102
OY	90118	CTCGTCCACACACACAAAGTGTTCGGGAAAACGTTCCGCTCCCAATTTGGAATATATCCA	90177
Db	88103	CTCGTCCACACACACAAAGTGTTCGGGAAAACGTTCCGCTCCCAATTTGGAATATATCCA	88162
OY	90178	TCTTTCGAGGTGATTTGTGAGTATTTCTATCTCGGTCAATTTGAACTTGTCACAGAAA	90237
Db	88163	TCTTTCGAGGTGATTTGTGAGTATTTCTATCTCGGTCAATTTGAACTTGTCACAGAAA	88222

QY	90238	CTAATCTAAGAAAGCCCTCACACCTCCCTCTAACTGTAGCTGAAATTTTATGTCCACCTTATA	90237
Db	88223	CTAACTCTAAGAAAGCCCTCACACCTCCCTCTAACTGTAGCTGAAATTTTATGTCCACCTTATA	88282
QY	90298	GGGGCGACGCTACGTATATATGCCCCGTGAAAGAACTGCACTTCCTCATTAATTAATCCCA	90357
Db	88283	GGGGCGACGCTACGTATATATGCCCCGTGAAAGAACTGCACTTCCTCATTAATTAATCCCA	88342
QY	90358	AAGCGTTTCGGGTGCGTCTACCTTAACTGACGTGACATTCACAGGTTCTATGTGTCGGG	90417
Db	88343	AAGCGTTTCGGGTGCGTCTACCTTAACTGACGTGACATTCACAGGTTCTATGTGTCGGG	88402
QY	90418	GTTTTCGCACTCCCCACCGCGACAGAGAAACGTAATTTTAAAGGCCACCAAGC	90477
Db	88403	GTTTTCGCACTCCCCACCGCGACAGAGAAACGTAATTTTAAAGGCCACCAAGC	88462
QY	90478	TCAACTTATTTTAAAGGAGAAAAAACCCGCCATAGAAAGGTTTCGGAGGCACACACC	90537
Db	88463	TCAACTTATTTTAAAGGAGAAAAAACCCGCCATAGAAAGGTTTCGGAGGCACACACC	88522
QY	90538	CCCAAGACCTATTTCCTGGCGAGTTTCGGCGCACGCTGTAGTTTTCGTATTTTGTAAAT	90597
Db	88523	CCCAAGACCTATTTCCTGGCGAGTTTCGGCGCACGCTGTAGTTTTCGTATTTTGTAAAT	88582
QY	90598	TTCGCATCAATTCGCCCCCAACATAGTCAATAAAAAACCGTAAACACACACTCTGGTG	90657
Db	88583	TTCGCATCAATTCGCCCCCAACATAGTCAATAAAAAACCGTAAACACACACTCTGGTG	88642
QY	90658	AACAAATTTATGCGTCTCTGGCCCCCAAGACGTGCGTGAAGGTCAAGCAGCACAGCGCTGCT	90717
Db	88643	AACAAATTTATGCGTCTCTGGCCCCCAAGACGTGCGTGAAGGTCAAGCAGCACAGCGCTGCT	88702
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QY	90778	CCAACGTGGAAGACAAAAAATATAGTACAAAGTCCGAGGAGCAGAGCGCTGTCAGGCCA	90837
Db	88763	CCAACGTGGAAGACAAAAAATATAGTACAAAGTCCGAGGAGCAGAGCGCTGTCAGGCCA	88822
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Db	88823	ACAGACAGCGTACCOCGGCGCGCCCTCAATCAAAAAACGTACGAGATTAATAAGTCCCAT	88882
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Db	89123	TAGTATCTGTGGGCAATCTGTGGGGCAATAATATATACCAGCTATTTCGCGCAACACACAG	89182
QY	91198	AGCAGCAGGCAAGGCAAGCAAGCCCAACAAAAATGGAACGTGAACCTATGGAAGGTCAACG	91257
Db	89183	AGCAGCAGGCAAGGCAAGCAAGCCCAACAAAAATGGAACGTGAACCTATGGAAGGTCAACG	89242
QY	91258	CCGAGGGGTGATGTCATAGAAACCGGGGGTAAATTAAGAAAGCGGAGATGTGTGCACGGTACA	91317
Db	89243	CCGAGGGGTGATGTCATAGAAACCGGGGGTAAATTAAGAAAGCGGAGATGTGTGCACGGTACA	89302
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QY 95398 ACGAGACATCATCCACAGCTGACCTGATGAGGAGAGGAGGAGCACTTCATGAA 95457
D 93383 ACGAGACATCATCCACAGCTGACCTGATGAGGAGAGGAGGAGCACTTCATGAA 93442
QY 95458 GTGCTTGAAGGTTTGTCTCGGTGCGCATGAGACGCTTTAAATAAACAGCTAGAA 95517
D 93443 GTGCTTGAAGGTTTGTCTCGGTGCGCATGAGACGCTTTAAATAAACAGCTAGAA 93502
QY 95518 GCTGACCTCGCGGAAGCCGCGCTGACCTTAATACAGCGTTGCGGACACATCTGTG 95577
D 93503 GCTGACCTCGCGGAAGCCGCGCTGACCTTAATACAGCGTTGCGGACACATCTGTG 93562
QY 95578 ACGAGATGTAATGGAAGCGTAACCAACGAGTCAATCTCAAGCTCGTTGCGCT 95637
D 93563 ACGAGATGTAATGGAAGCGTAACCAACGAGTCAATCTCAAGCTCGTTGCGCT 93622
QY 95638 CCACGAGTGTCTAGGCTCTCCGCAAAACAGGAAATTTATACATGACAGGCAACAA 95697
D 93623 CCACGAGTGTCTAGGCTCTCCGCAAAACAGGAAATTTATACATGACAGGCAACAA 93682
QY 95698 AAACAGCACCCCTCATTAACATCTGGGCGACGCTTTCAAAAAATGGGTGAAGAACCTGGG 95757

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QY 95758 TTCTCAGCAGTACGTATGCTAAACCTTAACGGCAGACAGAGTACCGCGAGTTAACGAAT 95817
Db 93743 TTCTCAGCAGTACGTATGCTAAACCTTAACGGCAGACAGAGTACCGCGAGTTAACGAAT 93802
QY 95818 TTGTGTATGCTTGTCTGTCTGTTAAAGTCTGTAAAGACCGTCAAGGCCGCTTGTGT 95877
Db 93803 TTGTGTATGCTTGTCTGTCTGTTAAAGTCTGTAAAGACCGTCAAGGCCGCTTGTGT 93862
QY 95878 TTGACATTAACCGCGACACTGTGCTTACGCTTCCCGAATACCGGAGATACGTC 95937
Db 93863 TTGACATTAACCGCGACACTGTGCTTACGCTTCCCGAATACCGGAGATACGTC 93922
QY 95938 GCACCGTAAACGAGCAGCAGTGTCTCCATTATTTCTGCGAAAGAGACCGGTTAGTACG 95997
Db 93923 GCACCGTAAACGAGCAGCAGTGTCTCCATTATTTCTGCGAAAGAGACCGGTTAGTACG 93982
QY 95998 TGGCCCTATATGCTCCATCCAAAGTGTGCTTTAAACAAATTCACGAGTGAATTCGGCCATC 94042
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QY 96058 GTTCAGGCTCAAGGCTTGAAGCTACACCCCGAGTCCCGGCTGAGTACGAGGTTAAAG 96117
Db 94043 GTTCAGGCTCAAGGCTTGAAGCTACACCCCGAGTCCCGGCTGAGTACGAGGTTAAAG 94102
QY 96118 GTTTGGCAGATTTTGGCCGAGAGAAAGTTTCGGTGTTCATTTGTTAAAGAAATAGCTT 96177
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Db 94403 CTTAAAAAACCAGTCTAGGCGCGCTATTTATTTGCTTAATGTAGTTAAGCAAC 94462
QY 96478 ATTAATAGACAGTGGGGCGGCAAAAGCTGTGCGCAGGCTGAGCGGGCATGATCATC 96537
Db 94463 ATTAATAGACAGTGGGGCGGCAAAAGCTGTGCGCAGGCTGAGCGGGCATGATCATC 94522
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Db 94523 TAAATCCAAACATGTCTACTAGAGAGCTTAAGGCCAATATGTGTAAACAAGGCTCTCT 94582
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Db 94583 GGCAGTACGTTGCCCTTTAAGCAGACGTCACTGTGTGACAAACGTACTGTGACCGT 94642
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Db 94643 TTGAACCAAGCGCCGACCGGCGCAAGAACTGATGAACGAGCGGTTTCCAACAATTTC 94702
QY 96718 TTCAAAATTTGGGTATGGGTCAAGTAGACCGCTCTGCTGGCTTACCAACACAGCTAT 96777
Db 94703 TTCAAAATTTGGGTATGGGTCAAGTAGACCGCTCTGCTGGCTTACCAACACAGCTAT 94762
QY 96778 TCTGTTGGTCTGGGGGACAGATCCGCGTCCATCTAGACAGTGGCGGACGAGGCTAG 96837
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QY 96838 CGTGAATTAACATGTCAATGAGAGACCCAGTGTCACTGTGTTTAAAGAAACAGTAGGT 96897
Db 94823 CGTGAATTAACATGTCAATGAGAGACCCAGTGTCACTGTGTTTAAAGAAACAGTAGGT 94882
QY 96898 GCCCGAGGTTCTGTGAACTCATGTGTGAGATTAATTCAAAAATTCATACGTTTG 96957
Db 94883 GCCCGAGGTTCTGTGAACTCATGTGTGAGATTAATTCAAAAATTCATACGTTTG 94942
QY 96958 ACATGTAGGAGACAGATAAAAATCCATCTTTGATGGGCTCCACCCAGTGTGTCGA 97017
Db 94943 ACATGTAGGAGACAGATAAAAATCCATCTTTGATGGGCTCCACCCAGTGTGTCGA 95002
QY 97018 CACACATATTTAGAGAGAGATCACGAACACCCCTTAGAAAAAGTCCGACCGGAGATTA 97077
Db 95003 CACACATATTTAGAGAGAGATCACGAACACCCCTTAGAAAAAGTCCGACCGGAGATTA 95062
QY 97078 CGAAACCCGGGTAGAGAGGCGGCGGAGTAGAGCATCAAACTATCTTACGCTTGTAC 97137
Db 95063 CGAAACCCGGGTAGAGAGGCGGCGGAGTAGAGCATCAAACTATCTTACGCTTGTAC 95122
QY 97138 GTTTGGCTCCCTGTCTTCATGAGCGTGTCAATTTCTGCGACGCGGCTGATTAACGCTGA 97197
Db 95123 GTTTGGCTCCCTGTCTTCATGAGCGTGTGTCAATTTCTGCGACGCGGCTGATTAACGCTGA 95182
QY 97198 CGAGAACACCGCGGCTTTACAAATTAACGTCAACACCTTAAACGTCGACCGGATCGT 97257
Db 95183 CGAGAACACCGCGGCTTTACAAATTAACGTCAACACCTTAAACGTCGACCGGATCGT 95242
QY 97258 ACACAGCTTAAACTCTGTATGAGTGTCCAACTAAACACCACTAACCCGACACTTTT 97317
Db 95243 ACACAGCTTAAACTCTGTATGAGTGTCCAACTAAACACCACTAACCCGACACTTTT 95302
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QY 97438 AGTCATTAAGACCCACCAAGGCGCAAAACGTCACAGGCTATCTCCGAGGTTGTGA 97497
Db 95423 AGTCATTAAGACCCACCAAGGCGCAAAACGTCACAGGCTATCTCCGAGGTTGTGA 95482
QY 97498 TGTCTTAATACAGTATTCGAAACACACAGAGTCCCGAGGCTTAAAGACAGATTA 97557
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QY 97558 TCTCGACAAACGTCGCATATTTGGCATGATTAACAGATATCATCATCACGTAATTCACG 97617
Db 95543 TCTCGACAAACGTCGCATATTTGGCATGATTAACAGATATCATCATCACGTAATTCACG 95602
QY 97618 TACGCCCTCGGGGATCCCGACCAACCAATGGGTATCAGCAGTCTACGCTGGGTAGA 97677
Db 95603 TACGCCCTCGGGGATCCCGACCAACCAATGGGTATCAGCAGTCTACGCTGGGTAGA 95662
QY 97678 GCAAAATTTTACAGAAACACCGGCAATACTGGAACCTTAACCTCCCGAGTCCGATTT 97737
Db 95663 ACAAATTTTACAGAAACACCGGCAATACTGGAACCTTAACCTCCCGAGTCCGATTT 95722
QY 97738 TATCGACATGGCGAAGTGTGCTCTCCGTTCAAGAGTGGCTTAATCTATCTATTTGTA 97797
Db 95723 TATCGACATGGCGAAGTGTGCTCTCCGTTCAAGAGTGGCTTAATCTATCTATTTGTA 95782
QY 97798 AAAACTGCAACTGGACACACCGCCCTATTTCCACCTGTGACGAACTGGCCGCTGCT 97857
Db 95783 AAAACTGCAACTGGACACACCGCCCTATTTCCACCTGTGACGAACTGGCCGCTGCT 95842
QY 97858 GGTTAACGGGCAACAGATTTGTTGCTCCCTATTCAGAGTACGTAAGAACTATCATCAG 97917
Db 95843 GGTTAACGGGCAACAGATTTGTTGCTCCCTATTCAGAGTACGTAAGAACTATCATCAG 95902
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QY	97918	CATGCCGTTTCAAAAACGAGACGCTTTGAGATATACACGCTCTTTGCCAATTCAAAAA	97977
Dp	95903	CATGCCAGTATCAAAAACGAGACGCTTTGAGATATACACGCTCTTTGCCAATTCAAAAA	95962
QY	97978	CATAGTTGACGGCACACCAATTTTACGCTTACCGACGACAGAACTTACAGCTTCACCC	98037
Dp	95963	CATAGTTGACGGCACACCAATTTTACGCTTACCGACGACAGAACTTACAGCTTCACCC	96022
QY	98038	CGAAGCTTATTTCTCTGACAGCTTCTGAATCGAGTCCCTGTGCAGAAAACGACGATACGG	98097
Dp	96023	CGAAGCTTATTTCTCTGACAGCTTCTGAATCGAGTCCCTGTGCAGAAAACGACGATACGG	96082
QY	98098	GTTGTTCCGCGAACGCAATTGAGATTTTATTAGAAAGGTATCGATTTTATGCGGAGTT	98157
Dp	96083	GTTGTTCCGCGAACGCAATTGAGATTTTATTAGAAAGGTATCGATTTTATGCGGAGTT	96142
QY	98158	GGGGCGCTTCATTGAAAAACGTTGTGGCATCGATCAACCGTAAGCCTGTCCAGCGTAG	98217
Dp	96143	GGGGCGCTTCATTGAAAAACGTTGTGGCATCGATCAACCGTAAGCCTGTCCAGCGTAG	96202
QY	98218	AGCGCTTAAGCCACGGCTCGCGAGCTGTGGCTTATCCAAAAGAGCCTGTGAAGATTTCCG	98277
Dp	96203	AGCGCTTAAGCCACGGCTCGCGAGCTGTGGCTTATCCAAAAGAGCCTGTGAAGATTTCCG	96262
QY	98278	CGCAATGATCTGATGACACCGACGACGAGACGCCAAAGTGAGGAAAAATTTTACGAGCTT	98337
Dp	96263	CGCAATGATCTGATGACACCGACGACGAGACGCCAAAGTGAGGAAAAATTTTACGAGCTT	96322
QY	98338	TTTTGAAATGTGTAACCAATTAACACTATACGGGTCTATTTTACGAGTGTCTTAACCA	98397
Dp	96323	TTTTGAAATGTGTAACCAATTAACACTATACGGGTCTATTTTACGAGTGTCTTAACCA	96382
QY	98398	GTAACAGCCCACTAGCATATCGCTGGCGCAAAATTAATCTTAACCGAGTGCATGC	98457
Dp	96383	GTAACAGCCCACTAGCATATCGCTGGCGCAAAATTAATCTTAACCGAGTGCATGC	96442
QY	98458	CGAACAGAGGATCGCGCCCTGTGGCGCACTCCATTAAATGGGTCTTTCCCGTCCCTCG	98517
Dp	96443	CGAACAGAGGATCGCGCCCTGTGGCGCACTCCATTAAATGGGTCTTTCCCGTCCCTCG	96502
QY	98518	GAAATTTAACAACGCTGTGCGTTTTTTTAAAGCTTACACCCCGTGGACAGCTACAAAA	98577
Dp	96503	GAAATTTAACAACGCTGTGCGTTTTTTTAAAGCTTACACCCCGTGGACAGCTACAAAA	96562
QY	98578	AATCTACAAGCAATACCGTCTGTAATGAGGTCTTTGTTCGAATATGCGGCAACAA	98637
Dp	96563	AATCTACAAGCAATACCGTCTGTAATGAGGTCTTTGTTCGAATATGCGGCAACAA	96622
QY	98638	ATCGTGGGGTAAACATCGCGCTCGCAGAGAGCCCGCTTAACCGACATACAGACCGCGA	98697
Dp	96623	ATCGTGGGGTAAACATCGCGCTCGCAGAGAGCCCGCTTAACCGACATACAGACCGCGA	96682
QY	98698	ACCAAGACACAGAGTCCGCTGTGCGCCCAAGTTATTCGCAAAATATGAGCGCTGTCCAAAT	98757
Dp	96683	ACCAAGACACAGAGTCCGCTGTGCGCCCAAGTTATTCGCAAAATATGAGCGCTGTCCAAAT	96742
QY	98758	AAGCGCAGAGATTTATGACGACGACATCGTCTCCAGCCCGGGAATTCGCCCGAGTTCTAT	98817
Dp	96743	AAGCGCAGAGATTTATGACGACGACATCGTCTCCAGCCCGGGAATTCGCCCGAGTTCTAT	96802
QY	98818	TAAACAAAACTGTATTCGATTCCTTTAGCGAGGTGCTCCGAACACGTTCCAAAAAAATG	98877
Dp	96803	TAAACAAAACTGTATTCGATTCCTTTAGCGAGGTGCTCCGAACACGTTCCAAAAAAATG	96862
QY	98878	ATCGCTTTTCCAAATTTAGATGCGTCAATAGCTTTCGGGAGAGAGAGCCAGACACTAGC	98937
Dp	96863	ATCGCTTTTCCAAATTTAGATGCGTCAATAGCTTTCGGGAGAGAGAGCCAGACACTAGC	96922
QY	98938	CCCTATACAGAGCTCGCTGGCCCTGGCGTATTTTCAATATATGACATTTTGGAGAAAA	98997
Dp	96923	CCCTATACAGAGCTCGCTGGCCCTGGCGTATTTTCAATATATGACATTTTGGAGAAAA	96982

QY	98998	GCATTCTCCGGAGTCGTTTATCAACCGTCGTGACATATCTTCAGGAACATTTCGGTCAT	99057
Db	96983	GCATTCTCCGGAGTCGTTTATCAACCGTCGTGACATATCTTCAGGAACATTTCGGTCAT	97042
QY	99058	ACGACAGGTGATACCGGAAAGCCACGTCGCCACAAGAAATTTCTACAAATCTTGTTAACTT	99117
Db	97043	ACGACAGGTGATACCGGAAAGCCACGTCGCCACAAGAAATTTCTACAAATCTTGTTAACTT	97102
QY	99118	TCAAAACATTTCCAAATAGCAGCGAGCTTCATTCAAAATCCATGACCTTTGTAGACGCT	99177
Db	97103	TCAAAACATTTCCAAATAGCAGCGAGCTTCATTCAAAATCCATGACCTTTGTAGACGCT	97162
QY	99178	GAAAACCGCATTCGCCGCTAATCTGACGACTGTCTCTTGTAGTCGCCGCTTTAATACAT	99237
Db	97163	GAAAACCGCATTCGCCGCTAATCTGACGACTGTCTCTTGTAGTCGCCGCTTTAATACAT	97222
QY	99238	GAAACTACTGTACATTTCAACGCTAGACACCGTCGATTCACAGGAAAGGCGAAC	99297
Db	97223	GAAACTACTGTACATTTCAACGCTAGACACCGTCGATTCACAGGAAAGGCGAAC	97282
QY	99298	CATGTCGTGAGCATGTTCCGTAATTCAAATCCAGATTCGGGTCCTCGAAGAGCTCTTACA	99357
Db	97283	CATGTCGTGAGCATGTTCCGTAATTCAAATCCAGATTCGGGTCCTCGAAGAGCTCTTACA	97342
QY	99358	GGAAGCCGTTATCGCGTTAACTCAAAAGTCCGAACCGATGTAGCAGCGACATCCGCTC	99417
Db	97343	GGAAGCCGTTATCGCGTTAACTCAAAAGTCCGAACCGATGTAGCAGCGACATCCGCTC	97402
QY	99418	GATGCAACACCTCAGCTACGTACGAAAGATGCGCGGACAGCAAAATTAATGACACACAACT	99477
Db	97403	GATGCAACACCTCAGCTACGTACGAAAGATGCGCGGACAGCAAAATTAATGACACACAACT	97462
QY	99478	TCGATCCGCTGTTTCACGAATACAGAGGATATTTGCACTGTTTAAAGCTTTTAAAGC	99537
Db	97463	TCGATCCGCTGTTTCACGAATACAGAGGATATTTGCACTGTTTAAAGCTTTTAAAGC	97522
QY	99538	TCTCATGTAAACGTTACGGGAACCTGCTACTCACTGACCGGATATCTTGGATTCCCT	99597
Db	97523	TCTCATGTAAACGTTACGGGAACCTGCTACTCACTGACCGGATATCTTGGATTCCCT	97582
QY	99598	ATATCAACCCCCCTAATACCCGATACCATGCTGTACAAAATTTTAAACTTTAAGCAAA	99657
Db	97583	ATATCAACCCCCCTAATACCCGATACCATGCTGTACAAAATTTTAAACTTTAAGCAAA	97642
QY	99658	AACGGACAAACCGACGACATCTTAAAGAGCTGTCAAGCCGCTGAGACAAAGACCTCT	99717
Db	97643	AACGGACAAACCGACGACATCTTAAAGAGCTGTCAAGCCGCTGAGACAAAGACCTCT	97702
QY	99718	ATCGGCTGAAGAAGTAGCAGTGCAGCTCTCAAAAACACAGCTTGAGCTCTTCAAAA	99777
Db	97703	ATCGGCTGAAGAAGTAGCAGTGCAGCTCTCAAAAACACAGCTTGAGCTCTTCAAAA	97762
QY	99778	ACTGTACGACACATTTGSGAACCGGCTCCACAAAACAAATRAACCCGACCTTATTAACCTGA	99837
Db	97763	ACTGTACGACACATTTGSGAACCGGCTCCACAAAACAAATRAACCCGACCTTATTAACCTGA	97822
QY	99838	ATATTCCGGGTATATTATAAGAAACAAAGTGTCCGTAGATTGGAGCAATTAACCTGCT	99897
Db	97823	ATATTCCGGGTATATTATAAGAAACAAAGTGTCCGTAGATTGGAGCAATTAACCTGCT	97882
QY	99898	GACATATACCCGACCCGACGATACGTTAAATTCACCCCGGTTTAACAGGAGCAGTAGA	99957
Db	97883	GACATATACCCGACCCGACGATACGTTAAATTCACCCCGGTTTAACAGGAGCAGTAGA	97942
QY	99958	TCGCATGTTTGCAGAAATTAACGATGGAATTCGCCCAATTTTTCGAAATTTTAAATAGA	100017
Db	97943	TCGCATGTTTGCAGAAATTAACGATGGAATTCGCCCAATTTTTCGAAATTTTAAATAGA	98002
QY	100018	GGGGGTGGCAACGACGACGAGGCGGAGTGAAGTTTGGGCAATAAGCCGGCTCGCAGTG	100077
Db	98003	GGGGGTGGCAACGACGACGAGGCGGAGTGAAGTTTGGGCAATAAGCCGGCTCGCAGTG	98062
QY	100078	CTTAAGCAACTGCGTTATCTACCTCGGACAAAGTTATTTCAATAGAGAGTCCGCCGCTGAC	100137

Db 98063 CTTAAGCACTGCGTTATCTACCTCGACAAAGTTATTTCAATAGAGAGTCCCGCGTGC 98122
QY 100138 GGACACTAAAGACCTTGACAGAGCTTTTACGGCAAGGGGAGCGAGCTTGACTTTATACGTAG 100197
Db 98123 GGACACTAAAGACCTTGACAGAGCTTTTACGGCAAGGGGAGCGAGCTTGACTTTATACGTAG 98182
QY 100198 AGGCTCCGGGAGCGCTGGCTATACCAATATGCCCCAAGTGCACACATACCAAGCTTTAT 100257
Db 98183 AGGCTCCGGGAGCGCTGGCTATACCAATATGCCCCAAGTGCACACATACCAAGCTTTAT 98242
QY 100258 CAAGACCAAGAGTGAACCGCGCCATCTTTCAATGTCAGAGTACTTTGAGATTAATG 100317
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Db 98303 ACTTGAAGCGGCGCATCCGGGAACCTTTCAATGCAATCCCTAAATGCAATCCTTAAGCGGAAA 98362
QY 100378 TTACGGCGGCGCGTTCAATCTTCTGTTTATATGCGGCGACAAAGCGGGCGCTAAT 100437
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QY 100498 TCCGGCACAGTATATGTTGTCAGAACCCACCGGCATATAGAGTACGTGCACGCGC 100557
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Db 98543 AAGACAGATATACACTGCGAGTTTCTATACATATATGCCCGAGAAATATGTCATACAA 98602
QY 100618 GCACATACATACCAACCACTATAGAACTTAAAGTTCGCGCAAGTACAGCGCCGCGACAT 100677
Db 98603 GCACATACATACCAACCACTATAGAACTTAAAGTTCGCGCAAGTACAGCGCCGCGACAT 98662
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QY 100738 GCGGGATGAGGTCAAAATCAATCAACCTGCGACGCGTGCAGAGAACCAACCAACGACAC 100797
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QY 100858 AAGCTACCCAGACCCGGCAACCAACGAGCGGAGCAACAAACTCTTAACCTCCGCTCAGC 100917
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QY 101098 GATATCCGCGGAGTGTGATGAGAGACATATATCTCTCTATATTCACGCGTGC 101157
Db 99083 GATATCCGCGGAGTGTGATGAGAGACATATATCTCTCTATATTCACGCGTGC 99142
QY 101158 GACTCATGCTTGAAGAGCTGTGAGAGCGCCCAATGAGCCGGAATTACATAGCA 101217
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Db 99143 GACTCCATGCTTGAAGAGCTGTTCAGACACCCCAATGAGCCGGAATTACATAGCA 99202
QY 101218 AGACGGACAGAGACAGCATGAGCGCTTTCTAGAAAGATGCTCGAGACGGGAAC 101277
Db 99203 AGACGGACAGAGACAGCATGAGCGCTTTCTAGAAAGATGCTCGAGACGGGAAC 99262
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QY 101338 AATGAAAGATTAATCAATAGCAAGCGCCCTGCGACAGCTGCAACATCTCGGACAA 101397
Db 99323 AATGAAAGATTAATCAATAGCAAGCGCCCTGCGACAGCTGCAACATCTCGGACAA 99382
QY 101398 ACAAAAGCGGCGAGCCGTCGAGAAAGCGGCGCCCTCGAGCGGATGAGCAAAATATGAT 101457
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QY 102118 GGAGACCCCGCGCAACGAAGCAACATTAACCAATTCGAACCTTTTCATCATGCT 102177
Db 100103 GGAGACCCCGCGCAACGAAGCAACATTAACCAATTCGAACCTTTTCATCATGCT 100162
QY 102178 GGCAAAATATCATATCAGCTTAAATCTTAACGTAACGAGAAACGATGCAATTA 102237
Db 100163 GGCAAAATATCATATCAGCTTAAATCTTAACGTAACGAGAAACGATGCAATTA 100222
QY 102238 CATAAGCCCATGGAAGCTAAGGCGTACGCTGTTGTAACCTCGAGAGGAGTATGAAAC 102297
Db 100223 CATAAGCCCATGGAAGCTAAGGCGTACGCTGTTGTAACCTCGAGAGGAGTATGAAAC 100282
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QY	102298	CATCTTTAATTTAGAGTGGCCATACGAAACCGTGCACCGGTTCAAGAACTGCCCTCGT	102357
Db	100283	CATCTTTAATTTAGAGTGGCCATACGAAACCGTGCACCGGTTCAAGAACTGCCCTCGT	100342
QY	102358	GGCGGGGGCGAAAGCAAAAATGGAATCGGTAAACAAAATGGAAGAACCAACAGGCTCT	102417
Db	100343	GGCGGGGGCGAAAGCAAAAATGGAATCGGTAAACAAAATGGAAGAACCAACAGGCTCT	100402
QY	102418	CGACCAATTAATCTGGGAGAGCGCCGAAACGTTACTTTGACACAAATACCGCAACATCCGGA	102477
Db	100403	CGACCAATTAATCTGGGAGAGCGCCGAAACGTTACTTTGACACAAATACCGCAACATCCGGA	100462
QY	102478	TGAGAACCCCGGTCCGCGCCATGTCCATACCGATCTGTGAGACCTTACATTACAAAGCAGG	102537
Db	100463	TGAGAACCCCGGTCCGCGCCATGTCCATACCGATCTGTGAGACCTTACATTACAAAGCAGG	100522
QY	102538	GGCCCTGATPAGGCACTTCTCGAAACACGAGGTTGAAAAATGCAAGCGCGCATCCAGCA	102597
Db	100523	GGCCCTGATPAGGCACTTCTCGAAACACGAGGTTGAAAAATGCAAGCGCGCATCCAGCA	100582
QY	102598	CCTGGCATCATCGAGATGCTTCATATAATGCTGTCAAAACACGCGGCTGATTAACAT	102657
Db	100583	CCTGGCATCATCGAGATGCTTCATATAATGCTGTCAAAACACGCGGCTGATTAACAT	100642
QY	102658	ATCAGACAAATCTGGCGCAAGATGAGAGGCATCTGTAGACAAACACACGTTTCTTCAAA	102717
Db	100643	ATCAGACAAATCTGGCGCAAGATGAGAGGCATCTGTAGACAAACACACGTTTCTTCAAA	100702
QY	102718	CGCCCACTTTAGCAAAAGCGTCCAAACGCTGGGAGGACGCTTAATCGGGAATGCGTAGA	102777
Db	100703	CGCCCACTTTAGCAAAAGCGTCCAAACGCTGGGAGGACGCTTAATCGGGAATGCGTAGA	100762
QY	102778	AGCGCTAATAATAAAGAGGCCCTCTCCCTCAACAACGCGCTCTCCGCGTTCAAC	102837
Db	100763	AGCGCTAATAATAAAGAGGCCCTCTCCCTCAACAACGCGCTCTCCGCGTTCAAC	100822
QY	102838	CATACTGGGGGACGCGTCCGTTCCAGATACAGAGACGCTGACGCGAATGCTTCCGGCGT	102897
Db	100823	CATACTGGGGGACGCGTCCGTTCCAGATACAGAGACGCTGACGCGAATGCTTCCGGCGT	100882
QY	102898	CGCCAGCGCCACAAAAGAAATCCGCTGGCGGATATCCAGATAGGTGGAACCGAGTAAACCG	102957
Db	100883	CGCCAGCGCCACAAAAGAAATCCGCTGGCGGATATCCAGATAGGTGGAACCGAGTAAACCG	100942
QY	102958	TCACCTAAACGAGCTGGAAGCTGTGAATACCAACATGCGGTGACAAAACCAACAGCGG	103017
Db	100943	TCACCTAAACGAGCTGGAAGCTGTGAATACCAACATGCGGTGACAAAACCAACAGCGG	101002
QY	103018	CAAACTGTAATGATTAATTAACCCGAGACCTCAAGAGGGGGAGGTGCTCAGAGAAACGCT	103077
Db	101003	CAAACTGTAATGATTAATTAACCCGAGACCTCAAGAGGGGGAGGTGCTCAGAGAAACGCT	101062
QY	103078	CCTGGAACACAGCGTGGCAAGAAAGCGTCTAAAGTTTCAACCGTGCAGCTCCAAAGAAAT	103137
Db	101063	CCTGGAACACAGCGTGGCAAGAAAGCGTCTAAAGTTTCAACCGTGCAGCTCCAAAGAAAT	101122
QY	103138	CGAAGACTTTTACACAGTGGGACCGCTCAGCAAAAGCCGGAATTTGCAAGAAAACACT	103197
Db	101123	CGAAGACTTTTACACAGTGGGACCGCTCAGCAAAAGCCGGAATTTGCAAGAAAACACT	101182
QY	103198	ACGGACGCTGANTCACCCAATTCOAAGGGCAGAGAGGACCGCGTCCGAGGCAACGCGCGT	103257
Db	101183	ACGGACGCTGANTCACCCAATTCOAAGGGCAGAGAGGACCGCGTCCGAGGCAACGCGCGT	101242
QY	103258	TCGCATGAGACTACAGCGCGACCCCATACCCACGCGCACAGGCGTTTCTACGGCTACCGC	103317
Db	101243	TCGCATGAGACTACAGCGCGACCCCATACCCACGCGCACAGGCGTTTCTACGGCTACCGC	101302
QY	103318	GGAAAAGGAAAAGGCCGCATGGAATTAATTCACAGGCGCTTTCAGAGTTTCAACTTCA	103377
Db	101303	GGAAAAGGAAAAGGCCGCATGGAATTAATTCACAGGCGCTTTCAGAGTTTCAACTTCA	101362

QY	103378	CCTCATGCAGCCTTTCGATTTGGGCAAGAGATGGCATTCAGTAATCTTCAGACACGGCTGTC	103437
Db	101363	CCTCATGCAGCCTTTCGATTTGGGCAAGAGATGGCATTCAGTAATCTTCAGACACGGCTGTC	101422
QY	103438	CCTTCTCGGTACGGTTGGACCAAAAGCTGTGCGCTTCATGTGAGAGCATCTTCAACACCT	103497
Db	101423	CCTTCTCGGTACGGTTGGACCAAAAGCTGTGCGCTTCATGTGAGAGCATCTTCAACACCT	101482
QY	103498	GGAGACATCCTCAACGCAAGAAAGCTGGCATCTCTGCTTCCAAACGGGGCCGCTTCAGACC	103557
Db	101483	GGAGACATCCTCAACGCAAGAAAGCTGGCATCTCTGCTTCCAAACGGGGCCGCTTCAGACC	101542
QY	103558	CCGACGCTTTGACTGATTCGGCGCCTATCAAAACACGCGTTAAACGCGTTTCTTAAAAACAT	103617
Db	101543	CCGACGCTTTGACTGATTCGGCGCCTATCAAAACACGCGTTAAACGCGTTTCTTAAAAACAT	101602
QY	103618	AGGCGTGGCCATGGTGGGCAACCTGGGGGCAAGATCCATACCAATGCCAAACCTGTACG	103677
Db	101603	AGGCGTGGCCATGGTGGGCAACCTGGGGGCAAGATCCATACCAATGCCAAACCTGTACG	101662
QY	103678	TCACGCGGTGCATTCGCGAGACCTTTCACACAGGCCACGGTGGGAAACATTTAGAACGACC	103737
Db	101663	TCACGCGGTGCATTCGCGAGACCTTTCACACAGGCCACGGTGGGAAACATTTAGAACGACC	101722
QY	103738	CGCGGCCCAATATCTGTGCAATATCTCTGCAATGTCAAGTCCGCTTCAACGACACGGAAT	103797
Db	101723	CGCGGCCCAATATCTGTGCAATATCTCTGCAATGTCAAGTCCGCTTCAACGACACGGAAT	101782
QY	103798	CGCGCTTAAGATTCGAGGCGCGGGGCTACAGGACGCATTCAACTCGCGGGCAACGTCGT	103857
Db	101783	CGCGCTTAAGATTCGAGGCGCGGGGCTACAGGACGCATTCAACTCGCGGGCAACGTCGT	101842
QY	103858	GACTTCCCCGAAACCACCTAGAAAGCCCCACAGAAAGCTTAATTAACGGCACTGACGCGCT	103917
Db	101843	GACTTCCCCGAAACCACCTAGAAAGCCCCACAGAAAGCTTAATTAACGGCACTGACGCGCT	101902
QY	103918	AACGTCGAGACATTTCCAGATTTTCTTAAAAAGTCATCTCTTCAACAGGACACGCACT	103977
Db	101903	AACGTCGAGACATTTCCAGATTTTCTTAAAAAGTCATCTCTTCAACAGGACACGCACT	101962
QY	103978	CATTGCGGTCCAGAGAGCGGAATTTACACAACTAGAGGCCACAGCATCTGTGGGGCCGAACG	104037
Db	101963	CATTGCGGTCCAGAGAGCGGAATTTACACAACTAGAGGCCACAGCATCTGTGGGGCCGAACG	102022
QY	104038	GCTCCGCCAATCCACCCCTGACAGAGATGCGAGGCCAAGATGGCAACCCGCTATCAGCAACT	104097
Db	102023	GCTCCGCCAATCCACCCCTGACAGAGATGCGAGGCCAAGATGGCAACCCGCTATCAGCAACT	102082
QY	104098	CTTACCCCGCGCCCGCTGTGCGCAATATCATCGAGACCGTTGAACCTTATCAAAACCTATAGA	104157
Db	102083	CTTACCCCGCGCCCGCTGTGCGCAATATCATCGAGACCGTTGAACCTTATCAAAACCTATAGA	102142
QY	104158	CTTTTGGATTCAACGTTATCGAATCGCAAAATCCTGTGCAAGAGACGCTTTCGAGACAGCCAT	104217
Db	102143	CTTTTGGATTCAACGTTATCGAATCGCAAAATCCTGTGCAAGAGACGCTTTCGAGACAGCCAT	102202
QY	104218	AGCGGATTTGCGGTGGCTGGAATTCGCGACAAATCCGTAAATGTCATACGTCAACAAAA	104277
Db	102203	AGCGGATTTGCGGTGGCTGGAATTCGCGACAAATCCGTAAATGTCATACGTCAACAAAA	102262
QY	104278	CGAAACGCAACGTTAAACGTAATCTGTAGCGAGGTAGAAAAACAGACACCGTGGCGCA	104337
Db	102263	CGAAACGCAACGTTAAACGTAATCTGTAGCGAGGTAGAAAAACAGACACCGTGGCGCA	102322
QY	104338	GCGTCTACACATTTTGGAAACGTGTGGCGCAAAACACGAGACGTAACGTAAGGTGTGAAGCA	104397
Db	102323	GCGTCTACACATTTTGGAAACGTGTGGCGCAAAACACGAGACGTAACGTAAGGTGTGAAGCA	102382
QY	104398	GGCGGTACAGCAACTCGCGGCCCTTCAGGGTTAAAGGGCGGAAAAACACACCTGTAGCGGTG	104457
Db	102383	GGCGGTACAGCAACTCGCGGCCCTTCAGGGTTAAAGGGCGGAAAAACACACCTGTAGCGGTG	102442
QY	104458	GAAACAAAACTGGAAAGCATAGATCCCTGCTTCGCGCCACGAGGACGCGGCGGAAT	104517

D	102443	GAACAAAAAAGTGGAAAGCATATATCCCTGCTTCGGCCACGAGGAGCGCAGCGAAAT	102502
Q	104518	ATCATCGAGACTTGAACGATCGGCACACAGGGGTTGGCACCATCACCTCCGCGATT	104577
D	102503	ATCATCGAGACTTGAACGATCGGCACACAGGGGTTGGCACCATCACCTCCGCGATT	102562
Q	104578	AGGAGGCTCTCCGATCAATGCGGGGAGCGCCGAATTTCTTCAGAGAGCGCATACC	104637
D	102563	AGGAGGCTCTCCGATCAATGCGGGGAGCGCCGAATTTCTTCAGAGAGCGCATACC	102622
Q	104638	CGAAGGCTTCGAGATAGGCAAAATCAGAGGAGCTCAGGCGGTACATTAGTACAA	104697
D	102623	CGAAGGCTTCGAGATAGGCAAAATCAGAGGAGCTCAGGCGGTACATTAGTACAA	102682
Q	104698	AAAACAGTTTCTGGAGCATTTTGAACACCCAGCCCTAACGCTTTTCAACGCTTCCGCT	104757
D	102683	AAAACAGTTTCTGGAGCATTTTGAACACCCAGCCCTAACGCTTTTCAACGCTTCCGCT	102742
Q	104758	ATCCCAAAACATATACGAAAAAGTTCGGGCGCCCGCGCATGAGCTCGGTGGCCAGCT	104817
D	102743	ATCCCAAAACATATACGAAAAAGTTCGGGCGCCCGCGCATGAGCTCGGTGGCCAGCT	102802
Q	104818	GACCAATACACTTCAGCTGGCGGCGAGCGGCCCACTTACACGCGATAGAAAGCT	104877
D	102803	GACCAATACACTTCAGCTGGCGGCGAGCGGCCCACTTACACGCGATAGAAAGCT	102862
Q	104878	ACCGACGCTGATCCGAAAAAACCACTACGTCGCGCGCGCAGCGAGAGACCCCTTGCA	104937
D	102863	ACCGACGCTGATCCGAAAAAACCACTACGTCGCGCGCGCAGCGAGAGACCCCTTGCA	102922
Q	104938	CGCGCGATACGATCTCAAAAGCTCCTAGAGGGGTTGTTTCATATATGTTCCACACGCT	104997
D	102923	CGCGCGATACGATCTCAAAAGCTCCTAGAGGGGTTGTTTCATATATGTTCCACACGCT	102982
Q	104998	AACCCCGGTTCCAGACGGCCCGCGCTGGAATTCGAACACGAGGAGCAGCGCGGGGAGA	105057
D	102983	AACCCCGGTTCCAGACGGCCCGCGCTGGAATTCGAACACGAGGAGCAGCGCGGGGAGA	103042
Q	105058	GGCGCGACGATGATGAGACAGACAGTGGCCGACATGCTCAGACGCTCCAGACGTTCT	105117
D	103043	GGCGCGACGATGATGAGACAGACAGTGGCCGACATGCTCAGACGCTCCAGACGTTCT	103102
Q	105118	CGACAGTACGAGACACACCCGCGCAACGAGAAACGGGGCAATTTAACACATTTCT	105177
D	103103	CGACAGTACGAGACACACCCGCGCAACGAGAAACGGGGCAATTTAACACATTTCT	103162
Q	105178	GGCGATGTGGTTTTTACGCAATTCATAGGGGCGCTAGCAGAGCCGTGACGCTCCGAA	105237
D	103163	GGCGATGTGGTTTTTACGCAATTCATAGGGGCGCTAGCAGAGCCGTGACGCTCCGAA	103222
Q	105238	GTTACCGGACACCGCGCTGATTTTCCAGAGAGATGCTTAAACACCCAGGGAATGAC	105297
D	103223	GTTACCGGACACCGCGCTGATTTTCCAGAGAGATGCTTAAACACCCAGGGAATGAC	103282
Q	105298	AACACTGGTACCGCCATGAGGCGCCACCCGCGGGGCGCAATTTACGATTAATATCTA	105357
D	103283	AACACTGGTACCGCCATGAGGCGCCACCCGCGGGGCGCAATTTACGATTAATATCTA	103342
Q	105358	CTCGGAAGCCCTAGACTATGATGTTTCTCCGCTAATTTTCCAGGCGCTGCGCA	105417
D	103343	CTCGGAAGCCCTAGACTATGATGTTTCTCCGCTAATTTTCCAGGCGCTGCGCA	103402
Q	105418	CCTAACGCTAGAGGCCAGGTCAAAAAGCCACATTAACACCCGCTCAGTTGAGATG	105477
D	103403	CCTAACGCTAGAGGCCAGGTCAAAAAGCCACATTAACACCCGCTCAGTTGAGATG	103462
Q	105478	CTTTGCAAAACAGAGCAATTTCCGATTTTCCGGGCGCAATGCGCATGCGCAACTAGA	105537
D	103463	CTTTGCAAAACAGAGCAATTTCCGATTTTCCGGGCGCAATGCGCATGCGCAACTAGA	103522
Q	105538	GCAGAGCTGTGGGAGACAGCGACTTTTGCAAATCTGAGATTAACATCAACGCAAGG	105597

D	103523	GCAGAGCTGTGGGAGACAGCGACTTTTGCAAATCTGCGATTAACATCAACGCAAGG	103582
Q	105598	CAGGGTGGCGGCGCTGACCTTGGCGCTCAGACGATAGAGCGCGGTTTGGACCAACT	105657
D	103583	CAGGGTGGCGGCGCTGACCTTGGCGCTCAGACGATAGAGCGCGGTTTGGACCAACT	103642
Q	105658	GTTGGTCACTTTTAAACCCATGACAGCGCGGTGAGAGACAGTACTGACTAGTCA	105717
D	103643	GTTGGTCACTTTTAAACCCATGACAGCGCGGTGAGAGACAGTACTGACTAGTCA	103702
Q	105718	GACCTTACACTGACCACTTTTGGCGCGCGGTTCGAACGCGAGCGAGAAAGCAAC	105777
D	103703	GACCTTACACTGACCACTTTTGGCGCGCGGTTCGAACGCGAGCGAGAAAGCAAC	103762
Q	105778	CGAGACCGCGCTACGAGTACGAGACCCAGCGGCTACTGCTCGGGTCAATGAC	105837
D	103763	CGAGACCGCGCTACGAGTACGAGACCCAGCGGCTACTGCTCGGGTCAATGAC	103822
Q	105838	GAGCGCGTCCAGGCTTCAAAACACACCGGATCCGCTTTCGAGGCGGTGCTGGACGAT	105897
D	103823	GAGCGCGTCCAGGCTTCAAAACACACCGGATCCGCTTTCGAGGCGGTGCTGGACGAT	103882
Q	105898	GCTGTTACAGTACGATCAGATATTTTGGCGCGACGCGCAAGCGCTTGGCCAGG	105957
D	103883	GCTGTTACAGTACGATCAGATATTTTGGCGCGACGCGCGCAAGCGCTTGGCCAGG	103942
Q	105958	GGCGGGCGGATGGGCTCTCTCAACCCATCTGGAATGCGTCCGAGCTGAGCCCTT	106017
D	103943	GGCGGGCGGATGGGCTCTCTCAACCCATCTGGAATGCGTCCGAGCTGAGCCCTT	104002
Q	106018	CAAAAGCTGATTAAGGACACCCCGCAACCCCGGCAATTTG-AAAGGCTAACCCGCAATCC	106076
D	104003	CAAAAGCTGATTAAGGACACCCCGCAACCCCGGCAATTTGAAAGGCTAACCCGCAAT-CC	104061
Q	106077	TCCACCGCAGCAGAGCGACAGAGTCTTTTGAGACAGGACAGTGGTATCTTACCGAT	106136
D	104062	TCCACCGCAGCAGAGCGACAGAGTCTTTTGAGACAGGACAGTGGTATCTTACCGAT	104121
Q	106137	TCACACCAACGAAAGCGCGCGTCTGCACTCCGCGCTTGTGTGATATGACCTTG	106196
D	104122	TCACACCAACGAAAGCGCGCGTCTGCACTCCGCGCTTGTGTGATATGACCTTG	104181
Q	106197	AAAACGCTGTAAGGAGCAAGTATCTCCAGTGGCGGCTGCAATTTTCGAGAGAGGCGG	106256
D	104182	AAAACGCTGTAAGGAGCAAGTATCTCCAGTGGCGGCTGCAATTTTCGAGAGAGGCGG	104241
Q	106257	TTTACGTGATGCCCGGACCATATACCCCGAGACTGGCCAAAAAGCTGTGGAATCAA	106316
D	104242	TTTACGTGATGCCCGGACCATATACCCCGAGACTGGCCAAAAAGCTGTGGAATCAA	104301
Q	106317	ACACGTCGTTGACGACCTCAGCAGCAGAGAGATATGTAACTTTTACTAGCTATCC	106376
D	104302	ACACGTCGTTGACGACCTCAGCAGCAGAGAGATATGTAACTTTTACTAGCTATCC	104361
Q	106377	GAGAACAGGGAGCGGTCGAAGGAGGAGATATCTTCAGAGGCGTCCGACAAACGTAAC	106436
D	104362	GAGAACAGGGAGCGGTCGAAGGAGGAGATATCTTCAGAGGCGTCCGACAAACGTAAC	104421
Q	106437	CGGAAACACCGCAATCTCTCGGCAATGGGAAAAAGGATTAACGATTAATTAACGCAACAG	106496
D	104422	CGGAAACACCGCAATCTCTCGGCAATGGGAAAAAGGATTAACGATTAATTAACGCAACAG	104481
Q	106497	AAAACGCAAAAAACCTCATATATATCTGCGTCTCTTAAAGCGCGGACAGATCCACGG	106556
D	104482	AAAACGCAAAAAACCTCATATATATCTGCGGCTCTCTTAAAGCGCGGACAGATCCACGG	104541
Q	106557	TGGAACCAAGACCCGCAATTCACAGGGGCAAGCGTCGGAACACGGAACAGCAAGCTAA	106616
D	104542	TGGAACCAAGACCCGCAATTCACAGGGGCAAGCGTCGGAACACGGAACAGCAAGCTAA	104601
Q	106617	ACCAGCGCGTCAAAATTAATTCACACGCTCAAGTAAACACGCTCAACCGCACTCAG	106676
D	104602	ACCAGCGCGTCAAAATTAATTCACACGCTCAAGTAAACACGCTCAACCGCACTCAG	104661

QY	106677	CCTCATCTTACCGGAAAAATTCAACAGCAACGGTGCCTCGACTAATATCTCAACGT	106736
Db	104662	CCTCATCTTACCGGAAAAATTCAACAGCAACGGTGCCTCGACTAATATCTCAACGT	104721
QY	106737	CGGAAGGGCCCATTTAAACCGAGCGCTCGGGCAGGTCAACCGAAGGGAATCT	106796
Db	104722	CGGAAGGGCCCATTTAAACCGAGCGCTCGGGCAGGTCAACCGAAGGGAATCT	104781
QY	106797	TTGGAGCGTATAAACCCCGAGTGTCAACGAAACCCGCAAAACCGCGCGGTAG	106856
Db	104782	TTGGAGCGTATAAACCCCGAGTGTCAACGAAACCCGCAAAACCGCGCGGTAG	104841
QY	106857	CCTCTCGGCAACCAAGGCAACACACAGGTGCCCAAGTTACCGATTAATCCACCA	106916
Db	104842	CCTCTCGGCAACCAAGGCAACACACAGGTGCCCAAGTTACCGATTAATCCACCA	104901
QY	106917	CTAGGGTCTTTATAGGAGCCGGTCCAAACTCTCGCAGCGCTCGAAGAGCAACGGG	106976
Db	104902	CTAGGGTCTTTATAGGAGCCGGTCCAAACTCTCGCAGCGCTCGAAGAGCAACGGG	104961
QY	106977	CCACACCCGAGCGACATCATGTCGGAAGTATGATGGAAAAATACGCCGAGTCCGCTC	107036
Db	104962	CCACACCCGAGCGACATCATGTCGGAAGTATGATGGAAAAATACGCCGAGTCCGCTC	105021
QY	107037	GGCGGACCCACACCTCGAAGAGGGGCCAGGGAGCTCAGTCGAACACTCCAAACGAGG	107096
Db	105022	GGCGGACCCACACCTCGAAGAGGGGCCAGGGAGCTCAGTCGAACACTCCAAACGAGG	105081
QY	107097	CACACATAAACGTCCCTCTTAGCCAAAGTCAAAAAACAGTACACGGGCGCAAAATCCG	107156
Db	105082	CACACATAAACGTCCCTCTTAGCCAAAGTCAAAAAACAGTACACGGGCGCAAAATCCG	105141
QY	107157	GCCTTCAAAAGCACTCCGAGGGCCCCCAACCAACGCGATCAAAACCGCGCATTCAT	107216
Db	105142	GCCTTCAAAAGCACTCCGAGGGCCCCCAACCAACGCGATCAAAACCGCGCATTCAT	105201
QY	107217	ACACGCTCCCGGAAGCGGCGCGGTGTCTCAGAGCAATCGAGAGTGAATCGACCC	107276
Db	105202	ACACGCTCCCGGAAGCGGCGCGGTGTCTCAGAGCAATCGAGAGTGAATCGACCC	105261
QY	107277	CAACCGAGAGGTAAAGATGCGCCAAAACCAAGATGTGTCTCAACGGGCCGGAACCG	107336
Db	105262	CAACCGAGAGGTAAAGATGCGCCAAAACCAAGATGTGTCTCAACGGGCCGGAACCG	105321
QY	107337	ACGATCTCAGGTGAGACCGCGCGTGGTCAACCATAGATTCATCGACTGGAACACC	107396
Db	105322	ACGATCTCAGGTGAGACCGCGCGTGGTCAACCATAGATTCATCGACTGGAACACC	105381
QY	107397	CCCAATTTCTCAAAATATATACATCATCACCCTCCCACTCCACAGATCACCCCAATCC	107456
Db	105382	CCCAATTTCTCAAAATATATACATCATCACCCTCCCACTCCACAGATCACCCCAATCC	105441
QY	107457	CTCCAGCTAACGTCGATACCCGATTCACAGTCAAGTCAACGCAAGAAATCAAC	107516
Db	105442	CTCCAGCTAACGTCGATACCCGATTCACAGTCAAGTCAACGCAAGAAATCAAC	105501
QY	107517	GAGCCAAAGATGTGTTAATGCGATTTATCAAAAGTACGAAGAAAACTTCAAGCGTGT	107576
Db	105502	GAGCCAAAGATGTGTTAATGCGATTTATCAAAAGTACGAAGAAAACTTCAAGCGTGT	105561
QY	107577	CTGACGCTATTCGAGGCTATTTGCGAAGATTAAGTTTATATCTGTAACGCCCAATC	107636
Db	105562	CTGACGCTATTCGAGGCTATTTGCGAAGATTAAGTTTATATCTGTAACGCCCAATC	105621
QY	107637	TCACTTGGCTTTTTTATTTTGAAGAGAGCGTCTTGTCACAGTATGTTGCGTCTAG	107696
Db	105622	TCACTTGGCTTTTTTATTTTGAAGAGAGCGTCTTGTCACAGTATGTTGCGTCTAG	105681
QY	107697	TGATTAACGAATGAGACCCATATGCCAGAGAGCGCACGCTCCGGGTCCGCGCACCGG	107756
Db	105682	TGATTAACGAATGAGACCCATATGCCAGAGAGCGCACGCTCCGGGTCCGCGCACCGG	105741

QY	107757	CGCGGGGGCCCAATCGAGCCTATCAATGAATGGGGCCCCGCTGGAGATCTGTAGTAAAGCTATT	107816
Db	105742	CGCGGGGGCCCAATCGAGCCTATCAATGAATGGGGCCCCGCTGGAGATCTGTAGTAAAGCTATT	105801
QY	107817	TGACCCGAGGGGGGAGGGCCACCGGGGGCAACGCTCGGGGGGGCGAGAGCCGAGCCGGACAA	107876
Db	105802	TGACCCGAGGGGGGAGGGCCACCGGGGGCAACGCTCGGGGGGGCGAGAGCCGAGCCGGACAA	105861
QY	107877	AACGCCCGAGATACTAGAACTAGCGTCTCTTTTGGCGGAGAAAGCCCCGGAGGGTGGTCTTT	107936
Db	105862	AACGCCCGAGATACTAGAACTAGCGTCTCTTTTGGCGGAGAAAGCCCCGGAGGGTGGTCTTT	105921
QY	107937	GGCGAGAATTCATTCTCTTTTGCATATACATGTCTGATATGATGTTTGGCGGTTAAAA	107996
Db	105922	GGCGAGAATTCATTCTCTTTTGCATATACATGTCTGATATGATGTTTGGCGGTTAAAA	105981
QY	107997	CACCGAGATTAATAGCTTTTCGGGATGTGGCATACGTGGGGGGGAGACATCTCACCCCTGGGGAAG	108056
Db	105982	CACCGAGATTAATAGCTTTTCGGGATGTGGCATACGTGGGGGGGAGACATCTCACCCCTGGGGAAG	106041
QY	108057	GTTTGTTCATCTCGGCAACAGCGGGGGTATTTGGTAAATGTGCTCAAGGCGTCCCTGAAC	108116
Db	106042	GTTTGTTCATCTCGGCAACAGCGGGGGTATTTGGTAAATGTGCTCAAGGCGTCCCTGAAC	106101
QY	108117	GATTGGCTCTTAACCCCGAGGAGCAGCATCTCTTTTAACTTCTATTACATTTTCCACAG	108176
Db	106102	GATTGGCTCTTAACCCCGAGGAGCAGCATCTCTTTTAACTTCTATTACATTTTCCACAG	106161
QY	108177	GACAGGGAGCATATAGAGAGGTTCAAAATTAACAGCTCGGCCACACGGAAATGCTTTAAT	108236
Db	106162	GACAGGGAGCATATAGAGAGGTTCAAAATTAACAGCTCGGCCACACGGAAATGCTTTAAT	106221
QY	108237	AGGCGGGTCCGCACTCCGGCGACGCCAAACAGGCGACAGCAGCTTAACAGAGGAGTTTC	108296
Db	106222	AGGCGGGTCCGCACTCCGGCGACGCCAAACAGGCGACAGCAGCTTAACAGAGGAGTTTC	106281
QY	108297	GCGTCTCGTATGAGCATGTGCGCGCTGTTGGGAGACGCGACCGTAAATAGGAGATCTCA	108356
Db	106282	GCGTCTCGTATGAGCATGTGCGCGCTGTTGGGAGAGCGACCGTAAATAGGAGATCTCA	106341
QY	108357	ACACACGTGATCTCGAATTAAGATATTAACCCCGCATGTGGGATCCGGCACAAATTAAGGCAN	108416
Db	106342	ACACACGTGATCTCGAATTAAGATATTAACCCCGCATGTGGGATCCGGCACAAATTAAGGCAN	106401
QY	108417	TATACGCGCCCGGTGTAGCAGATCGAAACCTGCTCTCTTTTGGTGGGACGTGAA	108476
Db	106402	TATACGCGCCCGGTGTAGCAGATCGAAACCTGCTCTCTTTTGGTGGGACGTGAA	106461
QY	108477	AACACGTTGTGGTGGGAAATTTACGGTTTCAAAATTTACCCCGTCGGAATTTCAAAACAG	108536
Db	106462	AACACGTTGTGGTGGGAAATTTACGGTTTCAAAATTTACCCCGTCGGAATTTCAAAACAG	106521
QY	108537	TAACCGCACTCGAGGCACACACACACCTTCGGAGCTGGGACGGTCTTCTCCAGTACGCTC	108596
Db	106522	TAACCGCACTCGAGGCACACACACACCTTCGGAGCTGGGACGGTCTTCTCCAGTACGCTC	106581
QY	108597	CTGGCGACACACTCGGGAGCAACACAGGTAGAGATACAGGAAACAGTACGTTATACGCC	108656
Db	106582	CTGGCGACACACTCGGGAGCAACACAGGTAGAGATACAGGAAACAGTACGTTATACGCC	106641
QY	108657	AATACTTTTGAACCCAGGTGCGGGGATATCTCGTCTGGTGCAGTCCCTATATGGGCAAC	108716
Db	106642	AATACTTTTGAACCCAGGTGCGGGGATATCTCGTCTGGTGCAGTCCCTATATGGGCAAC	106701
QY	108717	ACACACGGGAGACATGCTCAGCAGGGGCCCTTAACGTCAGGCTCTCTAGAAAGGGCGTTAAAC	108776
Db	106702	ACACACGGGAGACATGCTCAGCAGGGGCCCTTAACGTCAGGCTCTCTAGAAAGGGCGTTAAAC	106761
QY	108777	GGGTTTCCGCGACGGGAGCGGTGCGGCGCAATTTCTCGAGGAGGAGCCGGAAGTCCCGCGTCC	108836
Db	106762	GGGTTTCCGCGACGGGAGCGGTGCGGCGCAATTTCTCGAGGAGGAGCCGGAAGTCCCGCGTCC	106821
QY	108837	GAAGGGCCCCGGACACTCTCATTTACAGTTTACGCTCCAGACGTCTGGAATTAAGACGGAACG	108906

Db	106822	GAAGGGCCCCGGACACTCTCATTTCAAGTTAGTCCAGACGTCGTGGAAATTCAGCGAAGC	106881
Oy	108897	TTCAACTGCATCGAGACACAAACGGCCCCGGTTCATATTTCTTCGCAAAACGGGCAGATCC	108956
Db	106882	TTCAACTGCATCGAGACACAAACGGCCCCGGTTCATATTTCTTCGCAAAACGGGCAGATCC	106941
Oy	108957	AACGGGTGCTGTGGCAACAGTAAACCAAGGGGAAACCGCTGGCGACACATTTAGGGTTTG	109016
Db	106942	AACGGGTGCTGTGGCAACAGTAAACCAAGGGGAAACCGCTGGCGACATTTAGGGTTTG	107001
Oy	109017	CACAGAGACACACGCCCCCTTGAAACGCACACAAACAGATACCTGGACACCGGCTCCG	109076
Db	107002	CACAGAGACACACGCCCCCTTGAAACGCACACAAACAGATACCTGGACACCGGCTCCG	107061
Oy	109077	GGAAAGGCGCTTAAACTTAAACCTTCGTCGTCGGGACAGCCACGGCGGTGCAGATACAC	109136
Db	107062	GGAAAGGCGCTTAAACTTAAACCTTCGTCGTCGGGACAGCCACGGCGGTGCAGATACAC	107121
Oy	109137	CTCAGACACCCACGCGTAGCGCTCTTAACAACGACACGGCGCATATCTGACAGCGCGATCTC	109196
Db	107122	CTCAGACACCCACGCGTAGCGCTCTTAACAACGACACGGCGCATATCTGACAGCGCGATCTC	107181
Oy	109197	ACGTGGCGGTTTTTAGGGGGTTATCCGGCCGACAGCGGGTAGCATCTGCTCAGGGG	109256
Db	107182	ACGTGGCGGTTTTTAGGGGGTTATCCGGCCGACAGCGGGTAGCATCTGCTCAGGGG	107241
Oy	109257	GCTCGAAAGATGGGGGAGAAATTTAACTGCACAGCCATATTTGGGGGTGTCGCTCCAG	109316
Db	107242	GCTCGAAAGATGGGGGAGAAATTTAACTGCACAGCCATATTTGGGGGTGTCGCTCCAG	107301
Oy	109317	GCACCGAGCCCGTAGCTACATAAACAACACATGACATTCGGGGCATATGTCGATGAGCGT	109376
Db	107302	GCACCGAGCCCGTAGCTACATAAACAACACATGACATTCGGGGCATATGTCGATGAGCGT	107361
Oy	109377	ATAGAGGGCGGGAGATCTTAGCGCCACGGCGAGAACCATCCAGCAACAGATGGGAGATAA	109436
Db	107362	ATAGAGGGCGGGAGATCTTAGCGCCACGGCGAGAACCATCCAGCAACAGATGGGAGATAA	107421
Oy	109437	GAACCGCGCCCATGACAGGACAGCTTCGTTTCAGCCAGGTTTAGCAAGCGGCCGACAGGC	109496
Db	107422	GAACCGCGCCCATGACAGGACAGCTTCGTTTCAGCCAGGTTTAGCAAGCGGCCGACAGGC	107481
Oy	109497	ATCCCCCAATTTGTAACCGATGTAATTTGGTTAATTTGGTCATCGCCGCA - CGCTCTCGGGCC	109555
Db	107482	ATCCCCCAATTTGTAACCGATGTAATTTGGTTAATTTGGTCATCGCCGCA - CGCTCTCGGGCC	107541
Oy	109556	CAATATCCTTCAACATCCGACCCCGGAAGGGGGGCCACGAGAGCCCGTTCCCTCAACGACAC	109615
Db	107542	CAATATCCTTCAACATCCGACCCCGGAAGGGGGGCCACGAGAGCCCGTTCCCTCAACGACAC	107601
Oy	109616	CGAGGCGCTCGGAGAGTA - CCGCTCAGGGCGAAACCCGTTCTTAAGAAAGGTTTTTAACGCT	109674
Db	107602	CGAGGCGCTCGGAGAGTA - CCGGAGTACCCCGTCAGGGCGAAACCCGTTCTTAAGAAAGGTTTTTAACGCT	107661
Oy	109675	TTAGCGCTTTTGGAGTCACGACCAAAAACTGTAAACCTGTGCGGTCTCCGTTAAAGTAG	109734
Db	107662	TTAGCGCTTTTGGAGTCACGACCAAAAACTGTAAACCTGTGCGGTCTCCGTTAAAGTAG	107721
Oy	109735	GTGGCGCATATGACCATGAGCTGTAAACGTTTAGTCTCCGGAGAAAACCAAGAGCTGCC	109794
Db	107722	GTGGCGCATATGACCATGAGCTGTAAACGTTTAGTCTCCGGAGAAAACCAAGAGCTGCC	10781
Oy	109795	TTAAATTTCAATAAATCGTCGGCGCCAGGGGACAGGAGAGATTCCTCTCAAGATPACAG	109854
Db	107782	TTAAATTTCAATAAATCGTCCTGTGGCGCCAGGGACAGGAGAGATTCCTCTCAAGATPACAG	107841
Oy	109855	TCCGAATTTATAGCGAGGTTTTTTTCCAACATGGGCGATCGGCTCAAGTGGCTTACACAA	109914
Db	107842	TCCGAATTTATAGCGAGGTTTTTTTCCAACATGGGCGATCGGCTCAAGTGGCTTACACAA	107901
Oy	109915	AAACAATTTACAGCGTGGTGGCCAAACCGTTGTTGATTAATTAACAAACACGGGGCAACGGG	109974

Db	1079020	AAACATTTTCAGCGTGGTGGCCACGACCCGTTGTGATATTTACAAACACGGGGCAAAACGGG	107961
QY	109975	TAGGCCAGTCTCTCTAGATTGTGGAGCCAAAACCTTATACACAACTCGAGATGATAGACG	110034
Db	107962	TAGGCGACAGCTCTCTAGTTTGTGGAGCCAAAACCTTATACAAACCTCGAGATGATAGACG	108021
QY	110035	CAGCCGTGCTGACAGCGCAGCGGTGCACACGGGGACCGCCGCCCTTTAGCGTATACGGGA	110094
Db	108022	CAGCCGTGCTGACAGCGCAGCGGTGCACACGGGGACCGCCGCCCTTTAGCGTATACGGGA	108081
QY	110095	GGCCCGTCTCTGACACTCTCTCCAAAGTCACAGGAGATTCACAGAGGTTCCACAGTAAGAGACA	110154
Db	108082	GGCCCGTCTCTGACACTCTCTCCAAAGTCACAGGAGATTCACAGAGGTTCCACAGTAAGAGACA	108141
QY	110155	ACTAAATCGCACAGCTCGTCAACTAAACGTTTTCCGGAACTCATCGTATATAAGATCTTT	110214
Db	108142	ACTAAATCGCACAGCTCGTCAACTAAACGTTTTCCGGAACTCATCGTATATAAGATCTTT	108201
QY	110215	TAGGTGCTGTGTGGTGGCTCCGCTAAAAACCGCGTCCGTCTTAACGATTTTGTGAAATGACC	110274
Db	108202	TAGGTGCTGTGTGGTGGCTCCGCTAAAAACCGCGTCCGTCTTAACGATTTTGTGAAATGACC	108261
QY	110275	TGTTTACGGCGCTTTACCTTTGGCGTCCAGAGACATGACAGTGTGTCACAGTAGTGACCGG	110334
Db	108262	TGTTTACGGCGCTTTACCTTTGGCGTCCAGAGACATGACAGTGTGTCACAGTAGTGACCGG	108321
QY	110335	GTCTGAGCACGATGTGACAGAGSAAAGTTTTTAAATACTGACAGTAGTTAATGGCGTTGAGC	110394
Db	108322	GTCTGAGCACGATGTGACAGAGSAAAGTTTTTAAATACTGACAGTAGTTAATGGCGTTGAGC	108381
QY	110395	CTGGAAATATATGTGTGGGAACATAATTTTCATGTCAATCGGGACAGAGGACATCGAACGCC	110454
Db	108382	CTGGAAATATATGTGTGGGAACATAATTTTCATGTCAATCGGGACAGAGGACATCGAACGCC	108441
QY	110455	AATAAATGCTACCCGAACATCAGAGAGACAGAGGAAAAAAGATGCTACACGCCGCGTACCG	110514
Db	108442	AATAAATGCTACCCGAACATCAGAGAGACAGAGGAAAAAAGATGCTACACGCCGCGTACCG	108501
QY	110515	CGTAACACGCGCAGCAGCCACCCCTTCAATATTTTAGCCTTAAAAAGCGGGGCCCTTAAA	110574
Db	108502	CGTAACACGCGCAGCAGCCACCCCTTCAATATTTTAGCCTTAAAAAGCGGGGCCCTTAAA	108561
QY	110575	GTCTGTCCAATCAGCTTAAAAACTCTACCCATTATGTTCTGTCGGTGGCACTGTGAGAC	110634
Db	108562	GTCTGTCCAATCAGCTTAAAAACTCTACCCATTATGTTCTGTCGGTGGCACTGTGAGAC	108621
QY	110635	CCTCATGTGACACCTGGCCCTCTCTCGGGGACATCGTAGAACATCTTCTCCCGCGTAC	110694
Db	108622	CCTCATGTGACACCTGGCCCTCTCTCGGGGACATCGTAGAACATCTTCTCCCGCGTAC	108681
QY	110695	CCCGGACGAGCTTTTAAACAGCCCGGTATTAACTCCAACTCAGACTCTCTCAACCCCG	110754
Db	108682	CCCGGACGAGCTTTTAAACAGCCCGGTATTAACTCCAACTCAGACTCTCTCAACCCCG	108741
QY	110755	CTCATCTGTGACAGGCTGTGTAGCTCTCTGTCTACTCTGTGTGTGCGGACATTTCCACCCCGCA	110814
Db	108742	CTCATCTGTGACAGGCTGTGTAGCTCTCTGTCTACTCTGTGTGTGCGGACATTTCCACCCCGCA	108801
QY	110815	CTCTTTCTTCCGAAGACTACAGGTGTGGTTGTGCTCATCAGTCCATATACGCCGCCGAGTATAG	110874
Db	108802	CTCTTTCTTCCGAAGACTACAGGTGTGGTTGTGCTCATCAGTCCATATACGCCGCCGAGTATAG	108861
QY	110875	GACGGCTACCCCAAGGTGTGGCTGCGCAGCTTTTGAAGCTTAAGCAGAGTACTTCCCGCA	110934
Db	108862	GACGGCTACCCCAAGGTGTGGCTGCGCAGCTTTTGAAGCTTAAGCAGAGTACTTCCCGCA	108921
QY	110935	ATGCGGTGAAGATGGGCCAGTATACACGCCCCCAAAGCATCTCGGAATTCGACGTCAGCT	110994
Db	108922	ATGCGGTGAAGATGGGCCAGTATACACGCCCCCAAAGCATCTCGGAATTCGACGTCAGCT	108981
QY	110995	GCACCTTCTTCCGAACCCGCTGCTTCCAGACCATGACAGAGAAACAAATACTCCACACATCT	110504
Db	108982	GCACCTTCTTCCGAACCCGCTGCTTCCAGACCATGACAGAGAAACAAATACTCCACACATCT	109041

QY	111055	TCATTTAAATTTTTTTACAAACCGAGTTATTATAGGGGCATGTTAGAGGCACGATTC	CGGG	111114
Dp	109042	TCATTTAAATTTTTTTACAAACCGAGTTATTATAGGGGCATGTTAGAGGCACGATTC	CGGG	109101
QY	111115	ATCGTTCGTTTTAAACGTCCTGGCCGGCGCACAGAAAAGSAGCCCAACCTAC	CGGT	111174
Dp	109102	ATCGTTCGTTTTAAACGTCCTGGCCGGCGCACAGAAAAGSAGCCCAACCTAC	CGGT	109161
QY	111175	TGCGTGTGTTCCGTTGGCGCGCGGAGTCCACACCAACGCGAGTAACCCGCTAC	CGGAGA	111234
Dp	109162	TGCGTGTGTTCCGTTGGCGCGCGGAGTCCACACCAACGCGAGTAACCCGCTAC	CGGAGA	109221
QY	111235	CCTGGAGAGCGCGTTCAACTCCAGAGACGCGGAGGAAAAACCAGCTCTCTCGG	CGTCTT	111294
Dp	109222	CCTGGAGAGCGCGTTCAACTCCAGAGACGCGGAGGAAAAACCAGCTCTCTCGG	CGTCTT	109281
QY	111295	TTGGGCAACGTGGGCGAGAAATCCAGCTCTTGGGCTCCGACACAAACAGGCA	AGATCCGA	111354
Dp	109282	TTGGGCAACGTGGGCGAGAAATCCAGCTCTTGGGCTCCGACACAAACAGGCA	AGATCCGA	109341
QY	111355	TTTACAAACCTCCCGCTTCCCAACCCCAAGAAAGATCTGACCAATCACAGGGCC	CGCTCGCT	111414
Dp	109342	TTTACAAACCTCCCGCTTCCCAACCCCAAGAAAGATCTGACCAATCACAGGGCC	CGCTCGCT	109401
QY	111415	GATGCACCCCAACGCTCAACCTTAAAAACAAAAACACACCGCATCTATGCGT	CTATAG	111474
Dp	109402	GATGCACCCCAACGCTCAACCTTAAAAACAAAAACACACCGCATCTATGCGT	CTATAG	109461
QY	111475	CGAGTGTGTGGCGCGACACCCGCGAGCGCGGTCCGGTTTGAAAGATCTGCGT	CGGCACAT	111534
Dp	109462	CGAGTGTGTGGCGCGACACCCGCGAGCGCGGTCCGGTTTGAAAGATCTGCGT	CGGCACAT	109521
QY	111535	TCTGGAAAAACATGAAAAACAGCTTAAAGTCTCATCGCATATCGTATACCTTA	ACGA	111594
Dp	109522	TCTGGAAAAACATGAAAAACAGCTTAAAGTCTCATCGCATATCGTATACCTTA	ACGA	109581
QY	111595	TCCGGACTCAGCTGTACACAGTGTGCGGACGAAACATCTGTGCGGCGCTTA	TTAAACGGTGTCTC	111654
Dp	109582	TCCGGACTCAGCTGTACACAGTGTGCGGACGAAACATCTGTGCGGCGCTTA	TTAAACGGTGTCTC	109641
QY	111655	GGCAACAACAANTCCACAGCATTTTTTTTTGGGACACCCGGGTGCTGCTCA	AAACCGTACCTC	111714
Dp	109642	GGCAACAACAANTCCACAGCATTTTTTTTTGGGACACCCGGGTGCTGCTCA	AAACCGTACCTC	109701
QY	111715	GCACGTGTCCCGGTTTTATTATTAATGCGCACCTCCGCAAAAGTATAAGAGT	CAAAAC	111774
Dp	109702	GCACGTGTCCCGGTTTTATTATTAATGCGCACCTCCGCAAAAGTATAAGAGT	CAAAAC	109761
QY	111775	TCGTCGTGGCAACCGGAGAGTTCCTAGACTGTCAACAGAAATATTTGACT	GTGGAGACCTTACA	111834
Dp	109762	TCGTCGTGGCAACCGGAGAGTTCCTAGACTGTCAACAGAAATATTTGACT	GTGGAGACCTTACA	109821
QY	111835	GACCTGTGGCGCTCTCTTTAAGGGGTCTCACTGGCCAAATGCGCAAAAC	CGTGTGCT	111894
Dp	109822	GACCTGTGGCGCTCTCTTTAAGGGGTCTCACTGGCCAAATGCGCAAAAC	CGTGTGCT	109881
QY	111895	CGAGTATATCGGTGAAGTGTGATTTCACTGGGTGGACACAATTCCAATCA	CCCAACCC	111954
Dp	109882	CGAGTATATCGGTGAAGTGTGATTTCACTGGGTGGACACAATTCCAATCA	CCCAACCC	109941
QY	111955	GTTTCAAACTCCCAACTATACATTTAATCTTCAGAAAGGCAACAGACATG	CAAAACA	112014
Dp	109942	GTTTCAAACTCCCAACTATACATTTAATCTTCAGAAAGGCAACAGACATG	CAAAACA	110001
QY	112015	GCCCCAAGTGTGATTTGGCGTCTCGAGCGCGCTTACGCACTTAAGCGT	CAGGCGACCGGACG	112074
Dp	110002	GCCCCAAGTGTGATTTGGCGTCTCGAGCGCGCTTACGCACTTAAGCGT	CAGGCGACCGGACG	110061
QY	112075	GCCCCAGTCCACGCAACCGGCACTCCAGAGACGGCACTGTGCAAAAG	GAATATATGAGAGT	112134
Dp	110062	GCCCCAGTCCACGCAACCGGCACTCCAGAGACGGCACTGTGCAAAAG	GAATATATGAGAGT	110121

QY	112135	AAAAAGATTAGTTACAGACAGCACTTTTTTTTCTGCGCTTAACGGCGCGCACAGACTGGG	112194
Db	110122	GAAGAAAGTTAGTTTCAGACAGCACTTTTTTTTCTGCGCTTAACGGCGCGCACAGACTGGG	110181
QY	112195	GGTGGACTTTTAAAGAGAAATGGGAGACCCCGATATGACACTCCAAAGTCGGTATATTGGCC	112254
Db	110182	GCTGGACTTTTAAAGAGAAATGGGAGACCCCGATATGACACTCCAAAGTCGGTATATTGGCC	110241
QY	112255	GTTAAACCTAAAAACCATCGCCCCGGGTGCGGTGCTCTCTCTCATCATTTGGACACTTC	112314
Db	110242	GTTAAACCTAAAAACCATCGCCCCGGGTGCGGTGCTCTCTCTCATCATTTGGACACTTC	110301
QY	112315	GTCAAACTATGGGGTTCAACTGTTCGTGTGACGCCCACTGACAGSTGACGGGTGTCTCT	112374
Db	110302	GTCAAACTATGGGGTTCAACTGTTCGTGTGACGCCCACTGACAGSTGACGGGTGTCTCT	110361
QY	112375	GGAGCCAAACGGCGCTCGGGGAAAGATTCCGCGACGAAAAACACGCAAGCTGTGTTCACTGGC	112434
Db	110362	GGAGCCAAACGGCGCTCGGGGAAAGATTCCGCGACGAAAAACACGCAAGCTGTGTTCACTGGC	110421
QY	112435	GTTAAACCTTTTACCAACACGCGCGAAAAAGGTGCTGACGACCAAGGGCTTTTACCTGTCTCT	112494
Db	110422	GTTAAACCTTTTACCAACACGCGCGAAAAAGGTGCTGACGACCAAGGGCTTTTACCTGTCTCT	110481
QY	112495	GCTCAGCCACATCCATGGAAGTGGTTAGGAAAAAGCTTACGCAACCCGGGTGTCTACGC	112554
Db	110482	GCTCAGCCACATCCATGGAAGTGGTTAGGAAAAAGCTTACGCAACCCGGGTGTCTACGC	110541
QY	112555	CCACCTAGTCCGTAAGAAACCTTTGGGACAGATCTTTACCTATTTTACAGTGGATCCGA	112614
Db	110542	CCACCTAGTCCGTAAGAAACCTTTGGGACAGATCTTTACCTATTTTACAGTGGATCCGA	110601
QY	112615	TGAGAGACTCGCACTGTGGGGCGGTGTCCACACTAGAGACTTACACCTGGGGGAAACCAAG	112674
Db	110602	TGAGAGACTCGCACTGTGGGGCGGTGTCCACACTAGAGACTTACACCTGGGGGAAACCAAG	110651
QY	112675	TCTGCGACTCATTTATGAGCAACCTTCCAAATTATGACATACGGTGGACTGCATCAAGCA	112734
Db	110662	TCTGCGACTCATTTATGAGCAACCTTCCAAATTATGACATACGGTGGACTGCATCAAGCA	110721
QY	112735	AACGACATTAATGAAGTTTACACCCCTGGGACCGGCAACGCAACCGGTACGGTTCTCTG	112794
Db	110722	AACGACATTAATGAAGTTTACACCCCTGGGACCGGCAACGCAACCGGTACGGTTCTCTG	110781
QY	112795	CAACGACTTTTGGCGAGGCGGTGGCCACCCCTAGACTGCAACCGCACTTTTCGAGAAAGAAAT	112854
Db	110782	CAACGACTTTTGGCGAGGCGGTGGCCACCCCTAGACTGCAACCGCACTTTTCGAGAAAGAAAT	110841
QY	112855	TCAAAGGGGCGACGCCATCATTAACCTCCAGGGGGCTATTGTAACTTTCCCTAGACGGAA	112914
Db	110842	TCAAAGGGGCGACGCCATCATTAACCTCCAGGGGGCTATTGTAACTTTCCCTAGACGGAA	110901
QY	112915	ACAGATGTAATTCACCTACTTCAATAGTTAAGTTTTGTTTGAACATATCACCAATAAAA	112974
Db	110902	ACAGATGTAATTCACCTACTTCAATAGTTAAGTTTTGTTTGAACATATCACCAATAAAA	110961
QY	112975	ACAACTTATGTTTACACAAATTTGAAGAGCGTTTCAATTTTACCATTAAACATAGCAAAAA	113034
Db	110962	ACAACTTATGTTTACACAAATTTGAAGAGCGTTTCAATTTTACCATTAAACATAGCAAAAA	110211
QY	113035	CACGGTAACATAAACTCAATAGCAGATTTCCGATGGGATCCCTAGAGACCAATCGACGTG	113094
Db	111022	CACGGTAACATAAACTCAATAGCAGATTTCCGATGGGATCCCTAGAGACCAATCGACGTG	111081
QY	113095	CGCGCGTATTATTTACAGGGGAACGACGTTAAGTGTCTCTCCACGAAATTCGCAAACTCCGGC	113154
Db	111082	CGCGCGTATTATTTACAGGGGAACGACGTTAAGTGTCTCTCCACGAAATTCGCAAACTCCGGC	111411
QY	113155	TTTTTATAGCCATTGACGCGGCTTATATATTTGGCAGTAAACGCGAAAGGGCTACATCG	113214
Db	111142	TTTTTATAGCCATTGACGCGGCTTATATATTTGGCAGTAAACGCTACGAAAGGGCTACATCG	111201
QY	113215	CAGTATGATTTTACAGTGTGACACACTTTTCGCGGGTTTACCGCGCAACCAACAAACCGGG	113274

Db	111202	CAGTAGTAGTTTACGATGTGCACACCTTTCGGCGTTACCGCCACACAAACGCGG	111261
OY	113275	TCACGAGCAGCTAAATGCGCCGCGCCTTTATGCCAAAGTACAAAAGGAGCGCGTTC	113334
Db	111262	TCACGAGCAGCTAAATGCGCCGCGCCTTTATGCCAAAGTACAAAAGGAGCGCGTTC	111321
OY	113355	TACGTTACGACGACACACTGTTGATTCGCAAAATACATATAGTGTGTGGTGACCGCAACT	113394
Db	111322	TACGTTACGACGACCAACACTGTTGATTCGCAAAATACATATAGTGTGTGGTGACCGCAACT	111381
OY	113395	GCCAAATCCTAAATATGATGAGCATATAGTCTCTCAAAATCTAGAACGAATCTCCAAAACAT	113454
Db	111382	GCCAAATCCTAAATATGATGAGCATATAGTCTCTCAAAATCTAGAACGAATCTCCAAAACAT	111411
OY	113455	GGCGCAATTAACCAACCCCTTGCAGTTAAAGCAATCGTAACGAGACGGAATCCAAAGAC	113514
Db	111442	GGCGCAATTAACCAACCCCTTGCAGTTAAAGCAATCGTAACGAGACGGAATCCAAAGAC	111501
OY	113515	ACGCCGAGTCTTAAGACACGCGGACAGTCTTTGGGTTCCGGGGCGTTAGCATGGAAG	113574
Db	111502	ACGCCGAGTCTTAAGACACGCGGACAGTCTTTGGGTTCCGGGGCGTTAGCATGGAAG	111561
OY	113575	TTGATCACAACATATCCCATCAACCGTTACAAAAGCGTAAGATTAATGGTTTACAATA	113634
Db	111562	TTGATCACAACATATCCCATCAACCGTTACAAAAGCGTAAGATTAATGGTTTACAATA	111621
OY	113635	AACAAATAAAAAATAGTGCAGCAAGTTACATTCGCAATACAAAGCGGACCCCAAAAAACAC	113694
Db	111622	AACAAATAAAAAATAGTGCAGCAAGTTACATTCGCAATACAAAGCGGACCCCAAAAAACAC	111681
OY	113695	CCCAACGCAAAAACACTGAGACCTGTGTCTTTGGGTCCCTTCACAGTCCGCAATGAGATT	113754
Db	111682	CCCAACGCAAAAACACTGAGACCTGTGTCTTTGGGTCCCTTCACAGTCCGCAATGAGATT	111741
OY	113755	CTGGGACCGGTGTGCTGCTTAACGGGTTACAGTGTGTTTATGGTACGTAAACACAC	113814
Db	111742	CTGGGACCGGTGTGCTGCTTAACGGGTTACAGTGTGTTTATGGTACGTAAACACAC	111801
OY	113815	AATCTAGAATGCTTAACAGGTGCACGCGCTTAGGGCGCTTGTGCAACTAAGTGCATGA	113874
Db	111802	AATCTAGAATGCTTAACAGGTGCACGCGCTTAGGGCGCTTGTGCAACTAAGTGCATGA	111861
OY	113875	GGTACTACTCTTATTTTAAACAATAGCATATCCAACTGCATTAATTGCACTAAACCA	113934
Db	111862	GGTACTACTCTTATTTTAAACAATAGCATATCCAACTGCATTAATTGCACTAAACCA	111921
OY	113935	GTTTAGTCTTTTACTGAGTGGCGCCATAGTCTCATGAGAACCATATCATCTCCG	113994
Db	111922	GTTTAGTCTTTTACTGAGTGGCGCCATAGTCTCATGAGAACCATATCATCTCCG	111981
OY	113995	TCAACGGCGGTGTACTACCGTTGTATTTGCGGGAAAAACAGGCTGGGGGAAAAAAG	114054
Db	111982	TCAACGGCGGTGTACTACCGTTGTATTTGCGGGAAAAACAGGCTGGGGGAAAAAAG	112041
OY	114055	CAACATATGCTGATTTTAAACACTCAAGTTCTAAATCTCACCCACTCTGTAAACAAA	114114
Db	112042	CAACATATGCTGATTTTAAACACTCAAGTTCTAAATCTCACCCACTCTGTAAACAAA	112101
OY	114115	AACATCGAGTTAAGGTATGTATCCGGAACATTAACAACACAGTTTAAACACAGCT	114174
Db	112102	AACATCGAGTTAAGGTATGTATCCGGAACATTAACAACACAGTTTAAACACAGCT	112161
OY	114175	GGCGTAATTAACCCCATTTGCGACGCGTGCCTGCTAAGGTTTAAATTAACATTG	114234
Db	112162	GGCGTAATTAACCCCATTTGCGACGCGTGCCTGCTAAGGTTTAAATTAACATTG	112221
OY	114235	TGCGTTTAAACACCGCAGCATTAATCTCAGAGGCGGTTAAACGAGCGATATACATATTC	114294
Db	112222	TGCGTTTAAACACCGCAGCATTAATCTCAGAGGCGGTTAAACGAGCGATATACATATTC	112811
OY	114295	CCTAAACGCGGAACGCGCGCTGCACCGCCTTCCCAATACACACAGGAGCTACAAAGC	114354

Db	112822	CCTAACAACGGGACGGCGGTGACGCCGCTCCCAATACACAACAGGGACCTACAAAGC	112341
OY	114355	CTAGTGTATATATTAATCAAAATTAACAAAACACAGAAACCTTTATGTGTGCGCAACAACCTA	114414
Db	112342	CTAGTGTATATATTAATCAAAATTAACAAAACACAGAAACCTTTATGTGTGCGCAACAACCTA	112401
OY	114415	GCAAAAGTACACAGAGCTTTCCCTATACTTC - AAAAAACAGGGGGTATTATGACCA	114473
Db	112402	GCAAAAGTACACAGAGCTTTCCCTATACTTC AAAAAACAGGGGGTATTATGACCA	112461
OY	114474	CACGTAAAGTAAACACCCCTAAGAAATTTATCCGTTATCAAAAATGGAAAAATTAAGGCT	114533
Db	112452	CACGTAAAGTAAACACCCCTAAGAAATTTATCCGTTATCAAAAATGGAAAAATTAAGGCT	112522
OY	114534	TTGCGTAAATCTGCTTAACGCAAAAGGAGCCTTAATTTTCCAGTTTGACCTCGAACCTT	114595
Db	112532	TTGCGTAAATCTGCTTAACGCAAAAGGAGCCTTAATTTTCCAGTTTGACCTCGAACCTT	112581
OY	114594	TACCGCTAACGTTAAATTTAT	114655
Db	112582	TACCGCTAACGTTAAATTTAT	112641
OY	114654	AAACCTCTACAGCTTAAGTTAATTAACGCGGACCTTTGGGACGCAATAGTCTGTGCGCAA	114713
Db	112642	AAACCTCTACAGCTTAAGTTAATTAACGCGGACCTTTGGGACGCAATAGTCTGTGCGCAA	112701
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LOCUS	Macaca mulatta rhadinovirus 26-95	DNA	VRL 27-MAR-2000
DEFINITION	Macaca mulatta rhadinovirus 26-95	long unique region L-DNA,	
ACCESSION	AF210726	complete sequence.	
VERSION	AF210726.1	GI:73299990	
KEYWORDS	Macaca mulatta rhadinovirus 26-95		
SOURCE	Macaca mulatta rhadinovirus 26-95		
ORGANISM	Macaca mulatta rhadinovirus 26-95		
REFERENCE	1 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L., Knapp, A., Auerbach, M.R., Damanita, B. and Desrosters, R.C.		
TITLE	The primary sequence of rhesus monkey rhadinovirus isolate 26-95: sequence similarities to Kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 17577		
JOURNAL	J. Virol. 74 (7), 3388-3398		(2000)
MEDLINE	2 (bases 1 to 130733)		
PUBMED	10708456		
REFERENCE	Alexander, L., Denekamp, L.M., Knapp, A., Auerbach, M., Czejak, S., Damanita, B. and Desrosters, R.C.		
AUTHORS	Direct Submission		
TITLE	Submitted (02-DEC-1999)		
JOURNAL	Microbiology, New England Regional Primate		

Research Center, One Pinehill Dr, Southborough, MA 01772, USA

FEATURES
source

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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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LOCUS Macaca mulatta rhadinovirus 17577, complete genome.
DEFINITION AF083501
ACCESSION AF083501.3 GI:8714565
VERSION
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta rhadinovirus 17577
Macaca mulatta rhadinovirus 17577
Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
1 (bases 1 to 133719)
Seales,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.
Sequence and genomic analysis of a Rhesus macaque rhadinovirus with
similarity to Kaposi's sarcoma-associated herpesvirus/human
herpesvirus 8
J. Virol. 73 (4), 3040-3053 (1999)

JOURNAL
MEDLINE
99174001
10074154
2 (bases 1 to 133719)
Seales,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.
Direct Submission
TITLE
JOURNAL
Submitted (11-AUG-1998) Division of Pathobiology and Immunology,
Oregon Health Sciences University/ Oregon Regional Primate Research
Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA
3 (bases 1 to 133719)
Seales,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.
Direct Submission
TITLE
JOURNAL
Submitted (16-JUL-1999) Division of Pathobiology and Immunology,
Oregon Health Sciences University/ Oregon Regional Primate Research
Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA
REMARK
REFERENCE
4 (bases 1 to 133719)

AUTHORS
TITLE
JOURNAL
Seales,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.
Direct Submission
Submitted (26-JUN-2000) Division of Pathobiology and Immunology,
Oregon Health Sciences University/ Oregon Regional Primate Research
Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA
REMARK
COMMENT
Sequence update by submitter
On Jun 26, 2000 this sequence replaced gi:5508840.
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CDS

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Query 117543 ATATATATAGGGAAGTCTGTAAACAAACCAAC 117575
Db 23911 ATATATATAGGGAAGTCTGTAAACAAACCAAC 23879

RESULT 5
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LOCUS AF083424 108409 bp DNA linear VRL 07-JAN-2000
DEFINITION Ateine herpesvirus 3 complete genome.
ACCESSION AF083424
VERSION AF083424.1 GI:4019231
KEYWORDS
SOURCE Ateine herpesvirus 3
ORGANISM Ateine herpesvirus 3
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
1 (bases 1 to 108409)
Albrecht, J.C.
Primary structure of the Herpesvirus ateles genome
JOURNAL J. Virol. 74 (2), 1033-1037 (2000)
MEDLINE 20091363
PUBMED 10623770
2 (bases 1 to 108409)
Albrecht, J.-C. and Fleckenstein, B.
Direct Submission
Submitted (11-AUG-1998) Institut fuer klinische und molekulare
Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4,
Erlangen, Bayern 91054, Germany
location/Qualifiers
1. 108409
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CDS

CDS

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herpesvirus ORF -33"

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Query Match 0.1%; Score 26; DB 1; Length 108409;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 95614 CAAGAAATCCACAGCATTTTGTG 95639

RESULT 6
LOCUS U93872 133661 bp DNA linear VRL 09-JUL-2001
DEFINITION Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNA
replication protein, glycoprotein, DNA replication protein, FLICE
inhibitory protein and v-cyclin genes, complete cds, and tegument
protein gene, partial cds.
U93872
U93872.2 GI:14627174

ACCESSION
VERSION U93872.2
KEYWORDS

ORGANISM Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
Virusae; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
1 (bases 29032 to 30108; 117733 to 118431)
Zhong, W., Wang, H., Herndler, B. and Ganem, D.
Restricted expression of Kaposi sarcoma-associated herpesvirus
(human herpesvirus 8) genes in Kaposi sarcoma
(Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)

JOURNAL MEDLINE 96270595
PUBMED 8692871
2 (bases 17242 to 17856)
Neipel, F., Albrecht, J. C., Ensser, A., Huang, Y. Q., Li, J. J.,
Friedman-Kien, A. E. and Fleckenstein, B.
Human herpesvirus 8 encodes a homolog of interleukin-6
J. Virol. 71 (1), 839-842 (1997)

JOURNAL MEDLINE 97138401
PUBMED 8985427
3 (bases 123309 to 124082)
Li, M., Lee, H., Yoon, D. W., Albrecht, J. C., Fleckenstein, B., Neipel, F.,
and Jung, J. U.
Kaposi's sarcoma-associated herpesvirus encodes a functional cyclin
J. Virol. 71 (3), 1984-1991 (1997)

JOURNAL MEDLINE 97184528
PUBMED 9032330
4 (bases 122660 to 123226)
Thome, M., Schneider, P., Hofmann, K., Fickenscher, H., Mehl, E.,
Neipel, F., Matmann, C., Burns, K., Bodmer, J. L., Schrotter, M.,
Scheidt, C., Kramer, P. H., Peter, M. E. and Tschopp, J.
Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced
by death receptors
Nature 386 (6624), 517-521 (1997)

JOURNAL MEDLINE 97242415
PUBMED 9087414
5 (bases 1 to 133661)
Neipel, F., Albrecht, J. C. and Fleckenstein, B.

TITLE Cell-homologous genes in the Kaposi's sarcoma-associated
rhadinovirus human herpesvirus 8: determinants of its
pathogenicity?

JOURNAL MEDLINE 97296220
PUBMED 9151804
6 (bases 1 to 133661)
Neipel, F., Albrecht, J. C., Ensser, A., Huang, Y. Q., Li, J. J.,
Friedman-Kien, A. E. and Fleckenstein, B.
The genome of human herpesvirus 8 cloned from Kaposi's sarcoma
unpublished
7 (bases 1 to 133661)
Neipel, F., Albrecht, J. C., Ensser, A., Huang, Y. Q., Li, J. J.,
Friedman-Kien, A. E. and Fleckenstein, B.
Direct Submission.
Submitted (17-MAR-1997) Virology, University of Erlangen,
Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen
91054, Germany
8 (bases 1 to 133661)
Neipel, F., Albrecht, J. C., Ensser, A., Huang, Y. Q., Li, J. J.,
Friedman-Kien, A. E. and Fleckenstein, B.
Direct Submission
Submitted (09-JUL-2001) Virology, University of Erlangen,
Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen
91054, Germany
Sequence update by submitter
On Jul 9, 2001 this sequence version replaced gi:2246466.
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Db 115006 GTTTTAAATAGTCAGCAGTAGTT 115028
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RESULT 7
KSU75698 137508 bp DNA linear VRL 03-MAY-1997
LOCUS
DEFINITION
Kaposi's sarcoma-associated herpesvirus long unique region, 80
putative ORF's and kaposin gene, complete cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
U75698.1 GI:2065526

ORGANISM
Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
human herpesvirus 8)
Human herpesvirus 8
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

REFERENCE
AUTHORS
1 (bases 47193 to 47522): 135092 to 133729)
Chang, Y., Cesarman, E., Pessin, M.S., Lee, F., Culpepper, J.,
Knowles, D.M. and Moore, P.S.
Identification of herpesvirus-like DNA sequences in AIDS-associated
Kaposi's sarcoma
Science 266 (5192), 1865-1869 (1994)

REFERENCE
AUTHORS
2 (bases 35021 to 55726)
Moore, P.S., Gao, S.J., Domiguez, G., Cesarman, E., Lungu, O.,
Knowles, D.M., Garber, R., Pellett, P.E., McGeoch, D.J. and Chang, Y.
Primary characterization of a herpesvirus agent associated with
Kaposi's sarcoma
J. Virol. 70 (1), 549-558 (1996)

REFERENCE
AUTHORS
3 (bases 28661 to 29741: 117919 to 118103)
Zhong, W., Wang, H., Herndler, B. and Ganem, D.
Restricted expression of Kaposi sarcoma-associated herpesvirus
(human herpesvirus 8) genes in Kaposi sarcoma
Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)

REFERENCE
AUTHORS
4 (bases 122794 to 123567; 123809 to 127297; 129372 to 130400;
130531 to 134441)
Cesarman, E., Nador, R.G., Bai, F., Bohenzky, R.A., Russo, J.J.,
Moore, P.S., Chang, Y. and Knowles, D.M.
Kaposi's sarcoma-associated herpesvirus contains G protein-coupled
receptor and cyclin D homologs which are expressed in Kaposi's
sarcoma and malignant lymphoma
J. Virol. 70 (11), 8218-8223 (1996)

REFERENCE
AUTHORS
5 (bases 1 to 137508)
Moore, P.S., Boshoff, C., Weiss, R.A. and Chang, Y.
Molecular mimicry of human cytokine and cytokine response pathway
genes by KSHV
Science 274 (5293), 1739-1744 (1996)

REFERENCE
AUTHORS
6 (bases 1 to 137508)
Moore, P.S., Boshoff, C., Weiss, R.A. and Chang, Y.
Molecular mimicry of human cytokine and cytokine response pathway
genes by KSHV
Science 274 (5293), 1739-1744 (1996)

REFERENCE
AUTHORS
7 (bases 1 to 137508)
Moore, P.S., Boshoff, C., Weiss, R.A. and Chang, Y.
Molecular mimicry of human cytokine and cytokine response pathway
genes by KSHV
Science 274 (5293), 1739-1744 (1996)

AUTHORS Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and
Moore, P. S.
TITLE Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
(HHV8)
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14862-14867 (1996)
MEDLINE 97121480
PUBMED 8962146
REFERENCE 7 (bases 1 to 137508)
AUTHORS Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and
Moore, P. S.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-1996) Dept of Pathology/Genome Center/Division of
Epidemiology, Columbia University, 650 West 168th Street, New York,
NY 10032, USA
REFERENCE 8 (bases 1 to 137508)
AUTHORS Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and
Moore, P. S.
TITLE Direct Submission
JOURNAL Submitted (02-MAY-1997) Dept of Pathology/Genome Center/Division of
Epidemiology, Columbia University, 650 West 168th Street, New York,
NY 10032, USA
REMARK Sequence update by submitter
COMMENT On May 3, 1997 this sequence version replaced gi:1718251.
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RESULT 8

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DEFINITION Hepatitis A virus polypeptide RNA, complete cds.
ACCESSION M59808
VERSION M59808.1 GI:329585
KEYWORDS hepatitis A; polypeptide.
SOURCE Hepatitis A virus
ORGANISM Hepatitis A virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Hepatovirus.

REFERENCE 1 (bases 1 to 7423)
AUTHORS Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,
Cromeans, T., and Jansen, R.W.
TITLE Antigenic and genetic variation in cytopathic hepatitis A virus
variants arising during persistent infection: evidence for genetic
recombination
J. Virol. 65 (4), 2056-2065 (1991)

JOURNAL MEDLINE 91162758
COMMENT PUBMED 1705995
Original source text: Hepatitis A virus (strain HM175, isolate
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FEATURES

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5929..7395

mat_peptide

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/note="putative"
/label=3D
7396..7423

BASE COUNT

2173 a 1196 c 1622 g 2432 t

Query Match 0.1%; Score 21; DB 1; Length 7423;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 98116 TGAGCATTATTATAGAAAGG 98136
Db 5571 TGAGCATTATTATAGAAAGG 5591

RESULT 9

HPA24A 7436 bp ss-RNA linear VRL 02-AUG-1993
LOCUS HPA24A
DEFINITION Hepatitis A virus polypeptide RNA, complete cds.
ACCESSION M59810
VERSION M59810.1 GI:329587


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CDS
    <1..>207
    /codon_start=2
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    /protein_id="AA04604.1"
    /db_xref="GI:25807870"
    /translation="LEPRAKVISLTERLYCGGPMFNKGAQCGYRRCRASGLPTPS
    FGNITTCYKTAFAAKAGLNPP"

BASE COUNT      42 a      65 c      60 g      40 t

ORIGIN
Query Match      0.0%; Score 20; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86659 AGCGGCTCGAAGCCGCAG 86678
        |||||||
        169 AGCGGCTCGAAGCCGCAG 188

RESULT 11
LOCUS      HPCNS5AD      222 bp      DNA      linear      VRL 03-JAN-1994
DEFINITION      Hepatitis C virus type 3a (I4) nonstructural protein 5 (NS5) gene,
partial cds.
ACCESSION      L23464.1 GI:385086
VERSION      L23464
KEYWORDS      nonstructural protein 5.
SOURCE      Hepatitis C virus type 3a
ORGANISM      Hepatitis C virus type 3a
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnaviruses.
REFERENCE      1 (bases 1 to 222)
AUTHORS      Simmonds,P., Holmes,E.C., Cha,T.A., Chan,S.W., McOmish,F.,
Irvine,B., Beall,E., Yap,P.L., Kolberg,J. and Urcia,M.S.
TITLE      Classification of hepatitis C virus into six major genotypes and a
series of subtypes by phylogenetic analysis of the NS-5 region
JOURNAL      J. Gen. Virol. 74 (Pt 11), 2391-2399 (1993)
MEDLINE      94065665
PUBMED      8245854
COMMENT      Original source text: Hepatitis C virus type 3a (individual isolate
Italy I4) DNA.
FEATURES
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        location/Qualifiers
            1..222
            /organism="Hepatitis C virus type 3a"
            /mol_type="genomic DNA"
            /isolate="Italy I4"
            /db_xref="taxon:31652"
            1..222
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            /gene="NS5"
            /codon_start=1
            /product="nonstructural protein 5"
            /protein_id="AA045634.1"
            /db_xref="GI:385087"
            /translation="ITQCCNLEPRAKVISLTERLYCGGPMFNKGAQCGYRRCRAS
            GLPTPSFGNITTCYKTAFAAKAGLPTP"

BASE COUNT      47 a      67 c      63 g      45 t

ORIGIN
Query Match      0.0%; Score 20; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86659 AGCGGCTCGAAGCCGCAG 86678
        |||||||
        186 AGCGGCTCGAAGCCGCAG 205

RESULT 12
LOCUS      HPCNS5AE      222 bp      DNA      linear      VRL 03-JAN-1994
DEFINITION      Hepatitis C virus type 3a (S21) nonstructural protein 5 (NS5) gene,

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ACCESSION      partial cds.
VERSION        L23465
KEYWORDS       L23465.1 GI:385088
SOURCE         nonstructural protein 5.
ORGANISM       Hepatitis C virus type 3a
               Hepatitis C virus type 3a
               Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
               Hepacivirus.
REFERENCE      1 (bases 1 to 222)
AUTHORS       Slimmonds,P., Holmes,E.C., Cha,T.A., Chan,S.W., McOmish,F.,
               Irvine,B., Beall,E., Yap,P.L., Kolberg,J. and Urdea,M.S.
               Classification of hepatitis C virus into six major genotypes and a
               series of subtypes by phylogenetic analysis of the NS-5 region
               J. Gen. Virol. 74 (Pt 11), 2391-2399 (1993)
MEDLINE        8245854
PUBMED         8245854
COMMENT        Original source text: Hepatitis C virus type 3a (individual isolate
               Sweden S21) DNA.
FEATURES
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               /isolate="Sweden S21"
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               /gene="NS5"
               /codon_start=1
               /product="nonstructural protein 5"
               /protein_id="AA45635.1"
               /db_xref="GI:385088"
               /translation="ITVCCNIEPARVYISLTIRLYCGGPMENSKAQCCYRCRRAS
               GVLPSTSGNITTCIKATFAAKAGLNPD"
BASE COUNT    48 a 65 c 63 g 46 t
ORIGIN
Query Match      0.0% Score 20; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 7.9%
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      86659 AGCGGCTGCGAAGCGCGCAG 86678
Db      186 AGCGGCTGCGAAGCGCGCAG 205
RESULT 13
LOCUS       AY149712                223 bp RNA linear VRL 27-NOV-2002
DEFINITION  Hepatitis C virus isolate Bb11025 NS5 gene, partial cds.
ACCESSION   AY149712
VERSION     AY149712.1 GI:25807873
KEYWORDS
SOURCE      Hepatitis C virus
ORGANISM    Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE   1 (bases 1 to 223)
AUTHORS    Chinchai,T., Bedi,K., Jantaradsamee,P., Theamboonlers,A. and
               Poovorawan,Y.
               Direct Submission
               Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
               Ramad, Bangkok 10330, Thailand
               location/Qualifiers
               1..223
               /organism="Hepatitis C virus"
               /viralon
               /mol_type="genomic RNA"
               /isolate="Bb11025"
               /db_xref="taxon:11103"
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               /codon_start=2
               /product="NS5"
TITLE       JOURNAL
FEATURES
  source

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/protein_id="AA074606.1"
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/translation="LEPEARKYISLTERLYCGGPMFNSKGAGCGYRRCRASGVLPTS
FGNTTCYIKATRAAKAAGLRNDFVCGD"
BASE COUNT 44 a 68 c 66 g 45 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
169 AGCGGCTGCGAAGCCGCAG 188

RESULT 14
AY149695 224 bp RNA linear VRL 27-NOV-2002
LOCUS Hepatitis C virus isolate BB70646 NS5 gene, partial cds.
DEFINITION
ACCESSION AY149695
VERSION AY149695.1 GI:25807839
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinnchal,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
Poovorawan,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Ramad, Bangkok 10330, Thailand
FEATURES
source
1..224
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/mol_type="genomic RNA"
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/db_xref="taxon:11103"
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/product="NS5"
/protein_id="AA074589.1"
/db_xref="GI:25807840"
/translation="LEPEARKYISLTERLYCGGPMFNSKGAGCGYRRCRASGVLPTS
FGNTTCYIKATRAAKAAGLRNDFVCGD"
BASE COUNT 43 a 69 c 66 g 46 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
169 AGCGGCTGCGAAGCCGCAG 188

RESULT 15
AY149697 224 bp RNA linear VRL 27-NOV-2002
LOCUS Hepatitis C virus isolate BB1885 NS5 gene, partial cds.
DEFINITION
ACCESSION AY149697
VERSION AY149697.1 GI:25807843
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinnchal,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
Poovorawan,Y.

TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Ramad, Bangkok 10330, Thailand
FEATURES
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FGNTTCYIKATRAAKAAGLRNDFVCGD"
BASE COUNT 43 a 68 c 67 g 46 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
169 AGCGGCTGCGAAGCCGCAG 188

RESULT 16
AY149699 224 bp RNA linear VRL 27-NOV-2002
LOCUS Hepatitis C virus isolate BB10442 NS5 gene, partial cds.
DEFINITION
ACCESSION AY149699
VERSION AY149699.1 GI:25807847
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinnchal,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
Poovorawan,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Ramad, Bangkok 10330, Thailand
FEATURES
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1..224
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FGNTTCYIKATRAAKAAGLRNDFVCGD"
BASE COUNT 43 a 70 c 66 g 45 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
169 AGCGGCTGCGAAGCCGCAG 188

RESULT 17

AY149703 224 bp RNA linear VRL 27-NOV-2002
LOCUS
DEFINITION Hepatitis C virus isolate bb07893 NS5 gene, partial cds.
ACCESSION AY149703
VERSION AY149703.1 GI:25807855
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinchai,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
POOVORAWAN,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Rama4, Bangkok 10330, Thailand
FEATURES
source
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/product="NS5"
/protein_id="AA074597.1"
/db_xref="GI:25807856"
/translation="LEPARKYVSSLTRELYCGGPMFNSKGAQCGYRRCRASGVLPST
FGNTTCYIKATAAKAGLRNPDLVCGD"
BASE COUNT 44 a 68 c 66 g 46 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86659 AGCGGCTGCGAAGGCCGCGAG 86678
Db 169 AGCGGCTGCGAAGGCCGCGAG 188
RESULT 18
AY149713 224 bp RNA linear VRL 27-NOV-2002
LOCUS
DEFINITION Hepatitis C virus isolate BB1671 NS5 gene, partial cds.
ACCESSION AY149713
VERSION AY149713.1 GI:25807875
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinchai,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
POOVORAWAN,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Rama4, Bangkok 10330, Thailand
FEATURES
source
1..224
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/protein_id="AA074607.1"
/db_xref="GI:25807876"
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BASE COUNT 44 a 68 c 66 g 46 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86659 AGCGGCTGCGAAGGCCGCGAG 86678
Db 169 AGCGGCTGCGAAGGCCGCGAG 188
RESULT 19
AY149715 224 bp RNA linear VRL 27-NOV-2002
LOCUS
DEFINITION Hepatitis C virus isolate BB08720 3a NS5 gene, partial cds.
ACCESSION AY149715
VERSION AY149715.1 GI:25807879
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinchai,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
POOVORAWAN,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Rama4, Bangkok 10330, Thailand
FEATURES
source
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/db_xref="GI:25807880"
/translation="LEPARKYVSSLTRELYCGGPMFNSKGAQCGYRRCRASGVLPST
FGNTTCYIKATAAKAGLRNPDLVCGD"
BASE COUNT 42 a 67 c 68 g 47 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86659 AGCGGCTGCGAAGGCCGCGAG 86678
Db 169 AGCGGCTGCGAAGGCCGCGAG 188
RESULT 20
AY149717 224 bp RNA linear VRL 27-NOV-2002
LOCUS
DEFINITION Hepatitis C virus isolate BB92597 3a NS5 gene, partial cds.
ACCESSION AY149717
VERSION AY149717.1 GI:25807883
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinchai,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
POOVORAWAN,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Rama4, Bangkok 10330, Thailand
FEATURES
Location/Qualifiers

source
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/organism="Hepatitis C virus"
/vifion
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/db_xref="taxon:11103"
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/codon_start=2
/product="NS5"
/protein_id="AA074611.1"
/db_xref="GI:25807884"
/translation="LEPEARKVISLTERLYCGGPMFNSKGAQCGYRCRASGVLPPTS
FGNTTTCYIKATAAKAAGLRNPDLVCGD"
BASE COUNT 42 a 67 c 68 g 47 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGCTGCGAAGCGCGCAG 86678
|||||
Db 169 AGCGCTGCGAAGCGCGCAG 188

RESULT 21
AY149724 226 bp RNA linear VRL 27-NOV-2002
LOCUS Hepatitis C virus isolate BB09152 NS5 gene, partial cds.
DEFINITION
ACCESSION AY149724
VERSION AY149724.1 GI:25807897
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 226)
AUTHORS Chunchai,T., Bedi,K., Jantaradamee,P., Theamboonlers,A. and Poonvorawan,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University, Ramat, Bangkok 10330, Thailand
FEATURES
Location/Qualifiers
1. .226
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/db_xref="taxon:11103"
<1. .>226
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/product="NS5"
/protein_id="AA074611.1"
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FGNTTTCYIKATAAKAAGLRNPDLVCGD"
BASE COUNT 44 a 67 c 68 g 47 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGCTGCGAAGCGCGCAG 86678
|||||
Db 169 AGCGCTGCGAAGCGCGCAG 188

RESULT 22
AF388468 253 bp RNA linear VRL 08-JAN-2002
LOCUS Hepatitis C virus isolate 680 NS5B (NS5B) gene, partial cds.
DEFINITION
ACCESSION AF388468

VERSION AF388468.1 GI:18087222
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 253)
AUTHORS Kalina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Shift in predominating subtype of HCV from 1b to 3a in St. Petersburg mediated by increase in injecting drug use
JOURNAL J. Med. Virol. 65 (3), 517-524 (2001)
MEDLINE 11596087
PUBMED 11596087
REFERENCE 2 (bases 1 to 253)
AUTHORS Kalina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Department of Virology, Swedish Institute for Infectious Disease Control, 171 82 Solna, Sweden
FEATURES
Location/Qualifiers
1. .253
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/isolate="680"
/db_xref="taxon:11103"
/note="subtype: 3a"
<1. .>253
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/gene="NS5B"
/codon_start=1
/product="NS5B"
/protein_id="AA158782.1"
/db_xref="GI:18087223"
/translation="TYOCNLEPEARKVISLTERLYCGGPMFNSKGAQCGYRCRAS
GVLPSTFGNTTTCYIKATAAKAAGLRNPDLVCGDLYV"
BASE COUNT 50 a 71 c 75 g 57 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGCTGCGAAGCGCGCAG 86678
|||||
Db 186 AGCGCTGCGAAGCGCGCAG 205

RESULT 23
AF388469 253 bp RNA linear VRL 08-JAN-2002
LOCUS Hepatitis C virus isolate 590 NS5B (NS5B) gene, partial cds.
DEFINITION
ACCESSION AF388469
VERSION AF388469.1 GI:18087224
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 253)
AUTHORS Kalina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Shift in predominating subtype of HCV from 1b to 3a in St. Petersburg mediated by increase in injecting drug use
JOURNAL J. Med. Virol. 65 (3), 517-524 (2001)
MEDLINE 11596087
PUBMED 11596087
REFERENCE 2 (bases 1 to 253)
AUTHORS Kalina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Direct Submission

BASE COUNT	51 a	69 c	74 g	59 t
ORIGIN	/translation="TYOCCNLEPPARVYISLTLRLVCGGPMFMSKAGQCYRRCPA GVLPTEGNTTTCYIKATPAAKAAGLPDLVCGDDLV"			
Query Match	0.0%; Score 20; DB 1; Length 253;			
Best Local Similarity	100.0%; Pred. No. 8;			
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	86659	AGCGGCTGCGAAGCGCCGAG	86678	
DB	186	AGCGGCTGCGAAGCGCCGAG	205	
RESULT 25				
AF388475	253 bp RNA, linear VRL 08-JAN-2002			
LOCUS				
DEFINITION	Hepatitis C virus isolate 759 NS5B (NS5B) gene, partial cds.			
AF388475				
ACCESSION				
VERSION	AF388475.1 GI:18087236			
KEYWORDS				
SOURCE	Hepatitis C virus			
ORGANISM	Hepatitis C virus			
REFERENCE	Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.			
AUTHORS	1 (bases 1 to 253)			
TITLE	Kalinina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O. Shift in predominating subtype of HCV from 1b to 3a in St. Petersburg mediated by increase in injecting drug use J Med Virol. 65 (3), 517-524 (2001)			
JOURNAL	21479638			
MEDLINE	11596087			
PUBMED	2 (bases 1 to 253)			
REFERENCE	Kalinina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O. Direct Submission Submitted (06-JUN-2001) Department of Virology, Swedish Institute for Infectious Disease Control, 171 82 Solna, Sweden			
AUTHORS	Location/Qualifiers			
TITLE	1. .253			
JOURNAL	/organism="Hepatitis C virus"			
FEATURES	/vifion			
SOURCE	/mol_type="genomic RNA"			
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	/protein_id="AA158789.1"			
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BASE COUNT	53 a	72 c	72 g	56 t
ORIGIN				
Query Match	0.0%; Score 20; DB 1; Length 253;			
Best Local Similarity	100.0%; Pred. No. 8;			
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	86659	AGCGGCTGCGAAGCGCCGAG	86678	
DB	186	AGCGGCTGCGAAGCGCCGAG	205	
RESULT 26				
AF388516	253 bp RNA, linear VRL 08-JAN-2002			
LOCUS				
DEFINITION	Hepatitis C virus isolate 631 NS5B (NS5B) gene, partial cds.			

ACCESSION	AF388516
VERSION	AF388516.1 GI:18087318
KEYWORDS	
SOURCE	Hepatitis C virus
ORGANISM	Hepatitis C virus Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepadnavirus.
REFERENCE	1 (bases 1 to 253)
AUTHORS	Kalinnina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnius,L.O. Shift in predominating subtype of HCV from 1b to 3a in St. Petersburg mediated by increase in infecting drug use J. Med. Virol. 65 (3), 517-524 (2001)
JOURNAL	21479638
MEDLINE	11596087
PUBMED	11596087
REFERENCE	2 (bases 1 to 253)
AUTHORS	Kalinnina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnius,L.O. Direct Submission Submitted (06-JUN-2001) Department of Virology, Swedish Institute for Infectious Disease Control, 171 82 Solna, Sweden
TITLE	Location/Qualifiers
JOURNAL	1..253
FEATURES	/organism="Hepatitis C virus"
source	/vifion /mol_type="genomic RNA" /isolate="631" /db_xref="taxon:11103" /note="subtype: 3a" <1..>253 /gene="NS5B" /gene="NS5B" /protein_id="AA158830.1" /codon_start=1 /product="NS5B" /protein_id="AA158830.1" /db_xref="GI:18087319" /translation="TVCCNHEPPARVISLIERLYCGGPMENSKAGQCYRRCRAS GVLPSTSGNTTCYIKATPAAKAGLNPNPELVGGDDLVV"
BASE COUNT	51 a 69 c 74 g 59 t
ORIGIN	
Query Match	0.0%; Score 20; DB 1; Length 253;
Best Local Similarity	100.0%; Pred. No. 8;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY	86659 AGCGGTGCGAAGGCCGCAG 86678
DB	186 AGCGGTGCGAAGGCCGCAG 205
RESULT 27	
LOCUS	AF506554 318 bp RNA linear VRL_04-JUN-2002
DEFINITION	Hepatitis C virus isolate RIG398 polyprotein precursor gene, NS5B region, partial cds.
ACCESSION	AF506554
VERSION	AF506554.1 GI:21321465
KEYWORDS	
SOURCE	Hepatitis C virus
ORGANISM	Hepatitis C virus Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepadnavirus.
REFERENCE	1 (bases 1 to 318)
AUTHORS	Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Genetic variability of hepatitis C virus in Western Siberia Unpublished 2 (bases 1 to 318) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Direct Submission Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center "Vector", SRC VB "vector", Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES	location/Qualifiers
SOURCE	1. .318 /organism="Hepatitis C virus" /mol_type="genomic RNA" /isolate="RIG398" /db_xref="taxon:11103" /country="Russia" 1. .>318 /codon_start=1 /product="polyprotein precursor" /protein_id="AA047211.1" /db_xref="GI:21321466" /translation="OCCTLEPPAKKVISSLTERLYCGGPMFNKGAOCGYRRRASGV LPFSFGNTITCIYIKATATAAKAAGLRDPFLVCGDDLVTYVAESDGVDEDRKALAF7DA MTX"
CDS	<1. .>318 /product="NS5B"
mat_peptide	<1. .>318 /product="NS5B"
BASE COUNT	65 a 87 c 98 g 68 t
ORIGIN	
Query Match	0.0%; Score 20; DB 1; Length 318;
Best Local Similarity	100.0%; Pred. No. 8.1;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	86659 AGCGGTCGGAAGCCGCAG 86678
Db	180 AGCGGTCGGAAGCCGCAG 199
RESULT 28	
AF506566	AF506566 323 bp RNA linear VRL 04-JUN-2002
LOCUS	Hepatitis C virus isolate RIG403 polyprotein precursor gene, NS5B
DEFINITION	region, partial cds.
ACCESSION	AF506566
VERSION	AF506566.1 GI:21321487
KEYWORDS	Hepatitis C virus Hepatitis C virus Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
ORGANISM	1 (bases 1 to 323) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Genetic variability of hepatitis C virus in Western Siberia Unpublished
REFERENCE	2 (bases 1 to 323) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Direct submission Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia
FEATURES	Location/Qualifiers
source	1. .323 /organism="Hepatitis C virus" /mol_type="genomic RNA" /isolate="RIG403" /db_xref="taxon:11103" /country="Russia" 1. .>323 /codon_start=1 /product="polyprotein precursor" /protein_id="AA047221.1" /db_xref="GI:21321488" /translation="VTNAVTLTKPARKVISLTERLYCGGPMFNKGAOYLLARCARA SGVTFSEGNITCIYIKATATAAKAAGLRDPFLVCGDDLVTYVAESDGVDEDRVALRAF TEAM"
CDS	<1. .>323 /product="NS5B"
mat_peptide	<1. .>323 /product="NS5B"
BASE COUNT	68 a 86 c 99 g 70 t
ORIGIN	
Query Match	0.0%; Score 20; DB 1; Length 323;
Best Local Similarity	100.0%; Pred. No. 8.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 ACCGGCTGCGAAGCCGCAG 86678
|||||
Db 189 ACCGGCTGCGAAGCCGCAG 208

RESULT 29
HEC507267 327 bp RNA linear VRL 08-SEP-2002
LOCUS Hepatitis C virus partial gene for NS5B protein, isolate KGV244.
DEFINITION AJ507267
ACCESSION AJ507267.1 GI:22799051
VERSION
KEYWORDS NS5B protein.
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 327)
AUTHORS Shustov,A.V.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-2002) Shustov A. V., Inst. Molecular Biology,
State Research Center of Virology and Biotechnology VECTOR, 630559,
Koltsovo, Novosibirsk region, RUSSIA
Location/Qualifiers

FEATURES
source 1..327
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="KGV244"
/db_xref="taxon:11103"
<1..>327
/codon_start=1
/product="NS5B protein"
/protein_id="CAD45268.1"
/db_xref="GI:22799052"
/translation="EEIYCCDLEPEARKVYISLTERLYCGGPMFNSKGAOCGYRRC
RASGVLPISFGNTICYIKATPAKAAAGLRNDFVCGDDLVVAESDGVDEGALRL
AFTEAMT"
CDS
BASE COUNT 68 a 85 c 105 g 69 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 327;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 ACCGGCTGCGAAGCCGCAG 86678
|||||
Db 195 ACCGGCTGCGAAGCCGCAG 214

RESULT 30
AF506542 329 bp RNA linear VRL 04-JUN-2002
LOCUS Hepatitis C virus isolate KGV231 nonfunctional NS5B gene, partial
DEFINITION AF506542
ACCESSION AF506542
VERSION AF506542.1 GI:21321444
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE 1 (bases 1 to 329)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 329)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Direct Submission

JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
FEATURES
source 1..329
Location/Qualifiers
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="KGV231"
/db_xref="taxon:11103"
/country="Russia"
<1..>329
/note="nonfunctional NS5B protein due to mutation;
polyprotein precursor"

BASE COUNT 70 a 87 c 103 g 69 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 ACCGGCTGCGAAGCCGCAG 86678
|||||
Db 190 ACCGGCTGCGAAGCCGCAG 209

RESULT 31
AF506546 329 bp RNA linear VRL 04-JUN-2002
LOCUS Hepatitis C virus isolate RIG450 nonfunctional NS5B gene, partial
DEFINITION AF506546
ACCESSION AF506546.1 GI:21321450
VERSION AF506546
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE 1 (bases 1 to 329)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 329)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
Location/Qualifiers

FEATURES
source 1..329
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="RIG450"
/db_xref="taxon:11103"
/country="Russia"
<1..>329
/note="nonfunctional NS5B protein due to mutation;
polyprotein precursor"

BASE COUNT 71 a 86 c 105 g 67 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 ACCGGCTGCGAAGCCGCAG 86678
|||||
Db 191 ACCGGCTGCGAAGCCGCAG 210

RESULT 32
AY257434 332 bp RNA linear VRL 14-MAY-2003
LOCUS Hepatitis C virus isolate Mar14 NS5b (NS5b) gene, partial cds.
DEFINITION

ACCESSION AV257434
VERSION AV257434.1 GI:30720337
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE
AUTHORS 1 (bases 1 to 332)
Martal,J., Morice,Y., Abel,S., Cable,A., Rat,C., Lombard,F.,
Edouard,A., Pierre-Louis,S., Garsaud,P., Bera,O., Chout,R.,
Gordien,E., Dery,P. and Cesaire,R.
TITLE Hepatitis C virus (HCV) genotypes in the Caribbean island of Martinique: evidence for a large radiation of HCV-2 and for a recent introduction from Europe of HCV-4
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 332)
AUTHORS Martal,J., Morice,Y., Abel,S., Cable,A., Rat,C., Lombard,F.,
Edouard,A., Pierre-Louis,S., Garsaud,P., Bera,O., Chout,R.,
Gordien,E., Dery,P. and Cesaire,R.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-2003) Laboratoire de Virologie-Immunologie, Centre Hospitalier Universitaire de Fort-de-France, Hopital Pierre-Zobda-Quilman, Fort-de-France, Martinique 97261, France

FEATURES
source
1..332
Location/Qualifiers
/organism="Hepatitis C virus"
/viation
/mol_type="genomic RNA"
/isolate="Martia"
/db_xref="taxon:11103"
/country="Martinique"
/note="type: 3a"
<1..>332
/gene="NS5b"
<1..>332
/gene="NS5b"
/codon_start=2
/product="NS5b"
/protein_id="AAP33856.1"
/db_xref="GI:30720338"
/translation="TVTEODIRVEEETIYOCNLEPEARKYISSLTERLYCGGPMFNK
GAOCYRCRASGVLPFSFGNTTCYIKATAAKAAGLRNPDLVCGDDLVAESDG
VDEDRALV"

BASE COUNT 77 a 86 c 102 g 67 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86659 AGCGGCTGCGAAGCCGCGAG 86678
|||||
Db 223 AGCGGCTGCGAAGCCGCGAG 242

RESULT 33
AB081064 336 bp RNA linear VRL 06-AUG-2002
LOCUS Hepatitis C virus gene for polypeptide (NS5B region), partial cds,
strain:037.
ACCESSION AB081064
VERSION AB081064.1 GI:22122150
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE
AUTHORS 1
TITLE Kurbanov,F.M., Tanaka,Y., Orito,E., Mizokami,M. and Ruzhbayev,R.M.
JOURNAL Molecular epidemiology of hepatitis C virus in Uzbekistan
REFERENCE 2 (bases 1 to 336)
AUTHORS Tanaka,Y., Kurbanov,F. and Mizokami,M.

TITLE Direct Submission
JOURNAL Submitted (06-MAR-2002) Yasunito Tanaka, Nagoya City University Graduate School of Medical Sciences, Department of Clinical Molecular Informative Medicine, Kawasumi, Mizuno, Nagoya 467-8601, Japan (E-mail:ytanaka@med.nagoya-cu.ac.jp, Tel:81-52-851-5511(ex.8292), Fax:81-52-842-0021)

FEATURES
source
1..336
Location/Qualifiers
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/strain="U37"
/db_xref="taxon:11103"
<1..>336
/note="NS5B"
/codon_start=2
/product="polyprotein"
/protein_id="BAC07218.1"
/db_xref="GI:22122151"
/translation="TVTEODIRVEEETIYOCNLEPEARKYISSLTERLYCGGPMFNK
GAOCYRCRASGVLPFSFGNTTCYIKATAAKAAGLRNPDLVCGDDLVAESDG
VDEDRALRV"

BASE COUNT 77 a 82 c 105 g 72 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86659 AGCGGCTGCGAAGCCGCGAG 86678
|||||
Db 223 AGCGGCTGCGAAGCCGCGAG 242

RESULT 34
D14179 337 bp RNA linear VRL 03-FEB-1999
LOCUS Hepatitis C virus genomic RNA for NS5, partial cds.
ACCESSION D14179
VERSION D14179.1 GI:1783186
KEYWORDS NS5.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 337)
AUTHORS Okamoto,H.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 337)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1993) Hiroaki Okamoto, Jichi Medical School, Immunology Division, Minamikawachi-machi, Kawachi-gun, Tochigi 329-04, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:0285-44-2111(ex.3354), Fax:0285-44-1357)

FEATURES
source
1..337
Location/Qualifiers
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="Mal-HM"
/db_xref="taxon:11103"
<1..>337
/codon_start=2
/product="NS5"
/protein_id="BAA03214.1"
/db_xref="GI:1783187"
/translation="TVTEODIRVEEETIYOCNLEPEARKYISSLTERLYCGGPMFNK
GAOCYRCRASGVLPFSFGNTTCYIKATAAKAAGLRNPDLVCGDDLVAESDG
VDEDRALRV"

BASE COUNT 75 a 88 c 106 g 68 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
Db 223 AGCGGCTGCGAAGCCGCAG 242

RESULT 35
HPCNS5A22 337 bp RNA linear VRL 03-FEB-1999
LOCUS
DEFINITION Hepatitis C virus gene for NS5, partial cds, isolate HEM26.
ACCESSION D14214
VERSION D14214.1 GI:529638
KEYWORDS NS5.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
1 (bases 1 to 337)
REFERENCE
AUTHORS Tokita,H. and Okamoto,H.
JOURNAL Unpublished
2 (bases 1 to 337)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1993) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoto@ichi.ac.jp,
Tel:0285-44-2111(ex.334), Fax:0285-44-1557)
Location/Qualifiers
1..337
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="HEM26"
/db_xref="taxon:11103"
<1..>337
/codon_start=2
/product="NS5"
/protein_id="BAA03242.1"
/db_xref="GI:529638"
/translation="TVTEQDIVEEIEIYOCNLEPEARKYISLTERLYCGGPMNSK
GAOCGYRRCRASGVLPFSFGNTITCYIKATAAKAAGLRNPDFLVCGDDLVVAASDG
VDEDRALRA"

BASE COUNT 76 a 86 c 105 g 70 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
Db 223 AGCGGCTGCGAAGCCGCAG 242

RESULT 36
AF515972 339 bp RNA linear VRL 29-MAR-2003
LOCUS
DEFINITION Hepatitis C virus isolate P8.Don non-structural protein NS5-B
(NS5-b) gene, partial cds.
ACCESSION AF515972
VERSION AF515972.1 GI:29365772
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
1 (bases 1 to 339)
REFERENCE
AUTHORS Cantaloube,J.F., Bigini,P., Attoui,H., Gallian,P., de Micco,P. and
de Lamballerie,X.
TITLE Evolution of hepatitis C virus in blood donors and their respective
recipients
JOURNAL J. Gen. Virol. 84 (Pt 2), 441-446 (2003)
MEDLINE 22447295

PUBMED 12560577
REFERENCE 2 (bases 1 to 339)
AUTHORS Cantaloube,J.F., de Micco,P. and de Lamballerie,X.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Emerging Viruses Department, ERS
Alpes-Mediterranee, 149 Boulevard Baillie, Marseille 13005, France
Location/Qualifiers
1..339
/organism="Hepatitis C virus"
/virlon
/mol_type="genomic RNA"
/isolate="P8.Don"
/db_xref="taxon:11103"
/note="genotype: 3a"
<1..>339
/gene="NS5-D"
<1..>339
/gene="NS5-B"
/codon_start=1
/product="non-structural protein NS5-B"
/protein_id="AA083279.1"
/db_xref="GI:29365773"
/translation="STVTEQDIVEEIEIYOCNLEPEARKYISLTERLYCGGPMNS
KGAOCGYRRCRASGVLPFSFGNTITCYIKATAAKAAGLRNPDFLVCGDDLVVAASD
GVDEDRALRA"

BASE COUNT 77 a 88 c 104 g 70 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
Db 225 AGCGGCTGCGAAGCCGCAG 244

RESULT 37
HCU61361 340 bp mRNA linear VRL 15-JUL-1996
LOCUS
DEFINITION Hepatitis C virus nonstructural protein (ns5b) mRNA, partial cds.
ACCESSION U61361
VERSION U61361.1 GI:1420933
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
1 (bases 1 to 340)
REFERENCE
AUTHORS Stuyver,L., Wyseur,A., van Arnhem,W., Hernandez,F. and Maertens,G.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-1996) Nucleic Acid Chemistry, Innogenetics,
Industriepark 7, Box 4, Gent 9052, Belgium
Location/Qualifiers
1..340
/organism="Hepatitis C virus"
/mol_type="mRNA"
/db_xref="taxon:11103"
/note="type 3a sequence from French blood donor"
1..340
/gene="ns5b"
<1..>340
/gene="ns5b"
/codon_start=2
/product="nonstructural protein"
/protein_id="AAB03842.1"
/db_xref="GI:1420934"
/translation="STVTEQDIVEEIEIYOCNLEPEARKYISLTERLYCGGPMNS
KGAOCGYRRCRASGVLPFSFGNTITCYIKATAAKAAGLRNPDFLVCGDDLVVAASD
GVDEDRALRA"

BASE COUNT 77 a 89 c 105 g 69 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
226 AGCGGCTGCGAAGCCGCAG 245

RESULT 38
LOCUS HPC1 340 bp RNA linear VRL 23-JUN-1999
DEFINITION Hepatitis C virus (HCV) T-1(HCV-Ta) gene, partial sequence.
ACCESSION D10078
VERSION D10078.1 GI:221678
KEYWORDS T-1(HCV-Ta).
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirus.
REFERENCE 1 (bases 1 to 340)
Mori, S., Kato, N., Yagyu, A., Tanaka, T., Ikeda, Y., Petchclai, B., Chiewslip, P., Kurimura, T. and Shimotohno, K.
A new type of hepatitis C virus in patients in Thailand
JOURNAL Biochem. Biophys. Res. Commun. 183 (1), 334-342 (1992)
MEDLINE 92181465
PUBMED 1311926
COMMENT Data kindly submitted in computer readable form by: Shigehisa Mori

FEATURES
source National Cancer Center
Research Institute
5-1-1 Tsukiji, Chuo-ku
Tokyo 104
Japan
Phone: 03-3542-2511 x4702
Fax: 813-3545-3567.
Location/Qualifiers
1..340
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/strain="T1"
/db_xref="taxon:11103"
1..340
/gene="T-1(HCV-Ta)"
<1..>340
/codon_start=2
/protein_id="BA00972.1"
/db_xref="GI:221679"
/translation="STVTEDIRVEEITYOCNLEPEARKVISSITERLYCGPMWNS
KGACGGRRCRAGSVLPSTFGNTITCYIKATAAKAAGLRNPDLVCGDDLVVAESD
GVDEDRALRA"

BASE COUNT 76 a 92 c 106 g 66 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
226 AGCGGCTGCGAAGCCGCAG 245

RESULT 39
LOCUS AF506608 378 bp RNA linear VRL 04-JUN-2002
DEFINITION Hepatitis C virus isolate SGF65 polypeptide precursor gene, NSSB
region, partial cds.
ACCESSION AF506608
VERSION AF506608.1 GI:21321566
KEYWORDS Hepatitis C virus
SOURCE

ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirus.
REFERENCE 1 (bases 1 to 378)
Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.
Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
2 (bases 1 to 378)
Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.
Direct Submission
Submitted (26-Apr-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
Location/Qualifiers
1..378
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="SGF65"
/db_xref="taxon:11103"
/country="Russia"
1..>378
/codon_start=3
/product="polypeptide precursor"
/protein_id="AAM47258.1"
/db_xref="GI:21321567"
/translation="CCPDSTVTEODIRVEEITYOCNLEPEARKVISSITERLYCGP
MNSKAGCGYRRCRAGSVLPSTFGNTITCYIKATAAKAAGLRNPDLVCGDDLVV
AESDGVDEDRALRAFTFEMTRY"
1..>378
/product="NSSB"

BASE COUNT 83 a 98 c 115 g 82 t

ORIGIN

mat_peptide

Query Match 0.0%; Score 20; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
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239 AGCGGCTGCGAAGCCGCAG 258

RESULT 40
LOCUS AF506582 391 bp RNA linear VRL 04-JUN-2002
DEFINITION Hepatitis C virus isolate RIG101 polypeptide precursor gene, NSSB
region, partial cds.
ACCESSION AF506582
VERSION AF506582.1 GI:21321517
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirus.
REFERENCE 1 (bases 1 to 391)
Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.
Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
2 (bases 1 to 391)
Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.
Direct Submission
Submitted (26-Apr-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
Location/Qualifiers
1..391
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="RIG101"
/db_xref="taxon:11103"
/country="Russia"
1..>391
/codon_start=1

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86659 AGCGGCTGCGAAGCCGCGAG 86678
        |||||||||||||||||||
Db      252 AGCGGCTGCGAAGCCGCGAG 271

RESULT 41
AF506586      392 bp      RNA      linear      VRL 04-JUN-2002
LOCUS      Hepatitis C virus isolate RI6132 polyprotein precursor gene, NS5B
DEFINITION      region, partial cds.
ACCESSION      AF506586
VERSION      AF506586.1 GI:21321525
KEYWORDS
SOURCE      Hepatitis C virus
ORGANISM      Hepatitis C virus
REFERENCE      1 (bases 1 to 392)
AUTHORS      Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE      Genetic variability of hepatitis C virus in Western Siberia
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 392)
AUTHORS      Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE      Direct Submission
JOURNAL      Submitted (26-APR-2002) Inst. Molecular Biology, State Research
        Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
        630559, Russia
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            /country="Russia"
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            <1..>392
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86659 AGCGGCTGCGAAGCCGCGAG 86678
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Db      252 AGCGGCTGCGAAGCCGCGAG 271

RESULT 42
AY100081

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LOCUS      AY100081      678 bp      RNA      linear      VRL 04-NOV-2002
DEFINITION      Hepatitis C virus isolate L6 NS5B protein (NS5B) gene, partial cds.
ACCESSION      AY100081
VERSION      AY100081.1 GI:21065079
KEYWORDS
SOURCE      Hepatitis C virus
ORGANISM      Hepatitis C virus
REFERENCE      1 (bases 1 to 678)
AUTHORS      Cochrane,A., Searle,B., Hardie,A., Robertson,R., Delahooke,T.,
        Cameron,S., Tedder,R.S., Dushenko,G.M., De Lamballerie,X. and
        Simmonds,P.
TITLE      A Genetic Analysis of Hepatitis C Virus Transmission between
        Injection Drug Users
JOURNAL      J. Infect. Dis. 186 (9), 1212-1221 (2002)
MEDLINE      22289487
PUBMED      12402190
REFERENCE      2 (bases 1 to 678)
AUTHORS      Cochrane,A. and Simmonds,P.
TITLE      Direct Submission
JOURNAL      Submitted (25-APR-2002) Laboratory for Clinical and Molecular
        Virology, University of Edinburgh, Summerhall, Edinburgh, Scotland
        EH9 1QH, United Kingdom
FEATURES
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            /mol_type="genomic RNA"
            /isolate="L6"
            /isolation_source="from serum of patient in risk group IDU
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            /db_xref="taxon:11103"
            /country="United Kingdom"
            /note="genotype: 3a"
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            RAAMEYVTRHTPVNSWGLNITMYAFTIVRWMTHTFESILOSIEDRPLDFMYGAT
            YSVXPLX"
BASE COUNT      146 a      193 c      179 g      156 t      4 others
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Query Match      0.0%; Score 20; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86659 AGCGGCTGCGAAGCCGCGAG 86678
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Db      202 AGCGGCTGCGAAGCCGCGAG 221

RESULT 43
AF516375
LOCUS      AF516375      681 bp      RNA      linear      VRL 04-NOV-2002
DEFINITION      Hepatitis C virus isolate 195 NS5B gene, partial cds.
ACCESSION      AF516375
VERSION      AF516375.1 GI:21591680
KEYWORDS
SOURCE      Hepatitis C virus
ORGANISM      Hepatitis C virus
REFERENCE      1 (bases 1 to 681)
AUTHORS      Cochrane,A., Searle,B., Hardie,A., Robertson,R., Delahooke,T.,
        Cameron,S., Tedder,R.S., Dushenko,G.M., De Lamballerie,X. and

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TITLE Simmonds, P.
A Genetic Analysis of Hepatitis C Virus Transmission between
Injection Drug Users
JOURNAL J Infect. Dis. 186 (9), 1212-1221 (2002)
MEDLINE 22289487
PUBMED 12402190
REFERENCE 2 (bases 1 to 681)
AUTHORS Cochrane, A. and Simmonds, P.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Laboratory of Clinical and Molecular
Virology, University of Edinburgh, Summerhall, Edinburgh EH9 1QH,
UK

FEATURES
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/note="genotype: 3a"
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RAAMETARHTPVSNSWLNINIMYAPTIWRYVMWMTHTFSLIOSQELDRPLDFEMGAT
YSVTPXDXP"

BASE COUNT 152 a 204 c 176 g 147 t 2 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86659 AGCGCTCGGAAGCCGCAG 86678
|||||
DB 202 AGCGCTCGGAAGCCGCAG 221

RESULT 44
AF516377 682 bp RNA linear VRL 04-NOV-2002
LOCUS Hepatitis C virus isolate GWS13 NS5B gene, partial cds.
DEFINITION
ACCESSION AF516377
VERSION AF516377.1 GI:21591684
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.

REFERENCE 1 (bases 1 to 682)
AUTHORS Cochrane, A., Seale, B., Hardie, A., Robertson, R., Delahooke, T.,
Cameron, S., Tedder, R.S., Dushenko, G.M., De Lamballerie, X. and
Simmonds, P.
TITLE A Genetic Analysis of Hepatitis C Virus Transmission between
Injection Drug Users
J. Infect. Dis. 186 (9), 1212-1221 (2002)

TITLE A Genetic Analysis of Hepatitis C Virus Transmission between
Injection Drug Users
J. Infect. Dis. 186 (9), 1212-1221 (2002)
MEDLINE 22289487
PUBMED 12402190
REFERENCE 2 (bases 1 to 682)
AUTHORS Cochrane, A. and Simmonds, P.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Laboratory of Clinical and Molecular
Virology, University of Edinburgh, Summerhall, Edinburgh EH9 1QH,
UK

FEATURES
source Location/Qualifiers
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/organism="Hepatitis C virus"
/mol_type="genomic RNA"

/isolate="GWS13"
/isolation_source="injecting drug user, Glasgow"
/db_xref="taxon:11103"
/country="United Kingdom"
/note="genotype: 3a"
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/product="NS5B"
/protein_id="AA064176.1"
/db_xref="GI:21591685"
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YSVTPXDXP"

CDS

BASE COUNT 150 a 197 c 179 g 155 t 1 others
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Query Match 0.0%; Score 20; DB 1; Length 682;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86659 AGCGCTCGGAAGCCGCAG 86678
|||||
DB 202 AGCGCTCGGAAGCCGCAG 221

RESULT 45
AY100067 683 bp RNA linear VRL 04-NOV-2002
LOCUS Hepatitis C virus isolate G12 NS5B protein (NS5B) gene, partial
DEFINITION
ACCESSION AY100067
VERSION AY100067.1 GI:21065051
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.

REFERENCE 1 (bases 1 to 683)
AUTHORS Cochrane, A., Seale, B., Hardie, A., Robertson, R., Delahooke, T.,
Cameron, S., Tedder, R.S., Dushenko, G.M., De Lamballerie, X. and
Simmonds, P.
TITLE A Genetic Analysis of Hepatitis C Virus Transmission between
Injection Drug Users
J. Infect. Dis. 186 (9), 1212-1221 (2002)

TITLE A Genetic Analysis of Hepatitis C Virus Transmission between
Injection Drug Users
J. Infect. Dis. 186 (9), 1212-1221 (2002)
MEDLINE 22289487
PUBMED 12402190
REFERENCE 2 (bases 1 to 683)
AUTHORS Cochrane, A. and Simmonds, P.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Laboratory for Clinical and Molecular
Virology, University of Edinburgh, Summerhall, Edinburgh, Scotland
EH9 1QH, United Kingdom

FEATURES
source Location/Qualifiers
1. .683
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
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/country="United Kingdom"
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/translation="RVEEIVQCCNLEPEARKVLSLTERLYCGGPMFNSKAGACGY

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CDS

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BASE COUNT 150 a 196 c 180 g 156 t 1 others
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Query Match 0.0%; Score 20; DB 1; Length 683;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGGCTGCGAGGCCGACG 86678
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Db 202 AGCGGCTGCGAGGCCGACG 221

Search completed: September 30, 2003, 02:54:01
Job time : 33895 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: September 29, 2003, 10:19:43 ; Search time 6306 Seconds
(without alignments)
12337.108 Million cell updates/sec

Title: US-09-831-000-1_COPY_104900_133719

Sequence: 1 ccaactcagctccgcyga.....cgggcaaccgcgccagatct 28820

Scoring table: OLIGO_NUC

Searched: 2552756 seqs, 1349719017 residues

word size :

Total number of hits satisfying chosen parameters: 5105512

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28820	100.0	128139	24	AA1664291	RRV genome nucleot.
2	28820	100.0	133719	21	AA1664254	Macaca mulatta rha
3	33	0.1	128139	24	AA1664291	RRV genome nucleot
4	33	0.1	133719	21	AAAC64754	Macaca mulatta rha
5	28	0.1	3571	21	AAAC81583	Mouse zveg3f DNA,
6	28	0.1	3571	21	AAAS1527	Murine vascular en
7	28	0.1	3571	22	AAAD0650	Mouse zveg3f DNA.
8	28	0.1	3571	24	AB568648	Mouse cDNA encodin

c	9	28	0.1	3571	25	AAIT2444	Mouse zvegf3 codon
c	10	28	0.1	3571	24	ABX93182	DNA encoding protein
c	11	27	0.1	2218	14	AAQ47928	Paired basic amino
c	12	27	0.1	4461	24	AAS94758	Human DNA sequence
c	13	27	0.1	4303	14	AAQ47927	Paired basic amino
c	14	27	0.1	4403	24	ABN59505	Gene #2403 used to
c	15	26	0.1	3132	24	AAS94759	Human DNA sequence
c	16	25	0.1	2870	24	ABY94750	Human pancreatic c
c	17	25	0.1	2876	18	AAT97303	Human plasmalogen
c	18	25	0.1	2876	22	AAS09460	Human cDNA encodin
c	19	25	0.1	2876	22	AAH02917	Human shear stress
c	20	25	0.1	2876	24	ABV77991	Hypoxia-regulated
c	21	25	0.1	2944	9	AAH80253	Insert of lambda 3
c	22	25	0.1	3171	24	AAS94905	Human DNA sequence
c	23	25	0.1	3172	25	ABX63842	Human cDNA #842 d1
c	24	25	0.1	7309	22	AAS46568	Tumour suppressor
c	25	25	0.1	7309	24	ABK34011	Human DNA for stag
c	26	25	0.1	7309	24	ABL33817	Human immune syste
c	27	25	0.1	17509	24	ABN55599	Gene #2097 used to
c	28	23	0.1	2307	24	ABK32842	DNA encoding human
c	29	23	0.1	6816	25	ABX08754	Angiogenesis-assoc
c	30	23	0.1	7752	24	ABL70224	Chemically treated
c	31	23	0.1	33207	20	AAV73805	KSHV LTR DNA (nucl
c	32	23	0.1	137507	19	AAV19941	KSHV long unique c
c	33	22	0.1	1044	24	ABK97604	Human prostate spee
c	34	22	0.1	3024	22	AAK90497	Human digestive sy
c	35	22	0.1	3024	22	AAK90501	Human digestive sy
c	36	22	0.1	4176	22	AAI57831	Human polynucleoti
c	37	22	0.1	13334	22	ABA15786	Human nervous syst
c	38	22	0.1	38997	24	AAD36069	Human snare XKT6 g
c	39	22	0.1	157875	24	ABK97972	Human CdkPLX genom
c	40	22	0.1	254366	25	ABZ23304	Human phosphatase
c	41	22	0.1	1082138	21	AAE22305	Arabidopsis thalli
c	42	21	0.1	414	22	AAH42781	Nucleotide sequence
c	43	21	0.1	597	24	ABQ41636	Oligonucleotide fo
c	44	21	0.1	597	24	ABQ41637	Oligonucleotide fo
c	45	21	0.1	607	22	AAK77708	Human immune/haema

ALIGNMENTS

RESULT	1
AAI64291	
ID	AAI64291 standard; DNA; 128139 BP.

AC AAI64291;

DT 22-APR-2002 (first entry)

DE RRV genome nucleotide sequence.

RRV; rhesus rhadinovirus; japanese macaque virus; multiple sclerosis;

KW vulnerable; gene therapy; leucopenia; thrombocytopaenia;

Macaca mulatta rhadiporia 17577

XX	Key	Location/Qualifiers
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CDS	/*+aa= 2

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/..product= "dihydrof
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/note= "has similarity to Kaposi's sarcoma-associated
FT

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FT	3676..5613
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FT      /tag= e
FT      /product= "transport protein"
FT      /label= RRV_ORF7
FT      /note="has similarity to KSHV ORF7"
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FT      /tag= f
FT      /product= "glycoprotein B"
FT      /label= RRV_ORF8
FT      /note="has similarity to KSHV ORF8"
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FT      /product= "DNA polymerase protein"
FT      /label= RRV_ORF9
FT      /note="has similarity to KSHV ORF9"
FT      17261..18511
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FT      /label= RRV_ORF10
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FT CDS   18520..19749
FT      /tag= i
FT      /label= RRV_ORF11
FT      /note="has similarity to KSHV ORF11"
FT      complement (19921..20544)
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FT      /product= "RVV R3"
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FT CDS   26846..27409
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FT      /product= "tegument protein"
FT      /label= RRV_ORF19
FT      /note="has similarity to KSHV ORF19"
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FT      /tag= q
FT      /label= RRV_ORF20
FT      /note="has similarity to KSHV ORF20"
FT CDS   32094..33767
FT      /tag= r
FT      /product= "thymidine kinase"
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FT      /product= "glycoprotein H"

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FT      /label= RRV_ORF23
FT      /note="has similarity to KSHV ORF23"
FT      complement (37123..39321)
FT CDS   /tag= u
FT      /label= RRV_ORF24
FT      /note="has similarity to KSHV ORF24"
FT      39323..44459
FT      /tag= v
FT      /product= "major capsid protein"
FT      /label= RRV_ORF25
FT      /note="has similarity to KSHV ORF25"
FT CDS   43491..44408
FT      /tag= w
FT      /product= "capsid protein"
FT      /label= RRV_ORF26
FT      /note="has similarity to KSHV ORF26"
FT CDS   44433..45242
FT      /tag= x
FT      /label= RRV_ORF27
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FT CDS   45408..45683
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FT      complement (45733..46779)
FT      /tag= z
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FT      /note="has similarity to KSHV ORF31"
FT CDS   47683..49077
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FT      complement (49977..50960)
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FT      /label= RRV_ORF29a
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FT CDS   50959..51942
FT      /tag= af
FT      /label= RRV_ORF34
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FT      /tag= ah
FT      /product= "kinase"
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FT /note= "has similarity to KSHV ORF38"
FT complement (55255..56391)
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FT /tag= a1
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FT /label= RRV_ORF40
FT /note= "has similarity to KSHV ORF40"
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Query Match 100.0% Score 28820; DB 24; Length 128139;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 28820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB GTCTAGAGGGGTTTTCATTATGTTCACACAGCTAACCCCGGTTCCAGCGCCCG 99439
QY 121 GGTCTGAAATCGCAACAGGCGACGCGGCGGAGAGCGCGCAACGTGATGACAGA 180
DB GGTCTGAAATCGCAACAGGCGACGCGGCGGAGAGCGCGCAACGTGATGACAGA 99440
QY 181 CAGTGGCCGCAATCGCTCAGACGCTCCAAAGAGTTTCGACACGTACGAACACACACC 240
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QY 361 TTTCAGAGAAGATGTTCTAAACACCGAAGGATGCACAACTGTGTCACCGCATGTGG 420
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Db 105740 GTTCTTGGCTCGACACACAGAGCAGATACCATTACAAACCTCCGCTTCCACAC 105799
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QY 6541 ACAAATAACACACCGCATCATATGCTTATGAGATGCTGAGCGCACACCCGAG 6600
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QY 6841 TGGCCACCTCCGGAAGATTAAGAAAGTCAAAAGCTGCTGGCAACGGAGATTCCTA 6900
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QY 7021 CAAGTGCCTGACACAACTTAATCAACCCGCTTCAAAACCTCAAACTATACAT 7080
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QY 7081 TAATCTTGAGAAAGCAGCAACAATGCCAAAACAGCCAGAAAGTGCATTCGCTCGA 7140
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Db 106460 GCGCGCTGACGACCTTAGGCTGAGCGACCGGAGCGGCCAGTCCAGCGGACCGCATCC 106519
QY 7201 AGGACGAGGAGCTGCAAAAAGCAAAATCATGAGTGGAAAAAGTTAGTTTCAACACGCGAG 7260
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Db 106520 AGGACGAGAGCTGCAAAAAGCAAAATCATGCAATGGAAGAAAGTTAGTTTCAGACGCGAG 106579
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QY 7381 GGTGCGTGGCTCTCTCATCATATGGAACCTGTCAACATGGGGTTCAACTGTGCG 7440
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OY	14881	AAGCCTTTGATTAATACAGACAAACCGGGGGCTTACTTAATAATGGTCTTGCAAAAT	14940
Db	114200	GAGCCTTTGATTAATACAGACAAACCGGGGGCTTACTTAATAATGGTCTTGCAAAAT	114259
OY	14941	TCGCCAAGGTGTGTGGCAACGACTCGGGGGCGCCGACAGAGGATTGCGCCGCAACGCCG	15000
Db	114260	TCGCCAAGGTGTGTGGCAACGACTCGGGGGCGCCGACAGAGGATTGCGCCGCAACGCCG	114319
OY	15001	ACGGCTTCGCCAATCTGGCCGGAGCGGCGCAGCGGCAACCGAGCTAAACAGCGCGAG	15060
Db	114320	ACGGCTTCGCCAATCTGGCCGGAGCGGCGCAGCGGCGCACCAGGCTAAACAGCGCGAG	114379
OY	15061	GGGGCGCCACACAGGAGCGGGGGGACAGCCGGGGGGGGGTCACAGATGGCTTGTGA	15120
Db	114380	GGGGCGCCACACAGGAGCGGGGGGACAGCCGGGGGGGGGTCACAGATGGCTTGTGA	114439
OY	15121	ACAGACTCCACCACCTGGCTGTGAAGGGCAAGAGCTGCTCTTTGTAAAGCGCTTTTA	15180
Db	114440	ACAGACTCCACCACCTGGCTGTGAAGGGCAAGAGCTGCTCTTTGTAAAGCGCTTTTA	114499
OY	15181	AACAGGGTGGGCCGATGAGCGTCCGTTGGTAAAGAGCGCTTAAGTTCCACTTAAAGCC	15240
Db	114500	AACAGGGTGGGCCGATGAGCGTCCGTTGGTAAAGAGCGCTTAAGTTCCACTTAAAGCC	114559
OY	15241	TTAAGATTTGATTTTTCGTTTCAGTAAATCCGACAGGAAAAATCCGCGCGGCGAA	15300
Db	114560	TTAAGATTTGATTTTTCGTTTCAGTAAATCCGACAGGAAAAATCCGCGCGGCGAA	114619
OY	15301	AAGCATAAAAAGCGCGCCTTGAAGAGATTCAAGTCTTAATCTTGCGGCTAAAAATAGA	15360
Db	114620	AAGCATAAAAAGCGCGCCTTGAAGAGATTCAAGTCTTAATCTTGCGGCTAAAAATAGA	114679
OY	15361	CAGCGGGCCCCAGCCTCTGAAAACCGCGAGCGGGGATGCTCGACACTCTAGATAGCA	15420
Db	114680	CAGCGGGCCCCAGCCTCTGAAAACCGCGAGCGGGGATGCTCGACACTCTAGATAGCA	114739
OY	15421	TCGAAATTAAGTAAAGCGCCAGTGGGAAAAAGCTAAGATCCGCGTGGGGGCCCTGGCAAA	15480
Db	114740	TCGAAATTAAGTAAAGCGCCAGTGGGAAAAAGCTAAGATCCGCGTGGGGGCCCTGGCAAA	114799
OY	15481	GACCGCATCAACAGTCCCAAGATACTGCAATGCCACCGTCACCTCCGTTTGTATCGTC	15540
Db	114800	GACCGCATCAACAGTCCCAAGATACTGCAATGCCACCGTCACCTCCGTTTGTATCGTC	114859
OY	15541	CCATAGCAGGCCCGTGATGTTACAAAGACGCTTCGTGGGCGAGGAGTTAGAGAGGCC	15600
Db	114860	CCATAGCAGGCCCGTGATGTTACAAAGACGCTTCGTGGGCGAGGAGTTAGAGAGGCC	114919
OY	15601	CGGTCTGTGTACAGGAGGGGGGCATATGTCCTCGGGGGCGACTGGGCGCAACAGACATT	15660
Db	114920	CGGTCTGTGTACAGGAGGGGGGCATATGTCCTCGGGGGCGACTGGGCGCAACAGACATT	114979
OY	15661	GTCAGAGCAAGTAAAGAAAGCAGATATTAAGTCTCACTCGCGGCTCACGAGGCTTAAATC	15720
Db	114980	GTCAGAGCAAGTAAAGAAAGCAGATATTAAGTCTCACTCGCGGCTCACGAGGCTTAAATC	115039
OY	15721	GAAGCTCCGGCTTAAACACAAATCTTCTTGCGCTATGTCGCTCCACTGGTCCCA	15780
Db	115040	GAAGCTCCGGCTTAAACACAAATCTTCTTGCGCTATGTCGCTCCACTGGTCCCA	115099
OY	15781	TGTCCTTCGCAAGTTACAGCCCTGCTGTTCCCGGAAAGCGGCGACTAGTGAACGCGGA	15840
Db	115100	TGTCCTTCGCAAGTTACAGCCCTGCTGTTCCCGGAAAGCGGCGACTAGTGAACGCGGA	115159
OY	15841	AGCGGCTTTGATTTAAAGTGATACAGCGGGGCAATTTGCCAAACGATAGCGGTTT	15900
Db	115160	AGCGGCTTTGATTTAAAGTGATACAGCGGGGCAATTTGCCAAACGATAGCGGTTT	115219
OY	15901	CCTGCAGTCTGGGTTTTCACCTGCGAACGCGCACTGTCTTCTTGCGACGCGCGCTGGGG	15960
Db	115220	CCTGCAGTCTGGGTTTTCACCTGCGAACGCGCACTGTCTTCTTGCGACGCGCGCTGGGG	115279
OY	15961	ATTTTTTTAGTGTGAATTTGGCAGTCTCTGTCATGCGGCACTAATGCTGGCCTGGAAGTG	16020

Db	115280	ATTTTTTAGTGTGAATTTGGCAGTCTCTGTCCATGCGCACTATGCTGGCCTGGAATG	115339
Qy	16021	GGGGGGGATGGGTGATGTCGTTCCACAGGGCGAGGGCGCTTTTGTAGCGGCTTGCGGT	16080
Db	115340	GGGGGGGATGGGTATGTGCTCCACCGGGGAGGGGCGCTTTTGTAGCGGCTTGCGGT	115399
Qy	16081	TTCCGGGCTTTGACGAGAACACCCGTATGTCAAAAAGCCGGGATGACGGGACTGCCAGTGC	16140
Db	115400	TTCCGGGCTTTGACGAGAACACCCGTATGTCAAAAAGCCGGGATGAGGGGACTGCCAGTGC	115459
Qy	16141	GTCCGGCAAAAGCGGACGCTGGATGCTCTATGCGCGGAAACTGTAGGCACTTGCCAG	16200
Db	115460	GTCCGGCAAAAGCGGACGCTGGATGCTCTATGCGCGGAAACTGTAGGCACTTGCCAG	115519
Qy	16201	GGCATACAGTAATAGGGGTCTGATTCAAAAAGATGACTCCGTGACACACAGGGCCGG	16260
Db	115520	GGCATACAGTAATAGGGGTCTGATTCAAAAAGATGACTCCGTGACACACAGGGCCGG	115579
Qy	16261	CCGAGGGGGGTGATCCTCGGGTCCCAATACCTGACGATAAATCTCTCTGTGGCGGTA	16320
Db	115580	CCGAGGGGGGTGATCCTCGGGTCCCAATACCTGACGATAAATCTCTCTGTGGCGGTA	115639
Qy	16321	TTTTCGTGGGTACTCTTCTCTGATAGAGGATACGTTATGGGAAATGGGGTATCGCGGGG	16380
Db	115640	TTTTCGTGGGTACTCTTCTCTGATAGAGGATACGTTATGGGAAATGGGGTATCGCGGGG	115699
Qy	16381	GGCGGGGGGGCGCGGGGGCGCGCGGTGCTGCTCGCGCTCTCCCGCTTGTGCTCTG	16440
Db	115700	GGCGGGGGGGCGCGGGGGCGCGCGGTGCTGCTCGCGCTCTCCCGCTTGTGCTCTG	115759
Qy	16441	TTGTCTTTCAGAGACTTGTCTCTCGTGGAGATTGTGACTCTGTGCACTGCAACGTAAACA	16500
Db	115760	TTGTCTTTCAGAGACTTGTCTCTCGTGGAGATTGTGACTCTGTGCACTGCAACGTAAACA	115819
Qy	16501	AGGAACCTCTCCGGCACGCTGAGGGGAGACCCCAACCCCTACCGGTACGAGTGGAGTGT	16560
Db	115820	AGGAACCTCTCCGGCACGCTGAGGGGAGACCCCAACCCCTACCGGTACGAGTGGAGTGT	115879
Qy	16561	ATGGCCAGAAACGGGGGTCTTGCGCAGACGGCCGGTGGGGTGGTCTGTGTGGCTCAC	16620
Db	115880	ATGGCCAGAAACGGGGGTCTTGCGCAGACGGCCGGTGGGGTGGTCTGTGTGGCTCAC	115939
Qy	16621	CGCCTGTTCGCTGTTAGAGGGATGGGGCTGTGTAGAGCGTTGGCGATTGGGTGTCGGG	16680
Db	115940	CGCCTGTTCGCTGTTAGAGGGATGGGGCTGTGTAGAGCGTTGGCGATTGGGTGTCGGG	115999
Qy	16681	TGAGTCGGGGGGGGATTTCGGAGGGGGGAGAGACGTGGCGGTTGGCCGATTGTGGGGTCC	16740
Db	116000	TGAGTCGGGGGGGGATTTCGGAGGGGGGAGAGACGTGGCGGTTGGCCGATTGTGGGGTCC	116059
Qy	16741	AGGTGAGTCGGGAGGGGGCAAGGAGAGCTGAGAGGCTCAGGCGCTCAGGTGAGTCTGTG	16800
Db	116060	AGGTGAGTCGGGAGGGGGCAAGGAGAGCTGAGAGGCTCAGGCGCTCAGGTGAGTCTGTG	116119
Qy	16801	CGATGTGTGCAAAAACGACGAGAGGCTGCTGATTGGCGATGATTTATCCGACGAGCGGG	16860
Db	116120	CGATGTGTGCAAAAACGACGAGAGGCTGCTGATTGGCGATGATTTATCCGACGAGCGGG	116179
Qy	16861	TGCGAGGTAGTGGGGGGCCGGGGGTGACAGGGGGGTGATGTGTGGGGCGAATCGATGGCGG	16920
Db	116180	TGCGAGGTAGTGGGGGGCCGGGGGTGACAGGGGGGTGATGTGTGGGGCGAATCGATGGCGG	116239
Qy	16921	GGATGCGGGGAGCAACCTTGACGTTGTTTGAAGTGACAGGCTGAGCTAACACCGGGCG	16980
Db	116240	GGATGCGGGGAGCAACCTTGACGTTGTTTGAAGTGACAGGCTGAGCTAACACCGGGCG	116299
Qy	16981	AGACCCGCTTGGCAGCGGCTTTGGAGATCCCAACACGATGACGAGCTCAGACCCCTGACCC	17040
Db	116300	AGACCCGCTTGGCAGCGGCTTTGGAGATCCCAACACGATGACGAGCTCAGACCCCTGACCC	116359
Qy	17041	TGATGCGGACCTTTGGGATGACCCGTGCTGTGATTCGGTGGCCGTTTCGGTGTCCGATCC	17100

Db	116360	GGATGAGACACCCCTTGGGATGACCCCTGCTTGGATTGCGTGGCCGCTTTTCGGTGTCCGATCC	116419
Qy	17101	GTGCCCTTGTCTCTGCAACCGCCCGCACTTTCGGCCCTGATGTGTGTGAGCGGGGGCGC	17160
Db	116420	GTGCCCTTGTCTCTGCAACCGCCCGCACTTTCGGCCCTGATGTGTGTGAGCGGGGGCGC	116479
Qy	17161	GGGTGGCGCGGCTGGCGCGCGCGCTGCGCACAGCCCCCTGCCGCGCCTCCCGGCTGTCTCT	17220
Db	116480	GGGTGGCGCGCGCTGGCGCGCGCGCTGCGCACAGCCCCCTGCCGCGCCTCCCGGCTGTCTCT	116539
Qy	17221	AGTGGCGCGCGGTCTTTCGGCAATGTCCCTTCGAGAACATGTGCAACCCGTGTCCGATAC	17280
Db	116540	AGTGGCGCGCGGTCTTTCGGCAATGTCCCTTCGAGAACATGTGCAACCCGTGTCCGATAC	116599
Qy	17281	TATGCGCGAAGCATGTGTCCGGCTCCCGCACATGTTCGGGTATCTACTGCGTGTAAAAAC	17340
Db	116600	TATGCGCGAAGCATGTGTCCGGCTCCCGCACATGTTCGGGTATCTACTGCGTGTAAAAAC	116659
Qy	17341	GGCAGATTAAGTAGATTGCCCTTTCACGAGCCCGACGCCACCTGAGCGCGCGACGACA	17400
Db	116660	GGCAGATTAAGTAGATTGCCCTTTCACGAGCCCGACGCCACCTGAGCGCGCGACGACA	116719
Qy	17401	ACCATGTATTAGTGGGATTTGGCATTTATGTCCCTTAGTGTGGCGGCTATTTTATCTGCG	17460
Db	116720	ACCATGTATTAGTGGGATTTGGCATTTATGTCCCTTAGTGTGGCGGCTATTTTATCTGCG	116779
Qy	17461	GGCGACGATTGACCGTTAGAGTGGGGGAGAGGGCGGTTAACCGCAGCGACCCGACGG	17520
Db	116780	GGCGACGATTGACCGTTAGAGTGGGGGAGAGGGCGGTTAACCGCAGCGACCCGACGG	116839
Qy	17521	CGGTTTTAGTTTCGTTACTATTACGTTTAAATTCGTTGAGTTCGTTGCGGATTTTGGTGGCAG	17580
Db	116840	CGGTTTTAGTTTCGTTACTATTACGTTTAAATTCGTTGAGTTCGTTGCGGATTTTGGTGGCAG	116899
Qy	17581	TGTGTAAATCAACGCCCGCGCGCGCCCTTACTGTGTGCGCGCGCAACCGCGGAAGTCT	17640
Db	116900	TGTGTAAATCAACGCCCGCGCGCGCCCTTACTGTGTGCGCGCGCAACCGCGGAAGTCT	116959
Qy	17641	GTTCCGCGCGGAGAGCGCGCGCGGTGCGGAACCAACCGCCTTGAATTTGCGGGGCGG	17700
Db	116960	GTTCCGCGCGGAGAGCGCGCGCGGTGCGGAACCAACCGCCTTGAATTTGCGGGGCGG	117019
Qy	17701	CTGGGCTTGTGTCAGTGATTCACACAGATGCGATGTGTTGGCGGTGTGCTCAACGTC	17760
Db	117020	CTGGGCTTGTGTCAGTGATTCACACAGATGCGATGTGTTGGCGGTGTGCTCAACGTC	117079
Qy	17761	ACTTGTTAACCCGTTAACTGGAATTTCTTGTTCGCGCGCGCGGTGATAGCCGCGGCCCTAA	17820
Db	117080	ACTTGTTAACCCGTTAACTGGAATTTCTTGTTCGCGCGCGCGGTGATAGCCGCGGCCCTAA	117139
Qy	17821	GCCATTATGTGCTGTGACGCGATCTCGAAGCTCGAAGCTGGCGCATTAACCCCGATAT	17880
Db	117140	GCCATTATGTGCTGTGACGCGATCTCGAAGCTCGAAGCTGGCGCATTAACCCCGATAT	117199
Qy	17881	GGCGTTGGGTGTGCGGTGGCAACCTTTTGGAAAAAGATTTATTTGCCCGCGGTTTAAGCA	17940
Db	117200	GGCGTTGGGTGTGCGGTGGCAACCTTTTGGAAAAAGATTTATTTGCCCGCGGTTTAAGCA	117259
Qy	17941	CCACACCGACCGCTGCGCTTTCATTTAGTGGGAGGAATTAACATTAACTGCTGCTGG	18000
Db	117260	CCACACCGACCGCTGCGCTTTCATTTAGTGGGAGGAATTAACATTAACTGCTGCTGG	117319
Qy	18001	CGAGCGTTGCCAGCGGTGTGGTGGCGCTTCAAAAGCACTATGAGGGGGTCCCGCTGACAT	18060
Db	117320	CGAGCGTTGCCAGCGGTGTGGTGGCGCTTCAAAAGCACTATGAGGGGGTCCCGCTGACAT	117379
Qy	18061	CTACCGCGTCCCTGGGGGTGCTGTTTAACACACACCCCGACAGCTTCTTATCGTTACCTGGC	18120
Db	117380	CTACCGCGTCCCTGGGGGTGCTGTTTAACACACACCCCGACAGCTTCTTATCGTTACCTGGC	117439
Qy	18121	AAAAACAGGAATGCCCTAGTCCCGTTAACGTGGCCACATATAGTTCGGAAGCGGACCG	18180
Db	117440	AAAAACAGGAATGCCCTAGTCCCGTTAACGTGGCCACATATAGTTCGGAAGCGGACCG	117499

QY	18181	TGTTTACAGCCCCCGTTCCGCGGTAGGGTTTGACATTTCCGACACAAAGTTGACAGACA	18240
Db	117500	TGGTTTACAGCCCCCGTTCCGCGGTAGGGTTTGACATTTCCGACACAAAGTTGACAGACA	1175599
QY	18241	CCCTGAAGTTTTTTTAAATGCGACACCTCGAGAGAGAGGGGTACCTGTAATCTTTAAAG	18300
Db	117560	CCCTGAAGTTTTTTTAAATGCGACACCTCGAGAGAGAGGGGTACCTGTAATCTTTAAAG	117619
QY	18301	CGTTTGAAGTGGGAAAGCTGTGCGGAAACCGCTGCTTGAAGTTTTACGTCGCCCTGTCCA	18360
Db	117620	CGTTTGAAGTGGGAAAGCTGTGCGGAAACCGCTGCTTGAAGTTTTACGTCGCCCTGTCCA	117679
QY	18361	TGTCGCGTACAGTTTTTACCACCCCGATTAACCCGACAGAGCTCGTCTCGGCGCAGACCA	18420
Db	117680	TGTCGCGTACAGTTTTTACCACCCCGATTAACCCGACAGAGCTCGTCTCGGCGCAGACCA	117739
QY	18421	GTCCCGCACCGTCGCGTCAACTGGACCGCGCTCCGCGCCAGAGCTGTGCACGAACTGAAG	18480
Db	117740	GTCCCGCACCGTCGCGTCAACTGGACCGCGCTCCGCGCCAGAGCTGTGCACGAACTGAAG	117799
QY	18481	TGTTTCCCGCGGCCAACGAGAACACCTGTGTGTGGGTGCTGTCAACGTACGTCGCTG	18540
Db	117800	TGTTTCCCGCGGCCAACGAGAACACCTGTGTGTGGGTGCTGTCAACGTACGTCGCTG	117859
QY	18541	ACCCGGAAGACCTTGAAGAACGCGACAGTGCCTGTCACTATATAGCGGGTTTGGCCGCG	18600
Db	117860	ACCCGGAAGACCTTGAAGAACGCGACAGTGCCTGTCACTATATAGCGGGTTTGGCCGCG	117919
QY	18601	CGCGGCCCCGTGAGACCCCGTGTGGGATCCCTGGGAAGGAGACGACCACTAGTGTG	18660
Db	117920	CGCGGCCCCGTGAGACCCCGTGTGGGATCCCTGGGAAGGAGACGACCACTAGTGTG	117979
QY	18661	GTGTGTGGACACGGCGCGCGTTTAAAGCATTTTTTAAAGGGTGTTTTGTATAGGT	18720
Db	117980	GTGTGTGGACACGGCGCGCGTTTAAAGCATTTTTTAAAGGGTGTTTTGTATAGGT	118039
QY	18721	CTATGTGAGCGCGGTGTCTCCCGGTCTAGTGTTTGTTTCCCACTGAGTGTCTCATG	18780
Db	118040	CTATGTGAGCGCGGTGTCTCCCGGTCTAGTGTTTGTTTCCCACTGAGTGTCTCATG	118099
QY	18781	ACAAATACAAATTTTGAAGGTGGCTTTTAAAGGTGTCTTGTGTGCAAGCTTCTGTGTA	18840
Db	118100	ACAAATACAAATTTTGAAGGTGGCTTTTAAAGGTGTCTTGTGTGCAAGCTTCTGTGTA	118159
QY	18841	ACTGCATACACCGGGGTGTGCGCAGGAAACCGCGTCCCTTATGTCCGCTCGGCCCTC	18900
Db	118160	ACTGCATACACCGGGGTGTGCGCAGGAAACCGCGTCCCTTATGTCCGCTCGGCCCTC	118219
QY	18901	CCAGAGCGAAAGTGAAGATGTTCCTGGGGCGTTTGGCGTTGAGAGAGTGGGGCATGT	18960
Db	118220	CCAGAGCGAAAGTGAAGATGTTCCTGGGGCGTTTGGCGTTGAGAGAGTGGGGCATGT	118279
QY	18961	TGCGGTAAAGGGGTGTGCGCAAAAGCTACCGCGTCTCGTTTTTTCTTTTGTGCAGACAA	19020
Db	118280	TGCGGTAAAGGGGTGTGCGCAAAAGCTACCGCGTCTCGTTTTTTCTTTTGTGCAGACAA	118339
QY	19021	CACATGAGACGCGCTTGAAACAATTAACCTTAACTGTGATGAGATTTTCTGTACTACTTC	19080
Db	118340	CACATGAGACGCGCTTGAAACAATTAACCTTAACTGTGATGAGATTTTCTGTACTACTTC	118399
QY	19081	GAATAGCTACAGTATGATTAAGACAGACAATATGTCTTACACTTATGACAGGAATCCACGCT	19140
Db	118400	GAATAGCTACAGTATGATTAAGACAGACAATATGTCTTACACTTATGACAGGAATCCACGCT	118459
QY	19141	GTGTGGCGTGAAGGTGTTCCTCCACCTACCGTTTATGGATATATATGCTTTTATTTTT	19200
Db	118460	GTGTGGCGTGAAGGTGTTCCTCCACCTACCGTTTATGGATATATATGCTTTTATTTTT	118519
QY	19201	TTGCATTAACGCTGTTTGGGACAGCGTGTGTGCTATATATTTTTTTTAAATTTAAACGCT	19260
Db	118520	TTGCATTAACGCTGTTTGGGACAGCGTGTGTGCTATATATTTTTTTTAAATTTAAACGCT	118579

QY	19261	CCGCCACACTCTGAGATGTA	CTACTGATAGTGGCTGGGTGTGTGTTGTA	ACTCCCTGTTTCTGTGCGC	19320
Db	118580	CGCCAACTCTGTGGATGTACT	GTATGCTCGGGTGTGTGTTGTA	ACTCCCTGTTTCTGTGCGC	118633
QY	19321	GTCTGTTTGTTCAGCTGGC	TGCTGTACGTCGGGCCACATAGTCTAC	AGTCCGGAGCTG	19380
Db	118640	GTCTGTTTGTTCAGCTGGC	TGCTGTACGTCGGGCCACATAGTCTAC	AGTCCGGAGCTG	118699
QY	19381	CAGGTGAAATCTTTTCTTTT	TACCTGTACAGCTACTTTGGCCTGTAC	ATTGTGTGTG	19440
Db	118700	CAAGGTGAAATCTTTTCTTTT	TACCTGTACAGCTACTTTGGCCTGTAC	ATTGTGTGTG	118755
QY	19441	TATCACCTTATACAGTGCCT	GTAGTTGTGTTTTCCCGCCCGCTGGGTCA	AGCACGG	19500
Db	118760	TATCACCTTATACAGTGCCT	GTAGTTGTGTTTTCCCGCCCGCTGGGTCA	AGCACGG	118811
QY	19501	GGCCTCCGGCTTTCTCTGCG	TGTGTGTCTTTAATGTGGCGCTGGCGCTGTG	CCAA	19560
Db	118820	GGCCTCCGGCTTTCTCTGCG	TGTGTGTCTTTAATGTGGCGCTGGCGCTGTG	CCAA	118877
QY	19561	CGCGAGCCTATATAGAGCG	CCCTTGGCTACCCAGAGACCAGCATGTATG	CTPACGA	19620
Db	118880	CGCGAGCCTATATAGAGCG	CCCTTGGCTACCCAGAGACCAGCATGTATG	CTPACGA	118933
QY	19621	ACATCGCGGGGAAGATACCG	TCACTAGGAAGCTGAGATAGAA	CCACCAGCGCATCTG	19680
Db	118940	ACATCGCGGGGAAGATACCG	TCACTAGGAAGCTGAGATAGAA	CCACCAGCGCATCTG	118999
QY	19681	CGGGTTTTTGTTCCGTTGG	GCGTGTANAGGTCCTTTACGGACTTACGTGGTAT	AGT	19740
Db	119000	CGGGTTTTTGTTCCGTTGG	GCGTGTANAGGTCCTTTACGGACTTACGTGGTAT	AGT	119055
QY	19741	TAAAGCACGAAGCTGGCC	CAGAAAGGAGCCGTAGGGGTGTAA	TTTGACGCTGTGCT	19800
Db	119060	TAAAGCACGAAGCTGGCC	CAGAAAGGAGCCGTAGGGGTGTAA	TTTGACGCTGTGCT	119111
QY	19801	GCTGTTTTTAATTTTTTGC	CTCCCTCACTACCTGTGTG	CACTTTTTTGTACACCTGTTGAG	19860
Db	119120	GCTGTTTTTAATTTTTTGC	CTCCCTCACTACCTGTGTG	CACTTTTTTGTACACCTGTTGAG	119177
QY	19861	GACCGGTTTTTCGGCCG	GAACGTCGTAACCTCAGGAGCGTATAC	AGCTGGCGATGSCAT	19920
Db	119180	GACCGGTTTTTCGGCCG	GAACGTCGTAACCTCAGGAGCGTATAC	AGCTGGCGATGSCAT	119233
QY	19921	ATGCTCCCTGCTACAGAG	CATGTATAGCGCGTGTGCTGC	AGTGTGTATTTCTGGCTTGG	19980
Db	119240	ATGCTCCCTGCTACAGAG	CATGTATAGCGCGTGTGCTGC	AGTGTGTATTTCTGGCTTGG	119299
QY	19981	GTCTCTGTTTACGAGAG	GGTATAGGATATACCTGTGCTCGTGT	TATAGTGTTTTCCACTTC	20040
Db	119300	GTCTCTGTTTACGAGAG	GGTATAGGATATACCTGTGCTCGTGT	TATAGTGTTTTCCACTTC	119355
QY	20041	AGGTAGTTTATAGAGAC	TACTCAGCGCACTTGGTTGGATGTTTGTAT	ATTATTTTC	20100
Db	119360	AGGTAGTTTATAGAGAC	TACTCAGCGCACTTGGTTGGATGTTTGTAT	ATTATTTTC	119411
QY	20101	ATTTTGTGTCAATTTATTT	TCATTAAAGGATCTGACCTGACAGAC	CTTACTGTGACTTTTA	20160
Db	119420	ATTTTGTGTCAATTTATTT	TCATTAAAGGATCTGACCTGACAGAC	CTTACTGTGACTTTTA	119477
QY	20161	CTGTCTGTTTCTTATGAC	CACAGAGAACAAGGCACTGGAAG	CCACGCGCCACAGGGGAAAC	20220
Db	119480	CTGTCTGTTTCTTATGAC	CACAGAGAACAAGGCACTGGAAG	CCACGCGCCACAGGGGAAAC	119539
QY	20221	TGTCAATGTCCGAAC	TGCGGGGGGCACGTACGCCCACTGCC	ACAGGGGTGGAACGTACAGGC	20280
Db	119540	TGTCAATGTCCGAAC	TGCGGGGGGCACGTACGCCCACTGCC	ACAGGGGTGGAACGTACAGGC	119599
QY	20281	GGGGTCGACACAGGAG	GGCGCGGCGCCGTCCGGTGCAGTATGGCG	GGCCACAGCGCGCA	20340
Db	119600	GGGGTCGACACAGGAG	GGCGCGGCGCCGTCCGGTGCAGTATGGCG	GGCCACAGCGCGCA	119655
QY	20341	GTTCGCACAGCGGTTG	CGTGGGTAGTGTCCGCGAATCTCTG	GGGTGTGGCGCTGTGCCCCT	20400

Db	119660	GTGGGAGACAGGGGTTCCGTGGTAGTCTCCGGAAATCTCGGGTCGGCCCT	11971
Qy	20401	GTGGTAGTTCAGGGCATGGCTGCTGCTGTTAGATGGTATCCATGAGCCGCGCG	20460
Db	119720	GTGGTAGTTCAGGGCCATGGCTGCTGCTGTTAGATGGTATCCATGAGCCGCGCG	11977
Qy	20461	GTATCTCACGCCAGGTATCCGGCCGTTGGCCACCTGGAGAGCAGAGGCCCGAAGAC	20520
Db	119780	GTATCTCACGCCAGGTATCCGGCCGTTGGCCACCTGGAGAGCAGAGGCCCGAAGAC	11983
Qy	20521	CCTAAACATGATCTGATGGTGGTCTGGGGGATGTGAGGTTTAGCCAGAGGCACTGCTG	20580
Db	119840	CCTAAACATGATCTGATGGTGGTCTGGGGGATGTGAGGTTTAGCCAGAGGCACTGCTG	11989
Qy	20581	GTTCCTGTATGCTTCCCTCCAGAGTGATGCCACATGGTCGGGGGTTTGGGATCCGGG	20640
Db	119900	GTTCCTGTATGCTTCCCTCCAGAGTGATGCCACATGGTCGGGGGTTTGGGATCCGGG	11995
Qy	20641	CGTGTGTAGAGGGGCTCTCTTAAGAAGACCGAGCCGCCAGAGACTGGAACCCAAATC	20700
Db	119960	CGTGTGTAGAGGGGCTCTCTTAAGAAGACCGAGCCGCCAGAGACTGGAACCCAAATC	12001
Qy	20701	CCCGACGATAGTGAATAATGTATCCGCTCGGCGGAGAGAGCCATTAAGGCCCATAGCA	20760
Db	120020	CCCGACGATAGTGAATAATGTATCCGCTCGGCGGAGAGAGCCATTAAGGCCCATAGCA	12007
Qy	20761	CCGAGGGTGTGAGAAGACCCATGATCGGCACTCGGGCCCCCAGTAGCTGTTTGAT	20820
Db	120080	CCGAGGGTGTGAGAAGACCCATGATCGGCACTCGGGCCCCCAGTAGCTGTTTGAT	12013
Qy	20821	GGCCACGGTTCACCCGATGGTTCAGACCCGAGAAATCCCGGAGAGATGTTCCCTCTTAAG	20880
Db	120140	GGCCACGGTTCACCCGATGGTTCAGACCCGAGAAATCCCGGAGAGATGTTCCCTCTTAAG	12019
Qy	20881	GTCTGTGGTGGAGACGGCCGCGACGTCGAACCCGAGCTGTGTGAAGCGGCATCAGCGC	20940
Db	120200	GTCTGTGGTGGAGACGGCCGCGACGTCGAACCCGAGCTGTGTGAAGCGGCATCAGCGC	12025
Qy	20941	CCTGGGAACCGGGGACCGGGGGGTGACCAAGGGGGCACTGCTGGCGGCTCGACGGCGT	21000
Db	120260	CCTGGGAACCGGGGACCGGGGGGTGACCAAGGGGGCACTGCTGGCGGCTCGACGGCGT	12031
Qy	21001	TGCAAACAGAGTCAGTTCCTGTTTCTGCAAACTCGGCGAGGTGGGCCAGGTGTGTG	21060
Db	120320	TGCAAACAGAGTCAGTTCCTGTTTCTGCAAACTCGGCGAGGTGGGCCAGGTGTGTG	12037
Qy	21061	GTTCGACCCGTAGTCTTCTCTGTAGAGTTCCTCGCGGGGCTGAAGCTGGGCCCATAGA	21120
Db	120380	GTTCGACCCGTAGTCTTCTCTGTAGAGTTCCTCGCGGGGCTGAAGCTGGGCCCATAGA	12043
Qy	21121	GTACCACTGTGTCGTCGAGAACAGAGGCCAGTTTGCGCCACCGAATGAGGGCTGTGA	21180
Db	120440	GTACCACTGTGTCGTCGAGAACAGAGGCCAGTTTGCGCCACCGAATGAGGGCTGTGA	12049
Qy	21181	ATGAGACTTATCGTTGTGTGTAGATGAGCATTTCTTGTAGACAGACCTCTGACCCAC	21240
Db	120500	ATGAGACTTATCGTTGTGTGTAGATGAGCATTTCTTGTAGACAGACCTCTGACCCAC	12055
Qy	21241	GGTGGCGACACGGTGGCCCGGACGTCAAAGTTTGGCACGCTGGCGCACCTGTGAC	21300
Db	120560	GGTGGCGACACGGTGGCCCGGACGTCAAAGTTTGGCACGCTGGCGCACCTGTGAC	12061
Qy	21301	GTGGTGGGGCTGATTTGCAAAATGAGCGCCCGGGGTTTGGAGACACGACCACTGCAAGGG	21360
Db	120620	GTGGTGGGGCTGATTTGCAAAATGAGCGCCCGGGGTTTGGAGACACGACCACTGCAAGGG	12067
Qy	21361	CGTTTCTCTGACGGGATCGAATCTGTAGGCTCGGTTACGGGCCAAGGCCAATCTGAT	21420
Db	120680	CGTTTCTCTGACGGGATCGAATCTGTAGGCTCGGTTACGGGCCAAGGCCAATCTGAT	12073
Qy	21421	AGCGGTAACCACTATGCTCGTGGTGAAGTCTGGCGGACACCAAGACCCCGGGA	21480

Db 120740 AGCGGTAAACCAACCATGCTCCGCTCGCTGACGTGTGGCCGACACCAACGACCCCGGGA 120799
Qy 21481 GACGAGGGCCTGTGTTAGATGAAGAAGTTGGCCAGGTGTGTCGCCGAACGTCGGGTAG 21540
Db 120800 GACGAGGGCCTGTGTTAGATGAAGAAGTTGGCCAGGTGTGTCGCCGAACGTCGGGTAG 120859
Qy 21541 GGTGGGACTGCGCAAGACACAGTGTCTCAAGGTCGATCCCTGGGTCAAGTGTGGCGAC 21600
Db 120860 GGTGGGACTGCGCAAGACACAGTGTCTCAAGGTCGATCCCTGGGTCAAGTGTGGCGAC 120919
Qy 21601 GGGGAAGGACACGACGACATGAGTTACCGGTGGCTTACAGTGTGACGCGTTG 21660
Db 120920 GGGGAAGGACACGACGATGAGTTACCGGTGGCTTACAGTGTGACGCGTTG 120979
Qy 21661 CCTGAGGACTTACCTCGCGGGTGGGCGGTGATGACGACATGCGTTAAACGGGACGGGGG 21720
Db 120980 CTTGAGGACTTACCTCGCGGGTGGGCGGTGATGACGACATGCGTTAAACGGGACGGGGG 121039
Qy 21721 TACCGTCTGATGCTGTTGGGTGGCGCTGATCAAGTTCTTCCGACAGCGAGGCGTGC 21780
Db 121040 TACCGTCTGATGCTGTTGGGTGGCGCTGATCAAGTTCTTCCGACAGCGAGGCGTGC 121099
Qy 21781 GGGCGACGTGATGGCGAAGTTGATGCTCAAGTCCCTGCAATGTTCTTGAAGGCAAAAG 21840
Db 121100 GGGCGACGTGATGGCGAAGTTGATGCTCAAGTCCCTGCAATGTTCTTGAAGGCAAAAG 121159
Qy 21841 TGTGTCTGAGGAGCGAGGCTGTGTGCTCTCGGGTTCCAAACGACGACGCGGTAG 21900
Db 121160 TGTGTCTGAGGAGCGAGGCTGTGTGCTCTCGGGTTCCAAACGACGACGCGGTAG 121219
Qy 21901 CGTGTGTGCTTAAAGACGCGGACGTGCGCTAGCATGATGTTGGTGACCGGCTCGCAT 21960
Db 121220 CGTGTGTGCTTAAAGACGCGGACGTGCGCTAGCATGATGTTGGTGACCGGCTCGCAT 121279
Qy 21961 GGGGTATCTGGCCGCCACATGCGCGGTGATGCCCATCTGTATGCCGTGTCTCATATAGC 22020
Db 121280 GGGGTATCTGGCCGCCACATGCGCGGTGATGCCCATCTGTATGCCGTGTCTCATATAGC 121339
Qy 22021 CAGGCACTGTCCGACCCAGCGGTTCCGCGCTGCGCTGGGTGACCCAGGTTTCTGGGCT 22080
Db 121340 CAGGCACTGTCCGACCCAGCGGTTCCGCGCTGCGCTGGGTGACCCAGGTTTCTGGGCT 121399
Qy 22081 AACGAGCGTTCCGTGCGCTGTGCTGTGATGCGCTGGGGCGATATATGGGACCCG 22140
Db 121400 AACGAGCGTTCCGTGCGCTGTGCTGTGATGCGCTGGGGCGATATATGGGACCCG 121459
Qy 22141 CGGCATTCGTGCTGTAACACGACGATGTGTGACAAATGTGTAATCTGACAGCGGCCG 22200
Db 121460 CGGCATTCGTGCTGTAACACGACGATGTGTGACAAATGTGTAATCTGACAGCGGCCG 121519
Qy 22201 GCCCAGGGGTCCCACTTCCGACGTGTGAGCCAGACGCGTTGGAGCATGTGTCCACGTG 22260
Db 121520 GCCCAGGGGTCCCACTTCCGACGTGTGAGCCAGACGCGTTGGAGCATGTGTCCACGTG 121579
Qy 22261 TCGCGTGACAAACTCTTTCGTGCGCAACCGTGGACATCGGAGAACTGATCGACACGGA 22320
Db 121580 TCGCGTGACAAACTCTTTCGTGCGCAACCGTGGACATCGGAGAACTGATCGACACGGA 121639
Qy 22321 GGGCAGGGCGAATATAGGCCCCAGTGTGTCGGCGAGGGTGTCTTCCGACCATCTAGG 22380
Db 121640 GGGCAGGGCGAATATAGGCCCCAGTGTGTCGGCGAGGGTGTCTTCCGACCATCTAGG 121699
Qy 22381 TTTCTTGGGGCGGACGACGAGTTGGAGAAAGGGGTGTCTGTCGAACCCAAAGTTGC 22440
Db 121700 TTTCTTGGGGCGGACGACGAGTTGGAGAAAGGGGTGTCTGTCGAACCCAAAGTTGC 121759
Qy 22441 GATGACTTGGCGGATGTGGCTGTGATCGGCAACGCTCCGAGTTCCACAGCTCCAG 22500
Db 121760 GATGACTTGGCGGATGTGGCTGTGATCGGCAACGCTCCGAGTTCCACAGCTCCAG 121819
Qy 22501 GTGCTTACGAACTGAATTCGAAGCTTCTTGGCAGGTTTCCCAACGACGGCGAAAGGGCA 22560
Db 121820 GTGCTTACGAACTGAATTCGAAGCTTCTTGGCAGGTTTCCCAACGACGGCGAAAGGGCA 121879

Qy 22561 TCCGACAGATGCTGTGGGCCCTCTCGATGGCATCCAAAGGGGCCGGTTCCGGTCCGHTG 22620
Db 121880 TCCGACAGATGCTGTGGGCCCTCTCGATGGCATCCAAAGGGGCCGGTTCCGGTCCGHTG 121939
Qy 22621 GCGCGGAGGACGCGCAAAAGACACGACGAGGACGACGTTGTGAACCTTGTAACTAGAT 22680
Db 121940 GCGCGGAGGACGCGCAAAAGACACGACGAGGACGACGTTGTGAACCTTGTAACTAGAT 121999
Qy 22681 GTGCTTACGAGTTTCCCGTGAATGTCTGGCGTGGCGGTAGTTGGCTCGAATGGTTGG 22740
Db 122000 GTGCTTACGAGTTTCCCGTGAATGTCTGGCGTGGCGGTAGTTGGCTCGAATGGTTGG 122059
Qy 22741 TGGAGCTGAGACAAAGAGGCGGACGAGCGCCCGCGAGACGAGGCTCCAGAGTGGC 22800
Db 122060 TGGAGCTGAGACAAAGAGGCGGACGAGCGCCCGCGAGACGAGGCTCCAGAGTGGC 122119
Qy 22801 GATGACAGAGGCGGTTTCAATGAGCGCATTAATGCTGTGAATATAGGGGCCCTTCCAAAT 22860
Db 122120 GATGACAGAGGCGGTTTCAATGAGCGCATTAATGCTGTGAATATAGGGGCCCTTCCAAAT 122179
Qy 22861 CTGCTAAGCCAGGACAAAGTTGGGTGATGCGGGTAAATCTGCGGCGCTCCCGAGGTA 22920
Db 122180 CTGCTAAGCCAGGACAAAGTTGGGTGATGCGGGTAAATCTGCGGCGCTCCCGAGGTA 122239
Qy 22921 AAGCGAGCGCTGGTGGCATCGCCGTCACGCGGTTCAAAAGACCAAGACAGATGATAGG 22980
Db 122240 AAGCGAGCGCTGGTGGCATCGCCGTCACGCGGTTCAAAAGACCAAGACAGATGATAGG 122299
Qy 22981 CTGACTGAATTAAGACCTCTCTGAGAAATGTGTATGCTTGAAGCAGCAGATTAACGGA 23040
Db 122300 CTGACTGAATTAAGACCTCTCTGAGAAATGTGTATGCTTGAAGCAGCAGATTAACGGA 122359
Qy 23041 TGTGTGTGTAATACGTTGCGCTCGCGGTGGGTGGGCTGTGGAGCGGTTTAAAGAAAGCC 23100
Db 122360 TGTGTGTGTAATACGTTGCGCTCGCGGTGGGTGGGCTGTGGAGCGGTTTAAAGAAAGCC 122419
Qy 23101 ACCGAGACAGGCGTGGCGGTGGCGGACGCTGTGCAAGTGTGAGTGTGCTGTGTGTT 23160
Db 122420 ACCGAGACAGGCGTGGCGGTGGCGGACGCTGTGCAAGTGTGAGTGTGCTGTGTGTT 122479
Qy 23161 AATAGCTCTGTGGGTGGCGGAGAAATGCGCCACTGACGCGGTAGTGGCGTAATATCC 23220
Db 122480 AATAGCTCTGTGGGTGGCGGAGAAATGCGCCACTGACGCGGTAGTGGCGTAATATCC 122539
Qy 23221 ACAAGGGCGGATCTGATTTGCGCCCGGGGACAGGCTGGCAATGGAACAAGATGTTTG 23280
Db 122540 ACAAGGGCGGATCTGATTTGCGCCCGGGGACAGGCTGGCAATGGAACAAGATGTTTG 122599
Qy 23281 CAGCGCACTGCACTGTCTGAATGCGCTGTGAGGCTGTGAATGAGTCAAGTATGTG 23340
Db 122600 CAGCGCACTGCACTGTCTGAATGCGCTGTGAGGCTGTGAATGAGTCAAGTATGTG 122659
Qy 23341 GGTTCAGTTTTCGACGGGAGCGGCTGAAAAACGACGCTGATAGTCTCTCGGGCGCATATC 23400
Db 122660 GGTTCAGTTTTCGACGGGAGCGGCTGAAAAACGACGCTGATAGTCTCTCGGGCGCATATC 122719
Qy 23401 GGGGTATCTGGAACCTATAGCTGTGGGCTGGAGGCTGTGCAAGGCGGCGGTATAT 23460
Db 122720 GGGGTATCTGGAACCTATAGCTGTGGGCTGGAGGCTGTGCAAGGCGGCGGTATAT 122779
Qy 23461 GTTCGCTTGTAAAGGAGCATACCGCGGCGCATATATGGGTCTCTCGGCGCAACGCTCT 23520
Db 122780 GTTCGCTTGTAAAGGAGCATACCGCGGCGCATATATGGGTCTCTCGGCGCAACGCTCT 122839
Qy 23521 CCAAGCGGTGATTTGCAATGTACCGGGAGCTGGCGTGCACGCGCATATATTTCTAC 23580
Db 122840 CCAAGCGGTGATTTGCAATGTACCGGGAGCTGGCGTGCACGCGCATATATTTCTAC 122899
Qy 23581 TAGTGTGCAAGTGTACAGGGCGGCAAGGTGTCCCGGGGTATCCCGATCGCGCAAAAGCG 23640
Db 122900 TAGTGTGCAAGTGTACAGGGCGGCAAGGTGTCCCGGGGTATCCCGATCGCGCAAAAGCG 122959

QY	23641	TCCTGCTGGCAGCTCAGATGCTGCCACCTCTAACCGCAACGTTCTATCGAGCCGCT	23700
Db	122960	TCCTGCTGGCAGCTCAGATGCTGCCACCTCTAACCGCAACGTTCTATCGAGCCGCT	123019
QY	23701	GTCCTTAAGGCACTCAGATTTCCGTAGATCTTGATGAGTGGCGATCAGGCTGG	23760
Db	123020	GTCCTTAAGGCACTCAGATTTCCGTAGATCTTGATGAGTGGCGATCAGGCTGG	123079
QY	23761	GCCATAGGCGAGGATATATATATGATGAGCCCTGAGAGTGGCGCAAGTTTCCAGAG	23820
Db	123080	GCCATAGGCGAGGATATATATATGATGAGCCCTGAGAGTGGCGCAAGTTTCCAGAG	123139
QY	23821	TGCATATTTAACCAAGGCGCAGAGATGCGAGATTAACGCCACGCTGGCTCTCATC	23880
Db	123140	TGCATATTTAACCAAGGCGCAGAGATGCGAGATTAACGCCACGCTGGCTCTCATC	123199
QY	23881	GTCCTTGTCAAGTTATCAGAGGGGCGTGTTCAGAACCCAAAGTAAATAATCTCTAAGCA	23940
Db	123200	GTCCTTGTCAAGTTATCAGAGGGGCGTGTTCAGAACCCAAAGTAAATAATCTCTAAGCA	123259
QY	23941	CTGTTCTGGCAGACGCCCAAAACACTTCTGCGTCCGAAATGTCAATGATAAAGCCCTC	24000
Db	123260	CTGTTCTGGCAGACGCCCAAAACACTTCTGCGTCCGAAATGTCAATGATAAAGCCCTC	123319
QY	24001	CTCTTCTGGACTAAGGGGTGACAGGGGCCAGAGGGTTCGTTGGGCGCATTTTTC	24060
Db	123320	CTCTTCTGGACTAAGGGGTGACAGGGGCCAGAGGGTTCGTTGGGCGCATTTTTC	123379
QY	24061	TAACTCTAGCCGCGCAAAAGCAGCGGGTGGGACTTTAATAGGGCGTATAGGGTGT	24120
Db	123380	TAACTCTAGCCGCGCAAAAGCAGCGGGTGGGACTTTAATAGGGCGTATAGGGTGT	123439
QY	24121	AGGTAATGGGGTGGGAGCCGTCATGTTACATGCACTTCAATATTAATTTATGTTAGTTT	24180
Db	123440	AGGTAATGGGGTGGGAGCCGTCATGTTACATGCACTTCAATATTAATTTATGTTAGTTT	123499
QY	24181	TGGGCACTTGGGATGTTACACTTATTAATTTCCCAATGTCACAGTAATTCACCTTACAG	24240
Db	123500	TGGGCACTTGGGATGTTACACTTATTAATTTCCCAATGTCACAGTAATTCACCTTACAG	123559
QY	24241	TCGCCCTTCTAATCATAAACAAGTGGGGGTGTTGAGGTTACAGGTAAGGGTGGAGG	24300
Db	123560	TCGCCCTTCTAATCATAAACAAGTGGGGGTGTTGAGGTTACAGGTAAGGGTGGAGG	123619
QY	24301	GGAATGTAAGTGGGGAACCAAGCATAAAGTCGCGGGGGCGGAGTGGGAGCCCTTAAC	24360
Db	123620	GGAATGTAAGTGGGGAACCAAGCATAAAGTCGCGGGGGCGGAGTGGGAGCCCTTAAC	123679
QY	24361	CCAGAGATGTCACCTTACGCTTGTAGGCGATCGAACACTACCTCCGAAGAGTGTCTGT	24420
Db	123680	CCAGAGATGTCACCTTACGCTTGTAGGCGATCGAACACTACCTCCGAAGAGTGTCTGT	123739
QY	24421	TGGAATGTTTGTGATTAAGTAAGCAAGAAAGTGTGGAGAAAGTAACCTTAATAGATAC	24480
Db	123740	TGGAATGTTTGTGATTAAGTAAGCAAGAAAGTGTGGAGAAAGTAACCTTAATAGATAC	123799
QY	24481	CTTCTGCTGGCGGCGTGGGTGACAGCTGTTGTTATGATGAATGAACACTTCCCTGGGC	24540
Db	123800	CTTCTGCTGGCGGCGTGGGTGACAGCTGTTGTTATGATGAATGAACACTTCCCTGGGC	123859
QY	24541	GTTCTTGGGAGTGGGTGTGCTCACAATAAGAGCGCAACTCAACTAATCTCTCC	24600
Db	123860	GTTCTTGGGAGTGGGTGTGCTCACAATAAGAGCGCAACTCAACTAATCTCTCC	123919
QY	24601	CGTTTACAGCCGTGAGCGGTTTCTGTCTGAGCGCTTGTGAGGGGGTTCCTGAACCTT	24660
Db	123920	CGTTTACAGCCGTGAGCGGTTTCTGTCTGAGCGCTTGTGAGGGGGTTCCTGAACCTT	123979
QY	24661	GTTGCTGAACCAATCAAGTAACCGGTAATGACAGCGGTTCAGGGCGATTTGTAACAA	24720
Db	123980	GTTGCTGAACCAATCAAGTAACCGGTAATGACAGCGGTTCAGGGCGATTTGTAACAA	124039
QY	24721	CCTAAAAACGATATAAGTTTACAAACGATTTTGTGTAACAGTTTGTATATTTAGCC	24780

Db	124040	CCTAAAAACGATATAAGTTTACAAACGATTTTGTGTAACAGTTTGTATATTTAGCC	124099
QY	24781	CCAAAGTTTATCAAAAGCGAAACCTACTTACCGATTAGTAATATGCAAAACCGCAAGAGA	24840
Db	124100	CCAAAGTTTATCAAAAGCGAAACCTACTTACCGATTAGTAATATGCAAAACCGCAAGAGA	124159
QY	24841	TAAACATCAGATTTCTGTTCCAAATGTTGTTGGAATTAAGAAATGAGAGTAATTTGCC	24900
Db	124160	TAAACATCAGATTTCTGTTCCAAATGTTGTTGGAATTAAGAAATGAGAGTAATTTGCC	124219
QY	24901	CGCTGAGATGCTGGGAAATTAAGAGCGGCTTTTATCATGAGTACAGGGAGAGAAACC	24960
Db	124220	CGCTGAGATGCTGGGAAATTAAGAGCGGCTTTTATCATGAGTACAGGGAGAGAAACC	124279
QY	24961	TTGATGTTTCAAGTTAGTACACCCGCGCAACGTAACCCGCTAGAGTCTGCACCGGTTG	25020
Db	124280	TTGATGTTTCAAGTTAGTACACCCGCGCAACGTAACCCGCTAGAGTCTGCACCGGTTG	124339
QY	25021	TTGATGAGAGATGATCCTTAATTTTACTCTAAAGGGGTCTCTGTAAATTAATTT	25080
Db	124340	TTGATGAGAGATGATCCTTAATTTTACTCTAAAGGGGTCTCTGTAAATTAATTT	124399
QY	25081	AAGTATGAGTACTTACATATATCAATGATGATGATGATGATGATGATGATGATGAT	25140
Db	124400	AAGTATGAGTACTTACATATATCAATGATGATGATGATGATGATGATGATGATGAT	124459
QY	25141	AAAATGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	25200
Db	124460	AAAATGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	124519
QY	25201	TAAACCTATATGAGAAATTTTATTAAGTGTGTTGTTACTGTAACGTAATTAATTTTAA	25260
Db	124520	TAAACCTATATGAGAAATTTTATTAAGTGTGTTGTTACTGTAACGTAATTAATTTTAA	124579
QY	25261	ATAAATCTTATATATCAATGATGATGATGATGATGATGATGATGATGATGATGAT	25320
Db	124580	ATAAATCTTATATATCAATGATGATGATGATGATGATGATGATGATGATGATGAT	124639
QY	25321	GTAATCTAGTGTGAGGCAACTGATGATGATGATGATGATGATGATGATGATGATGAT	25380
Db	124640	GTAATCTAGTGTGAGGCAACTGATGATGATGATGATGATGATGATGATGATGATGAT	124699
QY	25381	ATAGGCAATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	25440
Db	124700	ATAGGCAATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	124759
QY	25441	CAATAGCTATAAAAAACAAGATGATGATGATGATGATGATGATGATGATGATGATGAT	25500
Db	124760	CAATAGCTATAAAAAACAAGATGATGATGATGATGATGATGATGATGATGATGATGAT	124819
QY	25501	AAATTAATAAATTAATATCCTGATTTTCCGTAATGATGATGATGATGATGATGATGAT	25560
Db	124820	AAATTAATAAATTAATATCCTGATTTTCCGTAATGATGATGATGATGATGATGATGAT	124879
QY	25561	TAAAGCTGTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	25620
Db	124880	TAAAGCTGTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	124939
QY	25621	AAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	25680
Db	124940	AAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	124999
QY	25681	GTCATACCTGCGTAATTTGCAACCAAGATCAATTAATCTTAAGTATGTTGTTTCCA	25740
Db	125000	GTCATACCTGCGTAATTTGCAACCAAGATCAATTAATCTTAAGTATGTTGTTTCCA	125059
QY	25741	CATAGCCACATATACATTAACACAAATGGCGTTAAATTAATCTGCAAGAGCGAGAT	25800
Db	125060	CATAGCCACATATACATTAACACAAATGGCGTTAAATTAATCTGCAAGAGCGAGAT	125119
QY	25801	ACTTGTAGTTTGAAGTCCACATTAAGAAATCCCTTAAGAAATTAAGTGTCTCATGTT	25860

Db	125120	ACCTTTGTAGTTTGGAGTCCACATTAAGAAATGCCGTAGACATTAACAGTGCCTATCCATGTT	125179
Qy	25861	GGTCCACAGAAAGACATGATGTGTTGTTTACTAGAAACAATTTTCGGTGGTTTATPACA	25920
Db	125180	GGTCCACAGAAAGACATGATGTGTTTACTAGAAACAATTTTCGGTGGTTTATPACA	125239
Qy	25921	AATATTAAATATGCTCGAAAAATATPAAACAAGATTAATTTAAGCCCAATPCTATGTAA	25980
Db	125240	AATATTAAATATGCTCGAAAAATATPAAACAAGATTAATTTAAGCCCAATPCTATGTAA	125299
Qy	25981	AACAAACGTTTAAACGGTAAAAAGTTACGTCCTTACTATGTAAAAATTTGGATPAGCATGC	26040
Db	125300	AACAAACGTTTAAACGGTAAAAAGTTACGTCCTTACTATGTAAAAATTTGGATPAGCATGC	125359
Qy	26041	AATAGCACTACACGTCGTGTACCAAAATACCTTCGTTGTCCAAAGGCCAATGCGATGTAA	26100
Db	125360	AATAGCACTACACGTCGTGTACCAAAATACCTTCGTTGTCCAAAGGCCAATGCGATGTAA	125419
Qy	26101	AACACACATGCTGCAAAACAGTACACAAAATATAATTAAATTTGCTAATTAAAAATTAA	26160
Db	125420	AACACACATGCTGCAAAACAGTACACAAAATATAATTAAATTTGCTAATTAAAAATTAA	125479
Qy	26161	TATTTCCAATGTATATATAAAATCAATACCTGTATCCATGCGAAAAAAATTTGAAGCAACG	26220
Db	125480	TATTTCCAATGTATATATAAAATCAATACCTGTATCCATGCGAAAAAAATTTGAAGCAACG	125539
Qy	26221	GAGTTAAATTTGACCTGCTGCTGCTGATTTCAATTAACAATTAATAGTTTCCATPAAAGAG	26280
Db	125540	GAGTTAAATTTGACCTGCTGCTGCTGATTTCAATTAACAATTAATAGTTTCCATPAAAGAG	125599
Qy	26281	AACACACGTAACAATGAACAATAATTTGTACGCTTGATTTAGAAGTCCCTGGCAT	26340
Db	125600	AACACACGTAACAATGAACAATAATTTGTACGCTTGATTTAGAAGTCCCTGGCAT	125659
Qy	26341	GTTGTACCAAGGCTATTATCCAAAACGTTAATGTAGAAGGTTTGTAACTAACCACTAC	26400
Db	125660	GTTGTACCAAGGCTATTATCCAAAACGTTAATGTAGAAGGTTTGTAACTAACCACTAC	125719
Qy	26401	TCCAATATAAAAAGGTATAGCTACACGCGCATTTTAAAAATPACAAAACGTAATPACAG	26460
Db	125720	TCCAATATAAAAAGGTATAGCTACACGCGCATTTTAAAAATPACAAAACGTAATPACAG	125779
Qy	26461	TTAAGGGGAGTTTGAGCTTTAAAAAGTTGTTTACATCGTTTCCAGGCAACCTCACACT	26520
Db	125780	TTAAGGGGAGTTTGAGCTTTAAAAAGTTGTTTACATCGTTTCCAGGCAACCTCACACT	125839
Qy	26521	GAGTACACAAAAGTTTCTGTGTGCCCCCTGTACGGSAAATCTGCTTATTTGCTATTTTGT	26580
Db	125840	GAGTACACAAAAGTTTCTGTGTGCCCCCTGTACGGSAAATCTGCTTATTTGCTATTTTGT	125899
Qy	26581	TGGCAACCAACCAAAAGAAATCATGTGAAAAGCAGAGTGGGAATATTGTTTGTTCGTTG	26640
Db	125900	TGGCAACCAACCAAAAGAAATCATGTGAAAAGCAGAGTGGGAATATTGTTTGTTCGTTG	125959
Qy	26641	GCGTGGATGCTTGGAACAATTCCTGTATTTTTGATGTTTAGGCCAAAACCTGTGAAAACATT	26700
Db	125960	GCGTGGATGCTTGGAACAATTCCTGTATTTTTGATGTTTAGGCCAAAACCTGTGAAAACATT	126019
Qy	26701	AAGAGTGTATTGAATAATATTTTGGTACAAAACCATGTTTATAGTCCAAAAGGAA	26760
Db	126020	AAGAGTGTATTGAATAATATTTTGGTACAAAACCATGTTTATAGTCCAAAAGGAA	126079
Qy	26761	CATATAAATGTTTATPAGAACATCGCTATGTACAGAACATTTTGTGTTAGCTAAACATA	26820
Db	126080	CATATAAATGTTTATPAGAACATCGCTATGTACAGAACATTTTGTGTTAGCTAAACATA	126139
Qy	26821	AAAAATATGTATGTTAAGGCTTAAGGGTTAAGGCAAGGGCTTAAGGCTTAAGGGTTAAGGCA	26880
Db	126140	AAAAATATGTATGTTAAGGCTTAAGGGTTAAGGCAAGGGCTTAAGGCTTAAGGGTTAAGGCA	126199
Qy	26881	AGGGTTAAGGGCAAGGGGTTAAGGGCAAGGGGTTAAGGGCAAGGGGTTAAGGGCAAGGGGTTA	26940
Db	126200	AGGGTTAAGGGCAAGGGGTTAAGGGCAAGGGGTTAAGGGCAAGGGGTTAAGGGCAAGGGGTTA	126259

QY	26941	GGGCAAGGGGTAAAGGGCAAGGGGGTAAGGGCAAGGGGTAAAGGGCTAAGGGGTAAAGGGCTAAGG	27000
Db	126260	GGGCAAGGGGTAAAGGGCAAGGGGGTAAGGGCAAGGGGGTAAGGGGTAAAGGGGTAAAGGGCTAAGG	126319
QY	27001	GGTAAAGGGCTAAGGGGTAAAGGGCTAAGGGTAAAGGTAAAGGTAAAGGTAAAGGTAAAGGTAAAG	27060
Db	126320	GGTAAAGGGCTAAGGGGTAAAGGGGTAAAGGGTAAAGGTAAAGGTAAAGGTAAAGGTAAAGGTAAAG	126379
QY	27061	GTAAATATATAGCCCTACGATTAATATGTCACATATATTTTAAATTTGGTTCAATTAA	27120
Db	126380	GTAAATATATAGCCCTACGATTAATATGTCACATATATTTTAAATTTGGTTCAATTAA	126439
QY	27121	CAGCCATGGTGTATTAGATTAAGGTAAAGGTTAAAGCTTCAATCAATATATCAAGTAATAAGTAA	27180
Db	126440	CAGCCATGGTGTATTAGATTAAGGTAAAGGTTAAAGCTTCAATCAATATATCAAGTAATAAGTAA	126499
QY	27181	CCACACGAATTTATATACATATTTTACAAAAGCGAACACAGCTGGACATGTAACTTACGC	27240
Db	126500	CCACACGAATTTATATACATATTTTACAAAAGCGAACACACAGCTGGACATGTAACTTACGC	126559
QY	27241	TACCCCTAAACGACATACCTGGGACGTAGAACCCAGAGGTAGTTAGAAATPATAGCGTATGTTA	27300
Db	126560	TACCCCTAAACGACATACCTGGGACGTAGAACCCAGAGGTAGTTAGAAATPATAGCGTATGTTA	126619
QY	27301	CAGAACTTTCAGATTCCCTTAGCGCAGCAGAGGGCTCTGCGGTTCAATTAATTAACAAAGTTTAA	27360
Db	126620	CAGAACTTTCAGATTCCCTTAGCGCAGCAGAGGGCTCTGCGGTTCAATTAATTAACAAAGTTTAA	126679
QY	27361	GATTAACGTAAACTTTAGGAAGTGCCTATGAGTGCATATGTTTCCAAATATAGGCGAAGGTT	27420
Db	126680	GATTAACGTAAACTTTAGGAAGTGCCTATGAGTGCATATGTTTCCAAATATAGGCGAAGGTT	126739
QY	27421	ACATAAAGCTGTTGCCCTAGAGGGCCGGGGCCCGGAGAGGGCCCGCGCGCGCGCGCGCGCGCC	27480
Db	126740	ACATAAAGCTGTTGCCCTAGAGGGCCGGGGCCCGGAGAGGGCCCGCGCGCGCGCGCGCGCGCC	126799
QY	27481	GCGGCGCGCATTTTCGCGCCGCGGGGCGAGAGGTCCCGCGCGCGCGCCCGCGGGCCCGCGCGCC	27540
Db	126800	GCGGCGCGCATTTTCGCGCCGCGGGGCGAGAGGTCCCGCGCGCGCGCCCGCGGGCCCGCGCGCC	126859
QY	27541	GGGGCGCGCGGCTTCCCGCGGCTTCCCGGCTTCGCGCCCGCGCGCGCGCGCGCGCGCGCGCC	27600
Db	126860	GGGGCGCGCGGCTTCCCGCGGCTTCCCGGCTTCGCGCCCGCGCGCGCGCGCGCGCGCGCGCC	126919
QY	27601	GCGCGCCCG	27660
Db	126920	GCGCGCCCG	126979
QY	27661	CCCGCGGGGGGCGCGGGGCG	27720
Db	126980	CCCGCGGGGGGCGCGGGGCG	127039
QY	27721	AGCGCCCGGTTCCGGCCGAGCCCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	27780
Db	127040	AGCGCCCGGTTCCGGCCGAGCCCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	127099
QY	27781	CCCAACAAGCCGCGGCGCGCGCGCGCTCCGATGCGCGGCGCGCGCGCGCGCGCGCGCGCGCTC	27840
Db	127100	CCCAACAAGCCGCGGCGCGCGCGCGCTCCGATGCGCGGCGCGCGCGCGCGCGCGCGCGCGCTC	127159
QY	27841	TCCGCGGGGCTTCCCTCCCGCCCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	27900
Db	127160	TCCGCGGGGCTTCCCTCCCGCCCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	127219
QY	27901	GGGGCGGGGCGCGGGGCGCTTGCAGGGGCGCGCGCGCGGGGCGCGAGCCGAGGGCCCGGGG	27960
Db	127220	GGGGCGGGGCGCGGGGCGCTTGCAGGGGCGCGCGCGGGGCGCGAGCCGAGGGCCCGGGG	127279
QY	27961	AGAACGGGGGATCGGGAAAAAGCGAGGGGAGCGGGGGACAGGGGAGCGCGTGTGCGTGCT	28020
Db	127280	AGAACGGGGGATCGGGAAAAAGCGAGGGGAGCGGGGGACAGGGGAGCGCGTGTGCGTGCT	127339

[illegible]

KM	ds.
OS	Macaqa mulatta rhadinovirus 17577.
XX	
PN	WO200028040-A2.
XX	
PD	18-MAY-2000.
XX	
PF	05-NOV-1999; 99WO-US26260.
XX	
PR	06-NOV-1998; 98US-0107507.
XX	
PA	20-NOV-1998; 98US-0109409.
XX	
PB	(UYOR-) UNIV OREGON HEALTH SCI.
PI	
DR	Wong SW, Axtheim MK, Searles RP;
XX	
XX	WPJ: 2000-376552/32.
PT	New rhesus rhadino virus for producing non-human primate model useful
PR	for testing potential treatments and efficacy of the candidate vaccine
PS	for conditions associated with RRV infection
XX	
XX	Claim 2; Page. 83-122; 141pp; English.
CC	The present invention describes a novel rhesus macaque rhadinovirus
CC	called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
CC	RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
CC	encoded by the genome sequence. The present invention also specifically
CC	claims the individual open reading frame (ORF) nucleotide sequences from
CC	the genome which encode the individual proteins, but these sequences are
CC	not given. A non-human animal infected with RRV can be used for testing
CC	the efficacy of drug in the treatment of condition associated with
CC	infection with RRV such as Kaposi's sarcoma, lymphoproliferative
CC	disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
CC	hyperimmunoglobulinemia or autoimmune haemolytic anaemia, by
CC	administering the drug to a immuno-compromised non-human primate
CC	preferably Rhesus macaque monkey obtained by as a result of infection
CC	by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
CC	non-human primate model for testing potential treatments for conditions
CC	associated with RRV infection. It is also useful for testing the
CC	efficacy of the candidate vaccine against RRV infection or conditions
CC	associated with its infection by administering the vaccine to the
CC	subject capable of infection with RRV, inoculating the subject with RRV
CC	and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
CC	to AAB53213 represent sequence used in the exemplification of the
CC	present invention.
XX	
SQ	Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;
	Query Match 100.0%; Score 28820; DB 21; Length 133719;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 28820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CCAACTACGTCCTCGGGGCACGAGAGAGGCCCTTGACCGCCAGATCAGTACTCAAC 60
DB	104900 CCAACTACGTCCTCGGGGCACGAGAGAGGCCCTTGACCGCCAGATCAGTACTCAAC 104959
OY	61 GTCTTAGAGGGGTGTTTATTATTAATGATTCACACAGCTAACCCCGGTTCCGAGGGCCCC 120
DB	104960 GTCTTAGAGGGGTGTTTATTATTAATGATTCACACAGCTAACCCCGGTTCCGAGGGCCCC 105019
OY	121 GGTTGGAATAATCCGACACAGGCGACGGCGGGGGACAAGGCCGCAAGCTGGATGAGAGA 180
DB	105020 GGTTGGAATAATCCGACACAGGCGACGGCGGGGGACAAGGCCGCAAGCTGGATGAGAGA 105079
OY	181 CAGTGGCCCGCATGCTCAGAGCGCTCCAAGAGCTTCTGACACGTACGAACACACCACC 240
DB	105080 CAGTGGCCCGCATGCTCAGAGCGCTCCAAGAGCTTCTGACACGTACGAACACACCACC 105139
OY	241 GCCACGCAAAACCGGGACGGGGCATTTAACAACATCTTTGGCGATGTCGGTTTTAGCAA 300
DB	105140 GCCACGCAAAACCGGGACGGGGCATTTAACAACATCTTTGGCGATGTCGGTTTTAGCAA 105199

QY	1381	CCCCCAGACTGGCCAAAAACGGTGTGCGTAATCATCAACAGCTCCGTGACGACACCTGCAC	1440
Db	106280	CCCCCAGACTGGCCAAAAACGGTGTGCGTAATCATCAACAGCTCCGTGACGACCTGCAC	106339
QY	1441	CACGACGAGATATGTAAACCTCTTTACTACGCTATCCCGAGAACACGGACCTGCNAAGC	1500
Db	106340	CACGACGAGATATGTAAACCTCTTTACTACGCTATCCCGAGAACACGGACCTGCNAAGC	106339
QY	1501	AGGATATCTTCGACGAGCGCTCCGCAAAACGTCACACCGGAAACAAACCGCAATCTCCG	1560
Db	106400	AGGATATCTTCGACGAGCGCTCCGCAAAACGTCACACCGGAAACAAACCGCAATCTCCG	106459
QY	1551	GCATGGGAAACGGATTAACCGATTAAATTAACGCAACGAACCCGCAAAAAACCTCTATTA	1620
Db	106460	GCATGGGAAACGGATTAACCGATTAAATTAACGCAACGAACCCGCAAAAAACCTCTATTA	106519
QY	1621	ATTCTGGGTCTCCCTAAAGCGGGACAGTATCCACGGGTGAAACCGACCCGCAATTTCA	1680
Db	106520	ATTCTGGGTCTCCCTAAAGCGGGACAGTATCCACGGGTGAAACCGACCCGCAATTTCA	106579
QY	1681	CAAGGGCAAGCGTCCCAACACGCAAAACGTAACACAGCCCGGTCAAAATTACTTGA	1740
Db	106580	CAAGGGCAAGCGTCCCAACACGCAAAACGTAACACAGCCCGGTCAAAATTACTTGA	106639
QY	1741	CACGCGTCACTGTAACACACCGTCAACACCGACTCAAGCCTCATCTTCACCGCAAAATTC	1800
Db	106640	CACGCGTCACTGTAACACACCGTCAACACCGACTCAAGCCTCATCTTCACCGCAAAATTC	106699
QY	1801	AACACGCAAAAGGTGCGCTGCACTAATATCTCAAAAGTGGGAAAGGGCCCATTAATTAACGAG	1860
Db	106700	AACACGCAAAAGGTGCGCTGCACTAATATCTCAAAAGTGGGAAAGGGCCCATTAATTAACGAG	106759
QY	1861	CCAGCGTCCGGCCAGGTCAACGCAACCAAGGGAATCTTTGGACGTATAAACCCGCAAGTG	1920
Db	106760	CCAGCGTCCGGCCAGGTCAACGCAACCAAGGGAATCTTTGGACGTATAAACCCGCAAGTG	106819
QY	1921	CTCACCGAACCCTGCCAACCAGCGCAAAACGCGCGGTAGCTCTTCGCAACAGAGCAACC	1980
Db	106820	CTCACCGAACCCTGCCAACCAGCGCAAAACGCGCGGTAGCTCTTCGCAACAGAGCAACC	106879
QY	1981	ACCACGGTCCCAAGTTCACGATTAATCCACACCGGTAAGGCTTTATAGGACCGCG	2040
Db	106880	ACCACGGTCCCAAGTTCACGATTAATCCACACCGGTAAGGCTTTATAGGACCGCG	106939
QY	2041	TCCAAACTCTCCGACGCGCTCGAAGAGACCAACGCGGCCACACCCGACGACATCTCAGTCG	2100
Db	106940	TCCAAACTCTCCGACGCGCTCGAAGAGACCAACGCGGCCACACCCGACGACATCTCAGTCG	106999
QY	2101	AAGATAGATCGGGAAAAATATAGCGCCGAGAGTCCGCGCTCCGCGACCCACACTCGAAGAG	2160
Db	107000	AAGATAGATCGGGAAAAATATAGCGCCGAGAGTCCGCGCTCCGCGACCCACACTCGAAGAG	107059
QY	2161	GGGCGCACGGGACCTCAGCTCAAACTCCAACACGAGGCACACATTAACGTCCTCTTAGC	2220
Db	107060	GGGCGCACGGGACCTCAGCTCAAACTCCAACACGAGGCACACATTAACGTCCTCTTAGC	107119
QY	2221	CAGGTCAAAAAAAGTACACAGCGGCGCGAAAAATCCCGGCTTCAAAACAGCAATCTCCAGC	2280
Db	107120	CAGGTCAAAAAAAGTACACAGCGGCGCGAAAAATCCCGGCTTCAAAACAGCAATCTCCAGC	107179
QY	2281	GCCGCCCAACCAACGCGCATCAAAACCCGCGATTCAATACAGCGTCCCGACGAACGAGCGC	2340
Db	107180	GCCGCCCAACCAACGCGCATCAAAACCCGCGATTCAATACAGCGTCCCGACGAACGAGCGC	107239
QY	2341	CGGTTGCTTCACGACGAATTCGAGGTGGAAATGACCCCAACGAGAGGTAAACGATCG	2400
Db	107240	CGGTTGCTTCACGAGAAATCGAGGTGGAAATGACCCCAACGAGAGGTAAACGATCG	107299
QY	2401	CCAAAAACAAGATGTGTCTACAGGGGCCGGAACCGGACGACTCCAGGTGGACCGGCCG	2460
Db	107300	CCAAAAACAAGATGTGTCTACAGGGGCCGGAACCGGACGACTCCAGGTGGACCGGCCG	107359
QY	2461	CTCGGCTCCAAACCATAGATTCGACTGACACTGGAACACCCCAAAATTCCTCAAAAAATATACA	2520

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Db 107360 CTGGTCACACCATAGATATCATGACGTGGAACACCCCAATTTCTCAAAATATTAACA 107419
QY 2521 TCACTCACCGTCCCACTCCAGAGTCAACCCCAATCCCTCCCACTAATCTGATATACC 2580
Db 107420 TCACTCACCGTCCCACTCCAGAGTCAACCCCAATCCCTCCCACTAATCTGATATACC 107479
QY 2581 CATCCACGTCAACATCCACACGAGAAATACACGAGCCCAAGATGTTATGCA 2640
Db 107480 CATCCACGTCAACATCCACACGAGAAATACACGAGCCCAAGATGTTATGCA 107539
QY 2641 TTTATCAAAAGCTACGAGAAACTTCAAGGTGCTGAGCGCTATCCGAGCTATT 2700
Db 107540 TTTATCAAAAGCTACGAGAAACTTCAAGGTGCTGAGCGCTATCCGAGCTATT 107599
QY 2701 GCGAGATAAAGTTTTTATATCTGTAAACGCGCCATCTCACTGCTTTTATTTATTTAG 2760
Db 107600 GCGAGATAAAGTTTTTATATCTGTAAACGCGCCATCTCACTGCTTTTATTTATTTAG 107659
QY 2761 ACAGCGCTTGTGTCTCAAGATAGTTGCGTCCGTAGGTATAACAGATGACCTATGC 2820
Db 107660 ACAGCGCTTGTGTCTCAAGATAGTTGCGTCCGTAGGTATAACAGATGACCTATGC 107719
QY 2821 CAGAAGACGCCAGCTCCCGGGTCCGCGCAACCGGGGCGGGGCCCATCGAGCTATCA 2880
Db 107720 CAGAAGACGCCAGCTCCCGGGTCCGCGCAACCGGGGCGGGGCCCATCGAGCTATCA 107779
QY 2881 ATGAATGGGGCCCGCTGAGATCTGTAAAGCTATTTGACCCGAGGTGAGAGCCACCG 2940
Db 107780 ATGAATGGGGCCCGCTGAGATCTGTAAAGCTATTTGACCCGAGGTGAGAGCCACCG 107839
QY 2941 GGGCAACGCTCGGGGGGGGGGGCGGAGCCGAGCCGAGCAAAACGCCGAGATCTAGAACTAG 3000
Db 107840 GGGCAACGCTCGGGGGGGGGGGCGGAGCCGAGCCGAGCAAAACGCCGAGATCTAGAACTAG 107899
QY 3001 CGTCTTTTGGCGCAAGGCCCGGAGAGTGTCTTTCGCGAGAAATTCATCTCTTTT 3060
Db 107900 CGTCTTTTGGCGCAAGGCCCGGAGAGTGTCTTTCGCGAGAAATTCATCTCTTTT 107959
QY 3061 GCATATACATGTCTGATATGATGTTGGCCGTTAAAAACACAGATATTTACGTTTCGCA 3120
Db 107960 GCATATACATGTCTGATATGATGTTGGCCGTTAAAAACACAGATATTTACGTTTCGCA 108019
QY 3121 TGGCAATACGTGGGGGGGAGACATGTCAACCTGGGGGAAGTGTTCATCTCGGCAACGACG 3180
Db 108020 TGGCAATACGTGGGGGGGAGACATGTCAACCTGGGGGAAGTGTTCATCTCGGCAACGACG 108079
QY 3181 GGTGATTTGGTAAATCGTCTCAAGCGCTCCCTGAAGCATGTGGCTCTTAACCCGCAAG 3240
Db 108080 GGTGATTTGGTAAATCGTCTCAAGCGCTCCCTGAAGCATGTGGCTCTTAACCCGCAAG 108139
QY 3241 ACGACATCTCTTTTAACTTCTATTAACACTTTCACAGACAGGAGCATATAGACAGGT 3300
Db 108140 ACGACATCTCTTTTAACTTCTATTAACACTTTCACAGACAGGAGCATATAGACAGGT 108199
QY 3301 CAATAATAAACACACTGGGCGCACACGCAATGCTTTAATAGCGGCTCGGCACTCGGCA 3360
Db 108200 CAATAATAAACACACTGGGCGCACACGCAATGCTTTAATAGCGGCTCGGCACTCGGCA 108259
QY 3361 CGCCAAACAGGGCAGACGAGCTAAACAGGAGTTCGGCTCGATGAGCATGTGCCG 3420
Db 108260 CGCCAAACAGGGCAGACGAGCTAAACAGGAGTTCGGCTCGATGAGCATGTGCCG 108319
QY 3421 GTTGTGGGAGACAGCAACCTAATAGGATCTCCACACACGATGATCCGAATAGAGA 3480
Db 108320 GTTGTGGGAGACAGCAACCTAATAGGATCTCCACACACGATGATCCGAATAGAGA 108379
QY 3481 TATTAACCGCATGTGCGATCGCCACAAATAGAGCAATATACGGCCGCGGTGTAGCACA 3540
Db 108380 TATTAACCGCATGTGCGATCGCCACAAATAGAGCAATATACGGCCGCGGTGTAGCACA 108439
QY 3541 GATGCAAAAGCTGCTCTTTTGGTCCGAGTGAAGAAACAGTGTGGGTGGCAATT 3600
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Db 108440 GATGCAAAAGCTGCTCTTTTGGTCCGAGTGAAGAAACAGCTTGGTGGGCAATT 108499
QY 3601 TAGGTTTCAAAATTTACCCCGTCCGAATTTCAAAACAGTAACCGCACTCGAGGACACAC 3660
Db 108500 TAGGTTTCAAAATTTACCCCGTCCGAATTTCAAAACAGTAACCGCACTCGAGGACACAC 108559
QY 3661 CACCTTGGAGCTGGGACAGGTCTTCTCCAGTACGCTCTCTGGCCACCACTGGGACCAAC 3720
Db 108560 CACCTTGGAGCTGGGACAGGTCTTCTCCAGTACGCTCTCTGGCCACCACTGGGACCAAC 108619
QY 3721 AGGTAGAGATTTACAGGAAACAGTACGTTATACGCCAATACTTTTGAACCAAGGTCCG 3780
Db 108620 AGGTAGAGATTTACAGGAAACAGTACGTTATACGCCAATACTTTTGAACCAAGGTCCG 108679
QY 3781 GGATATCTCGTCTCGGTGAGTCCCTTATGGGCAACACAGACGGGACATGTCACAG 3840
Db 108680 GGATATCTCGTCTCGGTGAGTCCCTTATGGGCAACACAGGACATGTCACAG 108739
QY 3841 GGGCCTTAAACGTACAGCTCTCTCAGAAAGGCGTTAAACGGGTTGCCACGGGACGTCG 3900
Db 108740 GGGCCTTAAACGTACAGCTCTCTCAGAAAGGCGTTAAACGGGTTGCCACGGGACGTCG 108799
QY 3901 CGCAGTTCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3960
Db 108800 CGCAGTTCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 108859
QY 3961 CAGGTTAGCTCCAGAGCTGTGGAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4020
Db 108860 CAGGTTAGCTCCAGAGCTGTGGAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 108919
QY 4021 GGGCCGCTTCATTTCTTCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4080
Db 108920 GGGCCGCTTCATTTCTTCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 108979
QY 4081 AACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4140
Db 108980 AACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 109039
QY 4141 AAACGACACACAGATACCTGTGACACGCGCTCTGTGGAGACGGCGTTAACTTAAC 4200
Db 109040 AAACGACACACAGATACCTGTGACACGCGCTCTGTGGAGAACGCGTTAACTTAAC 109099
QY 4201 TTGCTGCTGGGAGACGCCCGGCTGAGATATACACCTGACACCCAGCGTACGCCGC 4260
Db 109100 TTGCTGCTGGGAGACGCCCGGCTGAGATATACACCTGACACCCAGCGTACGCCGC 109159
QY 4261 TAAACAAGACCGGCGCATATCTGACAGCGCATCTCAGCTGGCGCTTTTATAGTGGT 4320
Db 109160 TAAACAAGACCGGCGCATATCTGACAGCGCATCTCAGCTGGCGCTTTTATAGTGGT 109219
QY 4321 ATCCGGCTTCAGCGCGGTAGCAATCTGTTCAAGGCGGTCTGAAGAGATGGGCGAGAAAT 4380
Db 109220 ATCCGGCTTCAGCGCGGTAGCAATCTGTTCAAGGCGGTCTGAAGAGATGGGCGAGAAAT 109279
QY 4381 TAAAGTGAAGGCCAATTTTGGGGGTGCTGCTCCAGGACCGGACCGCTTACTGACAAA 4440
Db 109280 TAAAGTGAAGGCCAATTTTGGGGGTGCTGCTCCAGGACCGGACCGCTTACTGACAAA 109339
QY 4441 ACACAGCTGATTCGGGCGATAGTCCGATTAAGCTATAGAGCGCGCAGATCTTAAGC 4500
Db 109340 ACACAGCTGATTCGGGCGATAGTCCGATTAAGCTATAGAGCGCGCAGATCTTAAGC 109399
QY 4501 CAGCGAGAACCATCCAGCCCAACGATGGGACAGATTAAGAACCGCGCCATGAACGACAC 4560
Db 109400 CAGCGAGAACCATCCAGCCCAACGATGGGACAGATTAAGAACCGCGCCATGAACGACAC 109459
QY 4561 TTGCTTTCAGCCAGGTTAGGCAAGGCGCCAGGCGATCCCAATTTTACCAGTTGAA 4620
Db 109460 TTGCTTTCAGCCAGGTTAGGCAAGGCGCCAGGCGATCCCAATTTTACCAGTTGAA 109519
QY 4621 TTGCTTAAATTTGATTCGCGGAGCGCTTCGCGGCGCAATATCTTCAACCTCGACCCG 4680
Db 109520 TTGCTTAAATTTGATTCGCGGAGCGCTTCGCGGCGCAATATCTTCAACCTCGACCCG 109579
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QY	4661	AAGGCGGGCCACGAGCCCGTTCCGCTC	AACGCACCGAGCCGCTCGAGTACCCCTCA	4740
Db	109580	AAGGGCGGGCCACGGAGCCCGCTTCGCTC	TAACGCACCGAGGCGCTCGGAGTACCCGCTCA	1096399
QY	4741	GGGCAAAAACCGTTCTAAGAAAGGGTTT	TAAACGTTTACGGCTTTTGAGTACGACCA	4800
Db	109640	GGGCAAAAACCGTTCTTAAGAAAGGGTTT	TAAACGTTTACGGCTTTTGAGTACGACCA	1096599
QY	4801	AAAACGTAAACCTGTGGTGCTCCGTAA	AGTGGGCGATATAGACATGAGACTGT	4860
Db	109700	AAAACGTAAAAACCTGTGGTGCTCCGTAA	AGTGGGCGATATAGACATGAGACTGT	109759
QY	4861	AAAGCTTAAAGCTCCGGGAAAAACCA	CGACGTCCTTAATTTTCATAAAATGCTCCTGGC	4920
Db	109760	AAAGCTTAAAGCTCCGGGAAAAACCA	CGACGTCCTTAATTTTCATAAAATGCTCCTGGC	109819
QY	4921	CCAGGACACGAGCAGTTCCCTCTCA	AGATATACAGCTCCGAATTTATAGCAGAGTTTTC	4980
Db	109820	CCAGGACACGAGCAGAGTTCCCTCTCA	AGATATACAGCTCCGAATTTATAGCAGAGTTTTC	109879
QY	4961	CAAACTGGGCATCGCGCTCAGCTGGCTT	ACAAAAACATTTCAACGTGTGGCCAAAC	5040
Db	109880	CAAACTGGGCATCGCGCTCAGCTGGCTT	ACAAAAACATTTCAACGTGTGGCCAAAC	1099399
QY	5041	CGTTTGTATATTTCAAAAACCGGGG	CAAAAGGGGACAGTCTCTAGTTTGTGA	5100
Db	109940	CGTTTGTATATTTCAAAAACCGGGG	CAAAAGGGGACAGTCTCTAGTTTGTGA	1099999
QY	5101	GCCAAAACCTTATACAAAACCTCGA	TGATGATAGACGAGCGCTGTGACAGCGCACGCTGC	5160
Db	110000	GCCAAAACCTTATACAAAACCTCGA	TGATGATAGACGAGCGCTGTGACAGCGCACGCTGC	110059
QY	5161	ACAGGGGACCGCCCCGCTTAAAGG	TATACGGGAGCCCGCTGTACACCTCTCCAACT	5220
Db	110060	ACAGGGGACCGCCCCGCTTAAAGG	TATACGGGAGCCCGCTGTACACCTCTCCAACT	110119
QY	5221	CCAGGAGATTCCAGAGGGTCCCA	GAGTAAAGAACAACTAAATCGCACACTGTCAACTA	5280
Db	110120	CCAGGAGATTCCAGAGGGTCCCA	GAGTAAAGAACAACTAAATCGCACACTGTCAACTA	110179
QY	5281	AACGTTTCCGGAACTCATCGTTAT	AAAGATCTCTTAAGTGTGTGCTGTGGCTCCCGCTAA	5340
Db	110180	AACGTTTCCGGAACTCATCGTTAT	AAAGATCTCTTAAGTGTGTGCTGTGGCTCCCGCTAA	110239
QY	5341	AAACGCGCTCGGTCTAAAGATTTT	TGTGATACCTGTTTACGGGCTTACCTTGGCGT	5400
Db	110240	AAACGCGCTCGGTCTAAAGATTTT	TGTGATACCTGTTTACGGGCTTACCTTGGCGT	110299
QY	5401	CCAGGACCATGCACTGTCTACAGT	AGCTGACCGGCTGTGAGACAGATGACAGAGAAAG	5460
Db	110300	CCAGGACCATGCACTGTCTACAGT	AGCTGACCGGCTGTGAGACAGATGACAGAGAAAG	110359
QY	5461	TTTTTAAATACGACAGTATGTTAA	TGAGGCTTGAAGCTGGAATATATGTTGGGAAACATTA	5520
Db	110360	TTTTTAAATACGACAGTATGTTAA	TGAGGCTTGAAGCTGGAATATATGTTGGGAAACATTA	110419
QY	5521	TTTTTCATGTCAATCGGGACAG	GAGACTCGAACGCCAATTAATGCTCACCGAATCATCACT	5580
Db	110420	TTTTTCATGTCAATCGGGACAG	GAGACTCGAACGCCAATTAATGCTCACCGAATCATCACT	110479
QY	5581	GAGACAGAGTAAAGATGCTTAC	CGCGGTACCGGCTTAACACGGACCAACGACACCCCTT	5640
Db	110480	GAGACAGAGTAAAGATGCTTAC	CGCGGTACCGGCTTAACACGGACCAACGACACCCCTT	110539
QY	5641	CAAAATTTTAAAGCCTTAAAAA	AGCGGGCCCTTAAAGTGTCTCAACACTCACCTTAAAAACATC	5700
Db	110540	CAAAATTTTAAAGCCTTAAAAA	AGCGGGCCCTTAAAGTGTCTCAACACTCACCTTAAAAACATC	110599
QY	5701	CTAACCATTTATGTTGCTCCG	TGCGCACTGAGACCCCTCATGAGACATGCGCCCTCTCTG	5760
Db	110600	CTAACCATTTATGTTGCTCCG	TGCGCACTGAGACCCCTCATGAGACATGCGCCCTCTCTG	110659

QY	5761	CGGGAGACTGTGAGAACATTCCTTCTCCCGGGTACCCCGGAGCGAGCTTTTAAACAGCCG	5820
Db	110660	CGGGAGACTGTGAGAACATTCCTTCTCCCGGGTACCCCGGAGCGAGCTTTTAAACAGCCG	110719
QY	5821	GTATTAAATCACAACACAGAGCTGTCTCAAAACCGGCTCAATCGGAGGGGGTGTATACCTC	5880
Db	110720	GTATTAAATCACAACACAGAGCTGTCTCAAAACCGGCTCAATCGGAGGGGGTGTATACCTC	110779
QY	5881	CTGTTCACCTGTGGTCCGGACATTTCCACCCCGCCGAGCTTTTCTTCCAGACATCGGGCTG	5940
Db	110780	CTGTTCACCTGTGGTCCGGACATTTCCACCCCGCGAGCTTTTCTTCCAGACATCGGGCTG	110839
QY	5941	TTGTGCTCTACCTGCTCTATACGCCCCCGCATCATGGAGCGGATACCTCATGTGTGCTGC	6000
Db	110840	TTGTGCTCTACCTGCTCTATACGCCCCCGCATCATGGAGCGGATACCTCATGTGTGCTGC	110899
QY	6001	GACCTTTTGGACCTAAGCAGCGTGTACTTCCGCGATGGGTGAAAGATGGGCGCAGTATAC	6060
Db	110900	GACCTTTTGGACCTAAGCAGCGTGTACTTCCGCGATGGGTGAAAGATGGGCGCAGTATAC	110959
QY	6061	ACCGGCCAAAGCATCTCGGAAATCGACGTCGACAGCTCAGCTTCTTCGCAACCCGCTGCTTC	6120
Db	110960	ACCGGCCAAAGCATCTCGGAAATCGACGTCGACAGCTCAGCTTCTTCGCAACCCGCTGCTTC	111019
QY	6121	CGACCCATCGACAGAGAACAAATCTCTCAACACATCTCATTTAAATTTTATACAAACGAG	6180
Db	111020	CGACCCATCGACAGAGAACAAATCTCTCAACACATCTCATTTAAATTTTATACAAACGAG	111079
QY	6181	TTTATTAGGGGCGATGTGTAGAAGGCACGATTCGGGGATCGTTCTGTTTTAAACGTCCTG	6240
Db	111080	TTTATTAGGGGCGATGTGTAGAAGGCACGATTCGGGGATCGTTCTGTTTTAAACGTCCTG	111139
QY	6241	CCGGCCACAGAAAGAGACACCAACAACCTACCGTGGCGTTCGCTCCGTTGGCCGCGGA	6300
Db	111140	CCGGCCACAGAAAGAGACACCAACAACCTACCGTGGCGTTCGCTCCGTTGGCCGCGGA	111199
QY	6301	AGTCACACCAACCGGGGATTAACCGCTTACCCGAGGACTGTGAAGAGGCGTTTCAACTCCAG	6360
Db	111200	AGTCACACCAACCGGGGATTAACCGCTTACCCGAGGACTGTGAAGAGGCGTTTCAACTCCAG	111259
QY	6361	AACGCGGAGAAAGCCCAAGCCTCTCGGGCGTCTTTTCGGCAACGTGGGCAAGATCCAG	6420
Db	111260	AACGCGGAGAAAGCCCAAGCCTCTCGGGCGTCTTTTCGGCAACGTGGGCAAGATCCAG	111319
QY	6421	CTTCTTGGCTCCGACACACAACAGGAGATTAACCATTTACAACCTCTCGGCTTCCCAAC	6480
Db	111320	CTTCTTGGCTCCGACACACAACAGGAGATTAACCATTTACAACCTCTCGGCTTCCCAAC	111379
QY	6481	CCAGAAGATGCTGACCAATCACAGGGGCCCTGCTGATGCACCCCAACGCTCAACCTPAAA	6540
Db	111380	CCAGAAGATGCTGACCAATCACAGGGGCCCTGCTGATGCACCCCAACGCTCAACCTPAAA	111439
QY	6541	ACAAAAAACACACCGCGATCCATATGCGCTTCTATGTGGAATGTCTGGCCGACACCCGGAC	6600
Db	111440	ACAAAAAACACACCGCGATCCATATGCGCTTCTATGTGGAATGTCTGGCCGACACCCGGAC	111499
QY	6601	GCGGCTCGGTTCTGAAAAGATCTGCGTCCGACATTTCTGAAAAACATGTGAAAAACAGTT	6660
Db	111500	GCGGCTCGGTTCTGAAAAGATCTGCGTCCGACATTTCTGAAAAACATGTGAAAAACAGTT	111559
QY	6661	AAGCTCGTCAATCGCATATCGTACATCTTAAACGATCCGGACTCACTGTTCACACGTGCGC	6720
Db	111560	AAGCTCGTCAATCGCATATCGTACATCTTAAACGATCCGGACTCACTGTTCACACGTGCGC	111619
QY	6721	GACGACATCTGCGCGGCTTAATTTAAACGGTGTCTGGCAACAAGAAATCCACAAGCATTTT	6780
Db	111620	GACGACATCTGCGCGGCTTAATTTAAACGGTGTCTGGCAACAAGAAATCCACAAGCATTTT	111679
QY	6781	TTTTCGAGCCGGTGGGTGCTCTGAAACAGTACTGCACTGTCCCGGGTTTATTATTA	6840
Db	111680	TTTTCGAGCCGGTGGGTGCTCTGAAACAGTACTGCACTGTCCCGGGTTTATTATTA	111739
QY	6841	TGCCACCTCCGAAAGATATTAAGAGCTCAAGAGCTGTCTGTGGCAACCGGAGAGTCTTA	6900

111740 TCCCAACCTCCGAAAAAGTATAGAGGCTCAAGGCTCGCTGCAACCGGAGAGTTCCTA 111799
QY GACTGCACAGAGATATTTGACTGCGAGACCTTACAGACCTGAGCCGTCTCTTTAAGGGG 6960
111800 GACTGCACAGAGATATTTGACTGCGAGACCTTACAGACCTGAGCCGTCTCTTTAAGGGG 111859
QY 6961 TCTCAACTGCGCAAAATCGGCAAAACCACTGCTCGAGATATTCGGTCACTCGGATTT 7020
Db 111860 TCTCAACTGCGCAAAATCGGCAAAACCACTGCTCGAGATATTCGGTCACTCGGATTT 111919
QY 7021 CAGCTGCGTGCAGACAACTTCAAAATCACCACCGCTTCAAACTCCCAACTATATCAT 7080
Db 111920 CAGCTGCGTGCAGACAACTTCAAAATCACCACCGCTTCAAACTCCCAACTATATCAT 111979
QY 7081 TATCTTTCAGAACGCGACAGACAAATGCCAAAACAGCCAGAGTCAATTTGGCGTCCGA 7140
Db 111980 TATCTTTCAGAACGCGACAGACAAATGCCAAAACAGCCAGAGTCAATTTGGCGTCCGA 112039
QY 7141 GCGCGGTACGACACTAGCGTCAAGCGACCGAGCGGCCCGCATCCAGCGGACCGGATCC 7200
Db 112040 GCGCGGTACGACACTAGCGTCAAGCGACCGAGCGGCCCGCATCCAGCGGACCGGATCC 112099
QY 7201 AGGACGCGGACGCTGCAAAAGCGAAATCATGCACTGGAAAAAGTTAGTTTACAGACAGCAG 7260
Db 112100 AGGACGCGGACGCTGCAAAAGCGAAATCATGCACTGGAAAAAGTTAGTTTACAGACAGCAG 112159
QY 7261 TTTTTCCTGCTTAAAGCGCGCCGCAAGAGTGGGGGTGAGCTTTTAAAGAAATGGGG 7320
Db 112160 TTTTTCCTGCTTAAAGCGCGCCGCAAGAGTGGGGGTGAGCTTTTAAAGAAATGGGG 112219
QY 7321 ACCCGATATGCACTCAAAAGTCCGTATGTTGCCGTTAAACCTTAAACCAATCGGCCG 7380
Db 112220 ACCCGATATGCACTCAAAAGTCCGTATGTTGCCGTTAAACCTTAAACCAATCGGCCG 112279
QY 7381 GGTGCGTGGCTCTCTCTCATCATATTCGAGACCTGCTCAACATGGGGTTTCAACTGTG 7440
Db 112280 GGTGCGTGGCTCTCTCTCATCATATTCGAGACCTGCTCAACATGGGGTTTCAACTGTG 112339
QY 7441 TCGTGACAGCCAACTGACAGGTGACGGGTGCTCTGAGAGCAAAAGCGCTGGCGAAGT 7500
Db 112340 TCGTGACAGCCAACTGACAGGTGACGGGTGCTCTGAGAGCAAAAGCGCTGGCGAAGT 112399
QY 7501 TCCGCCAGAAAAACAGGAGCTGTGTAGTGGGCTTAACCTTTACACCAACGCGGAA 7560
Db 112400 TCCGCCAGAAAAACAGGAGCTGTGTAGTGGGCTTAACCTTTACACCAACGCGGAA 112459
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Db	113960	CCATAGCTTCATGGAGAACCATCATCATCTCCGTCAACGGCGGTGGTTACCGTTGT	114019
QY	9121	TATTGCGGGGCAAAACAGGCTGGGGGGAAAAAGACCAATATTCGTACGTTTAAAAAAC	9180
Db	114020	TATTGCGGGGCAAAACAGGCTGGGGGGAAAAAGACCAATATTCGTACGTTTAAAAAAC	114079
QY	9181	TCAACTTCTAAAAATCTCAACCCCACTCGTAAACAAAAAACATCGACGTTAAGTGTATGTAC	9240
Db	114080	TCAACTTCTAAAAATCTCAACCCCACTCGTAAACAAAAAACATCGACGTTAAGTGTATGTAC	114139
QY	9241	CGAATATTAACACACAAAGTTTTTTAAAAACACAGCTGGGTAAGTAAACCCCATTTGGCACG	9300
Db	114140	CGAATATTAACACACAAAGTTTTTTAAAAACACAGCTGGGTAAGTAAACCCCATTTGGCACG	114199
QY	9301	CGTGTGCGGTGCTAAGTGTATTTAAAAATATCATTTGTGCTTTTACACACGACGACGTAT	9360
Db	114200	CGTGTGCGGTGCTAAGTGTATTTAAAAATATCATTTGTGCTTTTACACACGACGACGTAT	114259
QY	9361	CTCAGAGAGGCGGCTTAACGACGATATACATATTCCTTAACACGGGGAACGCGCTGAC	9420
Db	114260	CTCAGAGAGGCGGCTTAACGACGATATACATATTCCTTAACACGGGGAACGCGCTGAC	114319
QY	9421	CGCCCTCCCAATACAAACACAGGGGACTCAAAAGCCTAGTGTAAATATTAATCAAAATTA	9480
Db	114320	CGCCCTCCCAATACAAACACAGGGGACTCAAAAGCCTAGTGTAAATATTAATCAAAATTA	114379
QY	9481	AAACACAGAAACCTTTAGTGTGCGCAAAACACTAGCAAAAGTACCTAGAGCTTCCCT	9540
Db	114380	AAACACAGAAACCTTTAGTGTGCGCAAAACACTAGCAAAAGTACCTAGAGCTTCCCT	114439
QY	9541	ATACTTCAAAAAACAGCGGTGGGTATTGTGACACACAGTTAAGTAAACCCGTAAGAA	9600
Db	114440	ATACTTCAAAAAACAGCGGTGGGTATTGTGACACACAGTTAAGTAAACCCGTAAGAA	114499
QY	9601	TATTCCTCGTTTATCAAAATGAAAAATTAAGGCTTTGCTTAAATCTGCTAACGCAAG	9660
Db	114500	TATTCCTCGTTTATCAAAATGAAAAATTAAGGCTTTGCTTAAATCTGCTAACGCAAG	114559
QY	9661	GGCACTTAATTTTCCAGTTTGGACTCGGAACCTTAACGCTTAACGTTAAATTTAAT	9720
Db	114560	GGCACTTAATTTTCCAGTTTGGACTCGGAACCTTAACGCTTAACGTTAAATTTAAT	114619
QY	9721	GCAAAAGGACATATTTTTTTTTTGTGTAACTCTAAACCTCTACAGCTAAAGTTAATAAG	9780
Db	114620	GCAAAAGGACATATTTTTTTTTTGTGTAACTCTAAACCTCTACAGCTAAAGTTAATAAG	114679
QY	9781	GGCACTTTGGGACGGAATCAAGTGTCTGCGCAAAACCTGTTAAATTTAAACACACAG	9840
Db	114680	GGCACTTTGGGACGGAATCAAGTGTCTGCGCAAAACCTGTTAAATTTAAACACACAG	114739
QY	9841	GAGCGGACATTAACACGAGCTAAACGCTAATGCGGGCCGTGTGAACAACTGGTGTGCA	9900
Db	114740	GAGCGGACATTAACACGAGCTAAACGCTAATGCGGGCCGTGTGAACAACTGGTGTGCA	114799
QY	9901	ATGATTTAGGAATCTAAAAAACGAAATCTCGTGGTTAACACAGGAATTTCTTTAGTT	9960
Db	114800	ATGATTTAGGAATCTAAAAAACGAAATCTCGTGGTTAACACAGGAATTTCTTTAGTT	114859
QY	9961	CCTACAGCATCAACAAATTTGTAACCATTAACGTAACGGCGGTGGGGTTGGTGTG	10020
Db	114860	CCTACAGCATCAACAAATTTGTAACCATTAACGTAACGGCGGTGGGGTTGGTGTG	114919
QY	10021	AAATCGTTGGTCAACTGTTAATGCGGCGATTTGTAATGTGGTCTGTTGCAACAGGTG	10080
Db	114920	AAATCGTTGGTCAACTGTTAATGCGGCGATTTGTAATGTGGTCTGTTGCAACAGGTG	114979
QY	10081	GTGGGGTGCAGTCCCGCGGTGGGTGCAAGTCCCGGTGGGGTCCAGGTCCCGCGGTG	10140
Db	114980	GTGGGGTGCAGTCCCGCGGTGGGTGCAAGTCCCGGTGGGGTCCAGGTCCCGCGGTG	115039

QY	10141	GSGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGG	10200
Db	115040	GGGTCCAGAGTCCCGGTGGGTGCAGAGTCCCGGTGGGTGCAGAGTCCCCCGGTGGGG	115099
QY	10201	TGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGC	10260
Db	115100	TGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGC	115159
QY	10261	AAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAG	10320
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QY	10321	TCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCC	10380
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QY	10381	CCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCC	10440
Db	115280	CCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCC	115339
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QY	10861	CGGGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCC	10920
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QY	10981	GGTGGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCC	11040
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Db	116060	GCTCCGGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCC	116119
QY	11221	GCGGTGGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCCCCCGGTGGGTGCAGAGTCC	11280

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Db	118340	GGTGAATAGTTCTGATGACCGCGGCTTAAGTTTGCAGCGGTGTCAGCGGAACATAATTCT	118399
QY	13501	CCCCGGCTCCCAAGCCCGGGGGCCGGGGAGCCCGAGTGGGTTATTTAAAGTTTACGTAAAGG	13560
Db	118400	CCCCGGCTCCCAAGCCCGGGGGCCGGGGAGCCCGAGTGGGTTATTTAAAGTTTACGTAAAGG	118459
QY	13561	ATTAATTTTAAATCACAATAACCCCTTAATGTGCGGCTCGCCGCGACGCTGACGCC	13620
Db	118460	ATTAATTTTAAATCACAATAACCCCTTAATGTGCGGCTCGCCGCGACGCTGACGCC	118519
QY	13621	GGCGGGTTCGACCCCAATGACCGGCATCTCTGGTGGCGCGGGACAGAGCGCGCCGCGCAAAAG	13680
Db	118520	GGCGGGTTCGACCCCAATGACCGGCATCTCTGGTGGCGCGGGACAGAGCGCGCCGCGCAAAAG	118579
QY	13681	TGCGATCGCGGGGTCTGACCCACCCGCTGGGAGAAACCCCTCCGTTCTGTTGTTCTTGCC	13740
Db	118580	TGCGATCGCGGGGTCTGACCCACCCGCTGGGAGAAACCCCTCCGTTCTGTTGTTCTTGCC	118639
QY	13741	TGCGGTCCCTGGCCCCCTTGCCCCACCGGGGATGTCTTGAGACACTTTCCCGGTAGAA	13800
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QY	13801	TAGACAGAGAGATGCCCCGCAACATACGACGGGGTGGCCGTGGGGAACGGGAGCGCG	13860
Db	118700	TAGACAGAGAGATGCCCCGCAACATACGACGGGGTGGCCGTGGGGAACGGGAGCGCG	118759
QY	13861	CCGCTTGCCTGCGTAGAGTGTCCGCGGTGGCCCTATGACCCCGCAGCGAGGGGCCG	13920
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QY	13921	CTGGGGGGGAAATTTTCCCGAAGACGGCGCGCCGCTTGAGCGCGCGGTCTCTCCGCCA	13980
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QY	14281	TACCAAGCCCTTGTGGCGCGGCAACCGCGCTTAACCGGGTGGCTTGGCGCGCACAGCT	14340
Db	119180	TACCAAGCCCTTGTGGCGCGGCAACCGCGCTTAACCGGGTGGCTTGGCGCGCACAGCT	119239
QY	14341	TGGCCACGTGGCGCTTGGAGAGAGCGCTTGAGCAAGTCACTTTAAACATGTAGTTGAGG	14400
Db	119240	TGGCCACGTGGCGCTTGGAGAGAGCGCTTGAGCAAGTCACTTTAAACATGTAGTTGAGG	119299
QY	14401	GGCTGACCAAGGCGCCCTTTTCCATTTGGAGAGCCACCGAAAAAAGTGGGAGCATGGT	14460
Db	119300	GGCTGACCAAGGCGCCCTTTTCCATTTGGAGAGCCACCGAAAAAAGTGGGAGCATGGT	119359
QY	14461	TGCGCCTTGAGCAACGCTGTGTGCCCGTTAGAAAAAATAATTTTTCACGTCCCTTTCTG	14520
Db	119360	TGCGCCTTGAGCAACGCTGTGTGCCCGTTAGAAAAAATAATTTTTCACGTCCCTTTCTG	119419

QY	14521	AGAGCTGGCGGTCATATGGAGACATACAGTGTATTATAGACTAAAGTAACATCTGGGCTGG	14580
Db	119420	AGAGTGGGGGTCATATGGAGACATACAGTGTATTATAGACTAAAGTAACATCTGGGCTGG	119475
QY	14581	ACCGGAGCCTCTCGATTAATAAATATCCACGCTAGTAATAAAAAAGGTGGAGACCAAGGTCCA	14640
Db	119480	ACCGGAGCCTCTCGATTAATAAATATCCACGCTAGTAATAAAAAAGGTGGAGACCAAGGTCCA	119535
QY	14641	ATCCGCCAACGAAAAACAGGGCTCCAGCAACACCGGAGGGGAATACCGGATTCTCCAG	14700
Db	119540	ATCCGCCAACGAAAAACAGGGCTCCAGCAACACCGGAGGGGAATACCGGATTCTCCAG	119599
QY	14701	TTGAGGGGACAGCGCGTTTGCAAACCCCTCGGGGCTATATCTGGAGCGCGCGGTCAA	14760
Db	119600	TTGAGGGGACAGCGCGTTTGCAAACCCCTCGGGGCTATATCTGGAGCGCGCGGTCAA	119655
QY	14761	AAAGGCACAGCAAGGGCTCTGTGTGCTTCAGCCTTAGTGGGGGACAGCAATCCACTAAC	14820
Db	119660	AAAGGCACAGCAAGGGCTCTGTGTGCTTCAGCCTTAGTGGGGGACAGCAATCCACTAAC	119713
QY	14821	GCTTATGGGGAAATGGGTCCGGTGCAGGCGCTCGCGACACCCTCTTCACTACACTA	14880
Db	119720	GCTTATGGGGAAATGGGTCCGGTGCAGGCGCTCGCGACACCCTCTTCACTACACTA	119779
QY	14881	GAGCGTTTGATTAATTCACACGACGACCGCGGGCTTACTTAATATGTGTCTTGCTCAAT	14940
Db	119780	GAGCGTTTGATTAATTCACACGACGACGCGGGCTTACTTAATATGTGTCTTGCTCAAT	119833
QY	14941	TCCCGCAAGGTGTGGCAACGCACTCGGGGGCGCGCGAGGGGTGCGGGCGAAAGCCCG	15000
Db	119840	TCCCGCAAGGTGTGGCAACGCACTCGGGGGCGCGCGAGGGGTGCGGGCGAAAGCCCG	119899
QY	15001	ACGGGCTCCGCCAATCTGGCGCGAGGCGGCGACAGCGGACAGAGGCTAAACACGCGCAG	15060
Db	119900	ACGGGCTCCGCCAATCTGGCGCGAGGCGGCGACAGCGGACAGAGGCTAAACACGCGCAG	119955
QY	15061	GGCGCGCCACCAAGGAGCGGGGGCAGACCGCGGTGGCGGGTTACGATGTGCTTGTGA	15120
Db	119960	GGCGCGCCACCAAGGAGCGGGGGCAGACCGCGGTGGCGGGTTACGATGTGCTTGTGA	120019
QY	15121	ACAGACTCCACCACTGGCTGTGGAAGGGCAAGAGCGCTTTTGAAGCGCGCTTTA	15180
Db	120020	ACAGACTCCACCACTGGCTGTGGAAGGGCAAGAGCGCTTTTGAAGCGCGCTTTA	120077
QY	15181	AACAGGTTGGGCCGATGTGCGCTCTTGGTAAACAGCGGCTAGTTTCCACCTTAAAGCC	15240
Db	120080	AACAGGTTGGGCCGATGTGCGCTCTTGGTAAACAGCGGCTAGTTTCCACCTTAAAGCC	120133
QY	15241	TTAAGGATTAATTTTCTGTTCAGTAAATCCGCCACGGAAAAATCTCCGCGCGCAA	15300
Db	120140	TTAAGGATTAATTTTCTGTTCAGTAAATCCGCCACGGAAAAATCTCCGCGCGCAA	120199
QY	15301	AAGCATTAATAAAGCGGCGCTTGAAGAAGATTCAGTCTCTAATCTTTGGCGGCTAAAAATAGA	15360
Db	120200	AAGCATTAATAAAGCGGCGCTTGAAGAAGATTCAGTCTCTAATCTTTGGCGGCTAAAAATAGA	120255
QY	15361	CAGGGGGGCCCGCAGCCTCTGAAAACCGCCGACGGGGGATGCTGGGACACTCTAGATTAGCA	15420
Db	120260	CAGGGGGGCCCGCAGCCTCTGAAAACCGCCGACGGGGGATGCTGGGACACTCTAGATTAGCA	120313
QY	15421	TCCAGAAATTAATAAGGCCAGTGGGAAAAAGCCTAGCATCCGCTGTGTGGGCGCTGGCAACA	15480
Db	120320	TCCAGAAATTAATAAGGCCAGTGGGAAAAAGCCTAGCATCCGCTGTGTGGGCGCTGGCAACA	120377
QY	15481	GACCGCATTCACGTCGCCCAAGATTAATCGCATGCCACAGCTCACTTCGTTTGTATGTGC	15540
Db	120380	GACCGCATTCACGTCGCCCAAGATTAATCGCATGCCACAGCTCACTTCGTTTGTATGTGC	120435
QY	15541	CCATTAGCAGGGCGGTGGATGTTTCAAAAAGAGCGCTCTGTTGGGCGAGAGGTTAGAGAGGGCC	15600
Db	120440	CCATTAGCAGGGCGGTGGATGTTTCAAAAAGAGCGCTCTGTTGGGCGAGAGGTTAGAGAGGGCC	120499
QY	15601	CGGTCTCTGTATACAGGACGGGGTCAATGTGTCGGGTGGGCACTTGGGCAACAGAAAGCATTT	15660

Db	120500	CGGTCTGTGATACGAGCGGGGTCAATGTCGCCGTGGGACATGGGCAACAGAGCAATT	120559
Qy	15661	GTCAAGCAAGGTAAGAAGCGATATAGTCTTACCTCGGCTACGAGGCTTAAATAC	15720
Db	120560	GTCAAGCAAGGTAAGAAGCGATATAGTCTTACCTCGGCTACGAGGCTTAAATAC	120619
Qy	15721	GAACGTCCGGCTTAAACACAAATCTTTCGCTATATGTCGTCACACTGTGCCA	15780
Db	120620	GAACGTCCGGCTTAAACACAAATCTTTCGCTATATGTCGTCACACTGTGCCA	120679
Qy	15781	TGTCCTTCGAGTTCAGCCCTGCTGTCGCCGAAGCGGCGAGTACAGTGAACGCGCA	15840
Db	120680	TGTCCTTCGAGTTCAGCCCTGCTGTCGCCGAAGCGGCGAGTACAGTGAACGCGCA	120739
Qy	15841	AGCGCTGTTCAATTTAAGGTAGTCAACAGCGGGCAATTTGCCAACAGTACGCGTTT	15900
Db	120740	AGCGCTGTTCAATTTAAGGTAGTCAACAGCGGGCAATTTGCCAACAGTACGCGTTT	120739
Qy	15901	CCTGCAGTGGGTTTTCACCTGGCAAGCGCCACTGTGTTTGGCAGCCGCGGTGGG	15960
Db	120800	CCTGCAGTGGGTTTTCACCTGGCAAGCGCCACTGTGTTTGGCAGCCGCGGTGGG	120859
Qy	15961	ATTTTTCATGTCGATGATGGAGTCTGTCGTCATGCGCACTATGTCGCGCTGAAGTG	16020
Db	120860	ATTTTTCATGTCGATGATGGAGTCTGTCGTCATGCGCACTATGTCGCGCTGAAGTG	120919
Qy	16021	GGGGGCGATGGGTGATGTCCTCCACCGGCGAGCGGCTTTTTCAGCGCTTGGCGGT	16080
Db	120920	GGGGGCGATGGGTGATGTCCTCCACCGGCGAGCGGCTTTTTCAGCGCTTGGCGGT	120979
Qy	16081	TCCCGGCGCTTTCACAGAACACCGTATGCAAAAAAGCGGGATGACGGACTGCCAGTGC	16140
Db	120980	TCCCGGCGCTTTCACAGAACACCGTATGCAAAAAAGCGGGATGACGGACTGCCAGTGC	121039
Qy	16141	GTCCGCAAAAGCGGAGCGCTGATCTTAATGCGGGAACTGTAGGCACTTTCGAC	16200
Db	121040	GTCCGCAAAAGCGGAGCGCTGATCTTAATGCGGGAACTGTAGGCACTTTCGAC	121099
Qy	16201	GGGATACAGTGAATAGGGGTCTGAGTTACAAAAAGATGACTCCGTGACACACGCGCCCG	16260
Db	121100	GGGATACAGTGAATAGGGGTCTGAGTTACAAAAAGATGACTCCGTGACACACGCGCCCG	121159
Qy	16261	CGGAGGGGGTGCATCCTGGGTCCCAATCCTGACATAAATCTTCTGTGGGGGTA	16320
Db	121160	CGGAGGGGGTGCATCCTGGGTCCCAATCCTGACATAAATCTTCTGTGGGGGTA	121219
Qy	16321	TTTTTCGGGTACCTCTCTCTGATAGGAGTACGGTATGGAATGGGATATCGCGCGG	16380
Db	121220	TTTTTCGGGTACCTCTCTCTGATAGGAGTACGGTATGGAATGGGATATCGCGCGG	121279
Qy	16381	GGCGGGGGGGCGGGGGGGCGCGGTGTGTGCTGCTCCCTCTTTCCTCTG	16440
Db	121280	GGCGGGGGGGCGGGGGGGCGCGGTGTGTGCTGCTCCCTCTTTCCTCTG	121339
Qy	16441	TTGTCTTTAGGAGTCTGTCCTGCGGGAGTTGTGACGTGCACTAGACGTAATAA	16500
Db	121340	TTGTCTTTAGGAGTCTGTCCTGCGGGAGTTGTGACGTGCACTAGACGTAATAA	121399
Qy	16501	AGGAATCTCTCCGCAACCGTGGTGAACCCCAACCCCTACGATAGAGTGGAGT	16560
Db	121400	AGGAATCTCTCCGCAACCGTGGTGAACCCCAACCCCTACGATAGAGTGGAGT	121459
Qy	16561	ATGGCCAGGAAACGGGGGTCTGCGCGAGACGCGCGGTGGGTGTGTGTGGCTAC	16620
Db	121460	ATGGCCAGGAAACGGGGGTCTGCGCGAGACGCGCGGTGGGTGTGTGTGGCTAC	121519
Qy	16621	CGCTGTGTGCTTATAGGGGATGGGGCTGTGAGCGTTGGCGATTGGGTGTCCGG	16680
Db	121520	CGCTGTGTGCTTATAGGGGATGGGGCTGTGAGCGTTGGCGATTGGGTGTCCGG	121579
Qy	16681	TGAGTGGGGGGGATGGGAGGGGGAGACGTCGCGCGTGGCGATTGTGGGGTCC	16740
Db	121580	TGAGTGGGGGGGATGGGAGGGGGAGACGTCGCGCGTGGCGATTGTGGGGTCC	121639
Qy	16741	AGGTGATGCGGAGGGGGCAAGACGTCGAGGCTCAGCGGTTCAAGTACGTGTG	16800
Db	121640	AGGTGATGCGGAGGGGGCAAGACGTCGAGGCTCAGCGGTTCAAGTACGTGTG	121699
Qy	16801	CGATGTTTCAAAAACGACGAAGGCTGCTGATTGGGCGATGATATGTGACGACGGCGG	16860
Db	121700	CGATGTTTCAAAAACGACGAAGGCTGCTGATTGGGCGATGATATGTGACGACGGCGG	121759
Qy	16861	TGCAGTGAATGGGGGCGGGGCTGTGACGGGGGTGATGGTGGGGCAATGCGATGCGG	16920
Db	121760	TGCAGTGAATGGGGGCGGGGCTGTGACGGGGGTGATGGTGGGGCAATGCGATGCGG	121819
Qy	16921	GGATGCGGGGAGACACCTGACGCTGTTTGAAGTGAACAGCGCTGAAGCTAACCGGCGC	16980
Db	121820	GGATGCGGGGAGACACCTGACGCTGTTTGAAGTGAACAGCGCTGAAGCTAACCGGCGC	121879
Qy	16981	AGACCCGCTTGGCGAGCGGCTTGGAGATCCCAACAGATGACGAGTACAGCTGATCC	17040
Db	121880	AGACCCGCTTGGCGAGCGGCTTGGAGATCCCAACAGATGACGAGTACAGCTGATCC	121939
Qy	17041	TGATGGCGACCTTGGGATGACCCGCTGCTGATTCGATGCGGCTTTCGATTCGATTC	17100
Db	121940	TGATGGCGACCTTGGGATGACCCGCTGCTGATTCGATGCGGCTTTCGATTCGATTC	121999
Qy	17101	GTGCGCTTGTTCGACACCGCCCGACCTTGGCGCCCTGATGTTGTGAGCGGGGGCGC	17160
Db	122000	GTGCGCTTGTTCGACACCGCCCGACCTTGGCGCCCTGATGTTGTGAGCGGGGGCGC	122059
Qy	17161	GGGTGGGGGCTGGCGGGGGCGGTGACGCCCCCTGGCGGGCGCTCCCGGCTGTTCCT	17220
Db	122060	GGGTGGGGGCTGGCGGGGGCGGTGACGCCCCCTGGCGGGCGCTCCCGGCTGTTCCT	122119
Qy	17221	AGTCCGCGCGCTTTCGCAATGTCCTTCGAGAGTCTCCCAACCCCTGTCCGATAC	17280
Db	122120	AGTCCGCGCGCTTTCGCAATGTCCTTCGAGAGTCTCCCAACCCCTGTCCGATAC	122179
Qy	17281	TATCCGGAAGATGTTGCGGCTGCCACATGTTGCGGTTTACTGCTGTAAAAAC	17340
Db	122180	TATCCGGAAGATGTTGCGGCTGCCACATGTTGCGGTTTACTGCTGTAAAAAC	122239
Qy	17341	GGCAGATTAAGTATGATGCTTCCTTCACAGACCGGACGCACTGAGCGGCGGACAGCA	17400
Db	122240	GGCAGATTAAGTATGATGCTTCCTTCACAGACCGGACGCACTGAGCGGCGGACAGCA	122299
Qy	17401	ACCTATGTTTAAATGCGATTAATGTCGCTAGAGTGGCGGCTAATTTGATCCTGCG	17460
Db	122300	ACCTATGTTTAAATGCGATTAATGTCGCTAGAGTGGCGGCTAATTTGATCCTGCG	122359
Qy	17461	GGCGACGATTAACGCTTATGATGGGCGACAGCGCGCTTAACCGCACGACCGCACGG	17520
Db	122360	GGCGACGATTAACGCTTATGATGGGCGACAGCGCGCTTAACCGCACGACCGCACGG	122419
Qy	17521	CGGTATTAATTCGTTACTATTAAGCTTATTAATTCGTTGCGGATTTAGTGGTGGCAG	17580
Db	122420	CGGTATTAATTCGTTACTATTAAGCTTATTAATTCGTTGCGGATTTAGTGGTGGCAG	122479
Qy	17581	TGTTAAGTACAGCGCGCGCGCGCCCTTACTTGTGCGCGGCAACCGGAAAGTCT	17640
Db	122480	TGTTAAGTACAGCGCGCGCGCGCCCTTACTTGTGCGCGGCAACCGGAAAGTCT	122539
Qy	17641	GTTCCGCGCGGACGCGCGCGCTGCCGAACACGCGCTTGAATTTGCGGGCGG	17700
Db	122540	GTTCCGCGCGGACGCGCGCGCTGCCGAACACGCGCTTGAATTTGCGGGCGG	122599
Qy	17701	CTGGGCTGTGTCAAGTATTTACACAGATGGAGTGTATTTGGGGTGTGTCAACGTC	17760
Db	122600	CTGGGCTGTGTCAAGTATTTACACAGATGGAGTGTATTTGGGGTGTGTCAACGTC	122659
Qy	17761	ACTTGTAAACCGCTAAATCTGGAATTTCTTCCCGCGGCGGCTGAGCGCGGCGCTAA	17820
Db	122660	ACTTGTAAACCGCTAAATCTGGAATTTCTTCCCGCGGCGGCTGAGCGCGGCGCTAA	122719

OY	17821	GCCTTATATGCTGTGCACAGCATCTTGAAACTCGAAAGCTGGCCATATATAACCCAGTAT	17880
Db	122720	GCCTTATATGCTGTGCACAGCATCTTGAAACTCGAAAGCTGGCCATATATAACCCAGTAT	122779
OY	17881	GGCGTGGGTGTCGGGTGGCAACTTTTGGAAAAAGATTATATGCGCGGGGTGTAAAGA	17940
Db	122780	GGCGTGGGTGTCGGGTGGCAACTTTTGGAAAAAGATTATATGCGCGGGGTGTAAAGA	122839
OY	17941	CCAACACGACCGAGCTGCTTTTCCAAATTATGTCCGGAGGAATTTACATTACGTCGTGCTG	18000
Db	122840	CCAACACGACCGAGCTGCTTTTCCAAATTATGTCCGGAGGAATTTACATTACGTCGTGCTG	122899
OY	18001	CGACGCTTGCACACGTTGGGTGCGTCTTTCAAACGACATATGCGCGGTCCCGTCACT	18060
Db	122900	CGACGCTTGCACACGTTGGGTGCGTCTTTCAAACGACATATGCGCGGTCCCGTCACT	122959
OY	18061	CTACGCGTCCCTTGGGGGTGCCTGTTTAACGACACCCACAGCAGTTCCTTATCGTATCTGGC	18120
Db	122960	CTACGCGTCCCTTGGGGGTGCCTGTTTAACGACACCCACAGCAGTTCCTTATCGTATCTGGC	123019
OY	18121	AAAAACAGGAATCGCTATGCTCCGTTAACGTGGCCACATATATGTTCCGAAGCGGCACGG	18180
Db	123020	AAAAACAGGAATCGCTATGCTCCGTTAACGTGGCCACATATATGTTCCGAAGCGGCACGG	123079
OY	18181	TGGTTACAGCCCCCGTTTCCGGGTAGAGGTGACATTCGCCAACAACAAGTTAGACAGAAAG	18240
Db	123080	TGGTTACAGCCCCCGTTTCCGGGTAGAGGTGACATTCGCCAACAACAAGTTAGACAGAAAG	123139
OY	18241	CCCTGAATTTTTTAAATGCGCACCCCTGGAGAGAGGGGTCTACCTGATGTATCTTTAAGC	18300
Db	123140	CCCTGAATTTTTTAAATGCGCACCCCTGGAGAGAGGGGTCTACCTGATGTATCTTTAAGC	123199
OY	18301	CGTTTGGAGTGGGAAAGCTGTGCGGAAACCCGCTGCTTACAGGTTTACGTCCCTGTCCA	18360
Db	123200	CGTTTGGAGTGGGAAAGCTGTGCGGAAACCCGCTGCTTACAGGTTTACGTCCCTGTCCA	123259
OY	18361	TGTCGCTACAGTTTTTACCCTCCGATTAACCCGACGAGTCGTCTTCCGGGCGAGAGCCA	18420
Db	123260	TGTCGCTACAGTTTTTACCCTCCGATTAACCCGACGAGTCGTCTTCCGGGCGAGAGCCA	123319
OY	18421	GTCCCGCACCGTTCGGTCAACTGTGACCCGGCTGCGCCGAGCTGTGCACGAACTGAAAG	18480
Db	123320	GTCCCGCACCGTTCGGTCAACTGTGACCCGGCTGCGCCGAGCTGTGCACGAACTGAAAG	123379
OY	18481	TGTTTCCCGCGGCCCCAAGGAACAACCTGTTGTGGGTGCTGCAACGTAAAGTCGCTGG	18540
Db	123380	TGTTTCCCGCGGCCCCAAGGAACAACCTGTTGTGGGTGCTGCAACGTAAAGTCGCTGG	123439
OY	18541	ACCCGGAAGACCTTGAGAAAGCGCACGTGCTGTCATCATATAGCGGTTTGGCCGCGG	18600
Db	123440	ACCCGGAAGACCTTGAGAAAGCGCACGTGCTGTCATCATATAGCGGTTTGGCCGCGG	123499
OY	18601	CGCGGCCCCCTGGACCCCGGTTTTGGGAATCCCTCGAABAGGAGAACCCACTACGTGTGG	18660
Db	123500	CGCGGCCCCCTGGACCCCGGTTTTGGGAATCCCTCGAABAGGAGAACCCACTACGTGTGG	123559
OY	18661	GTTGTGTGGCAGCGCGCCGCTTATAGGCAATTTTTTAAAGGAGTGTTTTTTGTATAGGT	18720
Db	123560	GTTGTGTGGCAGCGCGCCGCTTATAGGCAATTTTTTAAAGGAGTGTTTTTTGTATAGGT	123619
OY	18721	CTATGTGAGCGCGCTGTCCCGGTGTCTAAGTGTTTTGTTCGCCAGTGAAGTGTCTCAATG	18780
Db	123620	CTATGTGAGCGCGCGCTGTCCCGGTGTCTAAGTGTTTTGTTCGCCAGTGAAGTGTCTCAATG	123679
OY	18781	ACAAATACAAATTTTGAAGCTGGCTTTTAAAGGTGTGTTTGTGACAGCCTTCCGTGTGA	18840
Db	123680	ACAAATACAAATTTTGAAGCTGGCTTTTAAAGGTGTGTTTGTGACAGCCTTCCGTGTGA	123739
OY	18841	ACTGCATACACCGGGGTGTCCGCACAGAAACGCGCTCTCCCTTATGTCCGCTGCGCCTTC	18900
Db	123740	ACTGCATACACCGGGGTGTCCGCACAGAAACGCGCTCTCCCTTATGTCCGCTGCGCCTTC	123799

QY	18901	CCAGACGGAAAGTGAAGATGGTTCCTCGGGCGCTTTTGGCGTTGACAGACTCGGGCATGT	18960
Db	123800	CCAGAGCGAAAGTGAAGATGGTTCCTCGGGCGCTTTTGGCGTTGACAGACTCGGGCATGT	123859
QY	18961	TGGCGTAGCGGCGTGCAGAAAGCTACCCGCTCTGTTTTTTCTTTTGTGCACACAA	19020
Db	123860	TGCCCTACGGGCGTGCAGAAAGCTACCCGCTCTGTTTTTTTCTTTTGTGCACACAA	123919
QY	19021	CACATGAGACGCGCTTGACAAATTAACCTTAACCTGCGATGGAATTTTCTGCTCAATATTC	19080
Db	123920	CACATGAGACGCGCTTGACAAATTAACCTTAACCTGCGATGGAATTTTCTGCTCAATATTC	123979
QY	19081	GAATAGCTACAGTACTTATGAGACAAATATGCTTACACTTAAACACGGAATCCACGCT	19140
Db	123980	GAATAGCTACAGTACTTATGAGACAAATATGCTTACACTTAAACACGGAATCCACGCT	124039
QY	19141	GTGTGGGCTGACGGTGGTTTTTCCACCTACCGTTATGCGATATATGCTTTTTTATTTT	19200
Db	124040	GTGTGGGCTGACGGTGGTTTTTCCACCTACCGTTATGCGATATATGCTTTTTTATTTT	124099
QY	19201	TTGCATTAACGCGTTTGGGAAACGCGTGGTGCATATATTTTTTTTAAATTTAAACGCT	19260
Db	124100	TTGCATTAACGCGTTTGGGAAACGCGTGGTGCATATATTTTTTTTAAATTTAAACGCT	124158
QY	19261	CGCCAACTCTGTGGATGTACTATGAGTGGTGGTTGTGTTAACCTCCCTGTTCTGTGCGC	19320
Db	124160	CGCCAACTCTGTGGATGTACTATGAGTGGTGGTTGTGTTAACCTCCCTGTTCTGTGCGC	124219
QY	19321	GTGCTTTTGTTCACCTGGCTGCTGTACGTCCGCGCACAGATGCTCAAGTCCGCGACGTG	19380
Db	124220	GTGCTTTTGTTCACCTGGCTGCTGTACGTCCGCGCACAGATGCTCAAGTCCGCGACGTG	124279
QY	19381	CAAAGTGGAAATCTTTTTCTTTTACCTGTACACGTCCTTTGGCGTACATTTGGGTTG	19440
Db	124280	CAAAGTGGAAATCTTTTTCTTTTACCTGTACACGTCCTTTGGCGTACATTTGGGTTG	124339
QY	19441	TATCAGCCTTATCAGATGCGCTGTAGTTGTGTTTTCCCGCCGCGTGGGTCAAGCACGG	19500
Db	124340	TATCAGCCTTATCAGATGCGCTGTAGTTGTGTTTTCCCGCCGCGTGGGTCAAGCACGG	124399
QY	19501	GGCCTCCGGCTTCTCTGCGTGTGTGTCTTTAATCGTGGCGCTGGCGCTGTCTGCCAA	19560
Db	124400	GGCCTCCGGCTTCTCTGCGTGTGTGTCTTTAATCGTGGCGCTGGCGCTGTCTGCCAA	124459
QY	19561	CGCGAGCCCTTATAGAGAGCGCCCTGGCGTACCACAGAGACAGAGAGTGGATATGTACGA	19620
Db	124460	CGCGAGCCCTTATAGAGAGCGCCCTGGCGTACCACAGAGACAGAGAGTGGATATGTACGA	124519
QY	19621	AGATCCCGGGGAAGATACCGTCAACTGGAAGCTGAAATACAGAACCCACGACGCGATCTG	19680
Db	124520	AGATCCCGGGGAAGATACCGTCAACTGGAAGCTGAAATACAGAACCCACGACGCGATCTG	124579
QY	19681	CGGCTTTTGGTCCGTTTGGGCTGATGCTCTTTTACGGACTTAACTGCTGTATGCT	19740
Db	124580	CGGCTTTTGGTCCGTTTGGGCTGATGCTCTTTTACGGACTTAACTGCTGTATGCT	124639
QY	19741	TAAAGCACAGAGCGGGCCAGAAAGGAGACCGTTAGGGGTAAATTTGACGGTGGTGGT	19800
Db	124640	TAAAGCACAGAGCGGGCCAGAAAGGAGACCGTTAGGGGTAAATTTGACGGTGGTGGT	124699
QY	19801	GCTGTTTTTAATTTTTTGGCTCCCTATACCTGTGCAACTTTTTTGACACCTGTTTGA	19860
Db	124700	GCTGTTTTTAATTTTTTGGCTCCCTATACCTGTGCAACTTTTTTGACACCTGTTTGA	124759
QY	19861	GACCGGTTTTTCGCCGAAACGTGCTACAGGACGTGATCAGCGTGGCCATGCACAT	19920
Db	124760	GACCGGTTTTTCGCCGAAACGTGCTACAGGACGTGATCAGCGTGGCCATGCACAT	124819
QY	19921	ATGCTCCCTGTCACAGAGATGTATTAAGCCCGTTCCGCCAGTCGTATTTCTGCTGTG	19980
Db	124820	ATGCTCCCTGTCACAGAGATGTATTAAGCCCGTTCCGCCAGTCGTATTTCTGCTGTG	124879
QY	19981	GTCTCTGTTTAGGAAGGTTTAGGATATCTGTGCTCGTGTATGCTGTTTTTCCACTTC	20040

Db	124880	GCTCTGTTTAGAGAAAGGTTAGGATACCTGGTCCGTGTTTAGGTTTTCACATTC	124939
Qy	20041	AGTAGTTTATGAGACACTCAAGACACTGTTGGATTGTTTGTGTACATTTATTTTC	20100
Db	124940	AGGTAGTTTATGAGACACTCAAGACACTGTTGGATTGTTTGTGTACATTTATTTTC	124999
Qy	20101	ATTTTGTGTACATTTATTTTATTTAATGAAGCATCTGACCTGTGACACTTACTGTACGTTTA	20160
Db	125000	ATTTTGTGTACATTTATTTTATTTAATGAAGCATCTGACCTGTGACACTTACTGTACGTTTA	125059
Qy	20161	CTGTCTGTTTCTTATGACCAAGAGAACAGGAGCTGGAAAGGCCAGGCCCAAGGGGAAAC	20220
Db	125060	CTGTCTGTTTCTTATGACCAAGAGAACAGGAGCTGGAAAGGCCAGGCCCAAGGGGAAAC	125119
Qy	20221	TGTCACTGCCCAAGCTCGGGGCGGACAGTACGCCACTGTCCAGGGGTGGAACGTCAAGCG	20280
Db	125120	TGTCACTGCCCAAGCTCGGGGCGGACAGTACGCCACTGTCCAGGGGTGGAACGTCAAGCG	125179
Qy	20281	GGGGTCACACAGGAGGCGCAGGTGGCCCGCTCCGGTGAAGTGAATGGCGCCACAGCGCGA	20340
Db	125180	GGGGTCACACAGGAGGCGCAGGTGGCCCGCTCCGGTGAAGTGAATGGCGCCACAGCGCGA	125239
Qy	20341	GTTGGCAACAGGGTGGCGTGGGTAGTGTGTGGCAACATCCTGGGGTGGCGGTTGCCCGT	20400
Db	125240	GTTGGCAACAGGGTGGCGTGGGTAGTGTGTGGCAACATCCTGGGGTGGCGGTTGCCCGT	125299
Qy	20401	GTGTAGTTCAGGCGGATGCGCTGCTGTGTGAGATGATGATCTCAATGGCGCGCGG	20460
Db	125300	GTGTAGTTCAGGCGGATGCGCTGCTGTGTGAGATGATGATCTCAATGGCGCGCGCGG	125359
Qy	20461	GTATCTACGCGCCACAGTACCGGCGCTGGGCCACCTGTGGAGAGACAGGCGCCGGAAGAC	20520
Db	125360	GTATCTACGCGCCACAGTACCGGCGCTGGGCCACCTGTGGAGAGACAGGCGCCGGAAGAC	125419
Qy	20521	CCTAAACATGATGCGATGGTGGTCTGGGGATGTGAAGGTTTAGCCAGAGGCACATCTGTG	20580
Db	125420	CCTAAACATGATGCGATGGTGGTCTGGGGATGTGAAGGTTTAGCCAGAGGCACATCTGTG	125479
Qy	20581	GTTCCTGTATCGTTCCTCTCCAGGTGATGTCCCATGTGGCGGGTTTGGTCCGGG	20640
Db	125480	GTTCCTGTATCGTTCCTCTCCAGGTGATGTCCCATGTGGCGGGTTTGGTCCGGG	125539
Qy	20641	CGTGTCTGAGGGGTCTCTCTAAGAAAGACGAGCGGCCACAGAGCTGGAACCCAAATCTC	20700
Db	125540	CGTGTCTGAGGGGTCTCTCTAAGAAAGACGAGCGGCCACAGAGCTGGAACCCAAATCTC	125599
Qy	20701	CCCGAGCATGTGTAATGTATCGCTCGCGGGAAGAAAGCCATAGGCCCCCATAGCA	20760
Db	125600	CCCGAGCATGTGTAATGTATCGCTCGCGGGAAGAAAGCCATAGGCCCCCATAGCA	125659
Qy	20761	CCAGAGGTCGTGGAAGAACCATGATCGGCATCGGGCCCCACAGTAGTGTCTTCGAT	20820
Db	125660	CCAGAGGTCGTGGAAGAACCATGATCGGCATCGGGCCCCACAGTAGTGTCTTCGAT	125719
Qy	20821	GCCCAAGGTTCCACCATGTGTCAAGACCGGGAATCCCGGAGAGTGTTCCTCTCTAAG	20880
Db	125720	GCCCAAGGTTCCACCATGTGTCAAGACCGGGAATCCCGGAGAGTGTTCCTCTCTCTAAG	125779
Qy	20881	GTCTGTCTGTGAAGACGGCCGCGAGCTGGAACCCGACGTTGGTGAAGCGCCCATCAAGCG	20940
Db	125780	GTCTGTCTGTGAAGACGGCCGCGAGCTGGAACCCGACGTTGGTGAAGCGCCCATCAAGCG	125839
Qy	20941	CCCTGGGAAGCGGGGACCGGGGGTGAACCAAGGGGCCACTGTGGGGGCTTCAGAGGGGT	21000
Db	125840	CCCTGGGAAGCGGGGACCGGGGGTGAACCAAGGGGCCACTGTGTGGGGGCTTCAGAGGGGT	125899
Qy	21001	TGCAAAACAGATCAAGTTCGCTGTTTCTGCAAAACCTCGGCGAGGTGGCCAGTGTGTTG	21060
Db	125900	TGCAAAACAGATCAAGTTCGCTGTTTCTGCAAAACCTCGGCGAGGTGGCCAGTGTGTTG	125959
Qy	21061	GTTCCACCCGATGCTCTTCTGTAGAGTTCCTCGCGGGCGTGAAGCTGGGCCCCCATAGA	21120
Db	125960	GTTTCACCCGATGCTCTTCTGTAGAGTTCCTCGCGGGCGTGAAGCTGGGCCCCCATAGA	126019
Qy	21121	GTACCACTGTTCGTCGGAAGACAGAGTCCAGTTTTCGCCACCGAAGTAGAGGTCTGTGA	21180
Db	126020	GTACCACTGTTCGTCGGAAGACAGAGTCCAGTTTTCGCCACCGAAGTAGAGGTCTGTGA	126079
Qy	21181	ATAGACTTCATCGTTGTGTGTGTGAGATATGACATTTCTTCTGACAGACCTTCGACCCAC	21240
Db	126080	ATAGACTTCATCGTTGTGTGTGTGAGATATGACATTTCTTCTGACAGACCTTCGACCCAC	126139
Qy	21241	GGTGGCGACACAGGTGGGCCCGGACAGTCAAAATTTTGGACGCCCTGGGCGACCTGTGAC	21300
Db	126140	GGTGGCGACACAGGTGGGCCCGGACAGTCAAAATTTTGGACGCCCTGGGCGACCTGTGAC	126199
Qy	21301	GTGCTGGGGCTGATTTCTGAAGATACGCCCGGGGTTTCGACACAGCCACTGACAGGG	21360
Db	126200	GTGCTGGGGCTGATTTCTGAAGATACGCCCGGGGTTTCGACACAGCCACTGACAGGG	126259
Qy	21361	CGTTTCTCTGACGGGATGCGAATCTGTAGGCTTCGGTTACGGGCGAGGGCATCTCGAT	21420
Db	126260	CGTTTCTCTGACGGGATGCGAATCTGTAGGCTTCGGTTACGGGCGAGGGCATCTCGAT	126319
Qy	21421	AGCGGTAACCAATGACCTCCGTGCTACAGTCTGAGGCGGACACACAGACCCCGGGA	21480
Db	126320	AGCGGTAACCAATGACCTCCGTGCTACAGTCTGAGGCGGACACACAGACCCCGGGA	126379
Qy	21481	GAGCAGGGGCTCTGTACCATGAAGAGGTTGGCCAGAGTGTGTCCCTGAAGTCCGGTAG	21540
Db	126380	GAGCAGGGGCTCTGTGTACATGAAGAGGTTGGCCAGAGTGTGTCCCTGAAGTCCGGTAG	126439
Qy	21541	GGTGGACCTCGGCAAGACACAGTGTCTCAAAGTGTGATCCTTGGGTCAAGTTCGGCAC	21600
Db	126440	GGTGGACCTCGGCAAGACACAGTGTCTCAAAGTGTGATCCTCCTGGGTCAAGTTCGGCAC	126499
Qy	21601	GGGGAAGGACACACACAGATGAGGTTACCGGTGGCCCTTCAGGTCAGGTGTGAAGCGTTG	21660
Db	126500	GGGGAAGGACACACACAGATGAGGTTACCGGTGGCCCTTCAGGTCAGGTGTGAAGCGTTG	126559
Qy	21661	CCTGGACGACTTCACCTCGGGGCTGGCCGCTGATGACAGTCTCGTTAAACGGCACGGGGG	21720
Db	126560	CCTGGACGACTTCACCTCGGGGCTGGCCGCTGATGACAGTCTCGTTAAACGGCACGGGGG	126619
Qy	21721	TACCGTCTGATGCTGTTGGGTGGCGCTGATATAGTTCTTCCGACAGGACGGGGTCTGCC	21780
Db	126620	TACCGTCTGATGCTGTTGGGTGGCGCTGATATAGTTCTTCCGACAGGACGGGGTCTGCC	126679
Qy	21781	GGCGAGCGATGGGGAAGTTGATGCTCAGGTTCCCTGATGTGTTCTTGCAGGCAAAACAG	21840
Db	126680	GGCGAGCGATGGGGAAGTTGATGCTCAGGTTCCCTGATGTGTTCTTGCAGGCAAAACAG	126739
Qy	21841	TGTGTCTGACAGGACCGAGGCTGTCTCTCCGGGTTCCAMCCGACCGACGCGCTGAG	21900
Db	126740	TGTGTCTGACAGGACCGAGGCTGTCTCTCCGGGTTCCAMCCGACCGACGCGCTGAG	126799
Qy	21901	CGTGAATGCTTAGACGCGCQACGTGCGCTAGCATGATGTTGGTGAACCGCCTCGCAGAT	21960
Db	126800	CGTGAATGCTTAGACGCGCGCCACAGTGTGCGATGATGTTGGTGAACCGCCTCGCAGAT	126859
Qy	21961	GGCGATATCGCGGCCACTGCGCGGGTGAATGCCATGCTGATGATGCCGTTCTCATATAGC	22020
Db	126860	GGCGATATCGCGGCCACTGCGCGGGTGAATGCCATGCTGATGATGCCGTTCTCATATAGC	126919
Qy	22021	CACGCACTGTCCGACCCACCGGTTCTGCCCCCTCCCTGGGTGACCCAGGTTTCTGGGCT	22080
Db	126920	CACGCACTGTCCGACCCACCGGTTCTGCCCCCTCCCTGGGTGACCCAGGTTTCTGGGCT	126979
Qy	22081	AAACAGGGGTTCCGTGCGGCTCTGCTGCTGATGAGGCTGGGGGCGATATATGGGCACCG	22140
Db	126980	AAACAGGGGTTCCGTCGCGGCTCTGCTGCTGATGAGGCTGGGGGCGATATATGGGCACCG	127039
Qy	22141	CGCCATTCTGTCCGTAACACCGACGTGTGTTATCAATGTGTAATCTCAACAGCGCGG	22200
Db	127040	CGCCATTCTGTCCGTAACACCGACGTGTGTTATCAATGTGTAATCTCAACAGCGCGG	127099

OY	22201	GCCACGGGGTCCCACTTGGCTGCTGAACCAACAAGTCCGTTGGAGCACTGTGCCACGTG	22260
Db	127100	GCCCCAGGGGGTCCCACTTGGCTGCTGAACCAACAAGTCCGTTGGAGCACTGTGCCACGTG	127159
OY	22261	TCGGCTGACAAACTTTTGCTGCCAACCGTGGGACATGACACAAAGTGTATGCAACGACGGA	22320
Db	127160	TCGGCTGACAAACTTTTGCTGCCAACCGTGGGACATGACACAAAGTGTATGCAACGACGGA	127219
OY	22321	GGCCAGCGGGAATAGCCCCCACTGCGTGGCGCAGAGGGTGGCTTTGGCCACCAATCCTCAG	22380
Db	127220	GGCCAGCGGGAATAGCCCCCACTGCGTGGCGCAGAGGGTGGCTTTGGCCACCAATCCTCAG	127279
OY	22381	TTCTTCTGGGGCCACCAGCCAGTGTGGAGAAACGGGCTGCTGTGCAACCCAAAGTTGC	22440
Db	127280	TTCTTCTGGGGCCACCAGCCAGTGTGGAGAAACGGGCTGCTGTGCAACCCAAAGTTGC	127339
OY	22441	GATGACTTCGGGCGGATGTGGGTGCTGTATCGGGCCACGCTCCCGGGTTCCACAGCTCCAG	22500
Db	127340	GATGACTTCGGGCGGATGTGGGTGCTGTATCGGGCCACGCTCCCGGGTTCCACAGCTCCAG	127399
OY	22501	GTCGTTACGAATCTGAATTTCCAAAGCTCTTCGAGGTTTCCCAACAGCAGCGCAAAAGGCA	22560
Db	127400	GTCGTTACGAATCTGAATTTCCAAAGCTCTTCGAGGTTTCCCAACAGCAGCGCAAAAGGCA	127459
OY	22561	TCCCGAGATGGGTGGGGCCCTCTATGGCATCCAAAGGGCCCGGTTCGGGCTCCGTGTC	22620
Db	127460	TCCCGAGATGGGTGGGGCCCTCTATGGCATCCAAAGGGCCCGGTTCGGGCTCCGTGTC	127519
OY	22621	GCGGGGAGAGACGGCAAAAGACACGACGACGACATACACAGTTTGAGAAACTTTTAACATGAGAT	22680
Db	127520	GCGGGGAGAGACGGCAAAAGACACGACGACGACATACACAGTTTGAGAAACTTTTAACATGAGAT	127579
OY	22681	GTCGTTACGCTTTCCGCTGAGATGCTGGCGTGGCGGCTCAGTTGGCTCAGATGGTTGG	22740
Db	127580	GTCGTTACGCTTTCCGCTGAGATGCTGGCGTGGCGGCTCAGTTGGCTCAGATGGTTGG	127639
OY	22741	TGGAAGCTGAGAGACAAAGAGGCGGACGCCGCCGCGAGACCAAGGCTCCCAAGTGGCC	22800
Db	127640	TGGAAGCTGAGAGACAAAGAGGCGGACGCCGCCGCGAGACCAAGGCTCCCAAGTGGCC	127699
OY	22801	GATGACAGAGCGGGTCTATGGGGCCGATTAATGCTGTGAATATAGGGGCTTCTCCAAAT	22860
Db	127700	GATGACAGAGCGGGTCTATGGGGCCGATTAATGCTGTGAATATAGGGGCTTCTCCAAAT	127759
OY	22861	CTCGTAAGCCACAGCCAAACGTTTGGGTGATGCGGGTAACTCGCGCGCTCCCCAGTAA	22920
Db	127760	CTCGTAAGCCACAGCCAAACGTTTGGGTGATGCGGGTAACTCGCGCGCTCCCCAGTAA	127819
OY	22921	AAGGAGGCGGTGGTGGCCATGCGCCGTCACAGGGTTCAAAAGACCCCAAGACAGATGATAG	22980
Db	127820	AAGGAGGCGGTGGTGGCCATGCGCCGTCACAGGGTTCAAAAGACCCCAAGACAGATGATAG	127879
OY	22981	CTGACTGAATAAAGACTCTGTAGAGAAATGTATATCTTGAGGCACGACAGATTAACGCGA	23040
Db	127880	CTGACTGAATAAAGACTCTGTAGAGAAATGTATATCTTGAGGCACGACAGATTAACGCGA	127939
OY	23041	TGTGGTGGTAATAACGTTCCGCTCGCTGGTGGTGGCGCTGTGAGCGGTTTAAAGAAAGCC	23100
Db	127940	TGTGGTGGTAATAACGTTCCGCTCGCTGGTGGTGGCGCTGTGAGCGGTTTAAAGAAAGCC	127999
OY	23101	ACCGAGGACAGCGCGTGGGTCGCGGCGCAGAGCTGTGGCAGTGGAGTGGGCTGGTGGTT	23160
Db	128000	ACCGAGGACAGCGCGTGGGTCGCGGCGCAGAGCTGTGGCAGTGGAGTGGGCTGGTGGTT	128059
OY	23161	AATAGCTCTGTGGCGTGGCGAGAAATATGCCCCACTGACGGCGTATAGTGGCTTAAATATCC	23220
Db	128060	AATAGCTCTGTGGCGTGGCGAGAAATATGCCCCACTGACGGCGTATAGTGGCGTAAATATCC	128119
OY	23221	ACACAGGGCCGATCTGATTTGGCCCCCGGGGACAGCGTGGCATGACACAGATGTTTGG	23280
Db	128120	ACACAGGGCCGATCTGATTTGGCCCCCGGGGACAGCGTGGCATGACACAGATGTTTGG	128179

QY	23281	TAGGCAACCTGACACCTGTCGTAAGAGGGCGCTGACAGTCGTGTAATAGATGACGATATG	23340
Db	128180	CAGGGCACTGACCTCTCTGAATGGCGCTGACAGTGTGTAATGATCAGCTATGTG	128233
QY	23341	GGTTACGTTTTGCGACGGAGGGCGCTGAAAAAGCAGCTGATGACTCTGCGGGCCATAC	23400
Db	128240	GGTTACGTTTTGCGACGGAGGGCGCTGAAAAAGCAGCTGATGACTCTGCGGGCCATGAC	128299
QY	23401	GGCCTATCTGACACCGTATAGCTGTTGGCCGTTGAGGGCTGACGGCCAGCGGTAAAT	23460
Db	128300	GGCCTATCTGACACCGTATAGCTGTTGGCCGTTGAGGGCTGACGGCCAGCGGTAAAT	12835
QY	23461	GTTCCGTTGTAACGGGAGCATCAACCGCGCGCATATTGGGTCTCTCTCGGGCAAGGCT	23520
Db	128360	GTTCCGTTGTAACGGGAGCATCAACCGCGCGCATATTGGGTCTCTCTCGGGCAAGGCT	12841
QY	23521	CCAGGCGGTGATTTGCATGTCAACCGGGAGTGGCGCTCAGCGCCACATCATATTCTAC	23580
Db	128420	CCAGGCGGTGATTTGCATGTCAACCGGGAGTGGCGCTCAGCGCCACATCATATTCTAC	12847
QY	23581	TATGTGCCAAGTGTCAAGGGCGCCAAAGTGCCCGGGGTACCCGATGGCGACAAACG	23640
Db	128480	TATGTGCCAAGTGTCAAGGGCGCCAAAGTGCCCGGGGTACCCGATGGCGACAAACG	128533
QY	23641	TCCTGCTGGCAGCTCAGATGTGTGCCCACTCTAACCCGCAAGCTTATGAGGCCCT	23700
Db	128540	TCCTGCTGGCAGCTCAGATGTGTGCCCACTCTAACCCGCAAGCTTATGAGGCCCT	12859
QY	23701	GTCCTTAAGCAGCTGCACCTATTTCCGTAGATCTTGTAAGGTGGCGCATCAGGTCGG	23760
Db	128600	GTCCTTAAGCAGCTGCACCTATTTCCGTAGATCTTGTAAGGTGGCGCATCAGGTCGG	12865
QY	23761	GCCATAGGGCAGGGATTAAGTATGATGCCCTGAGGTGCGCCGACCGAGTTTCCAGAG	23820
Db	128660	GCCATAGGGCAGGGATTAAGTATGATGCCCTGAGGTGCGCCGACCGAGTTTCCAGAG	12871
QY	23821	TGCATATTTAACAGAGAGGCCCAAGAGATGCAAGTACGCCAGCGCTGGCTCTAC	23880
Db	128720	TGCATATTTAACAGAGAGGCCCAAGAGATGCAAGTACGCCAGCGCTGGCTCTAC	12877
QY	23881	GTCCTTGTCAAAAGTTATCAGAGGGCGGTGTTACAAACCCAAAGTAAATAATCTCAACCA	23940
Db	128780	GTCCTTGTCAAAAGTTATCAGAGGGCGGTGTTACAAACCCAAAGTAAATAATCTCAACCA	12883
QY	23941	CTGTTCGGAACAAGCCCAAAACACTTCTGCGTCCGAATTTGATGATTAAGCTC	24000
Db	128840	CTGTTCGGAACAAGCCCAAAACACTTCTGCGTCCGAATTTGATGATTAAGCTC	12889
QY	24001	CTCTTCGACATAAGGCTGACAGGCCCAAGGAGGTCTGTCGTTGGGCATATTTC	24060
Db	128900	CTCTTCGACATAAGGCTGACAGGCCCAAGGAGGTCTGTCGTTGGGCATATTTC	12895
QY	24061	TAACTTCAGCCGGCGCAAAAGCAAGGGGGGACTTAAATAGGGGTATAGGGTGT	24120
Db	128960	TAACTTCAGCCGGCGCAAAAGCAAGGGGGGACTTAAATAGGGGTATAGGGTGT	12901
QY	24121	AGGATATCGGTGGGGAGCCGTCCTCATGTACATGACATTCATATTAATTATGTAAT	24180
Db	129020	AGGATATCGGTGGGGAGCCGTCCTCATGTACATGACATTCATATTAATTATGTAAT	12907
QY	24181	TGGGCACTTGGGATGTTACATTTAACTTCCCATATCTCAAGTAACTCACTTGACGA	24240
Db	129080	TGGGCACTTGGGATGTTACATTTAACTTCCCATATCTCAAGTAACTCACTTGACGA	129133
QY	24241	TCGCCCTTAACATCAACACCTGTTGGGGGTGAGGTAAACAGTAAGGGTGGAGG	24300
Db	129140	TCGCCCTTAACATCAACACCTGTTGGGGGTGAGGTAAACAGTAAGGGTGGAGG	129199
QY	24301	GGATGTTAGTGGCGCAACCAAGCATTAACGTTCGGGGCGGGAGCTGGAGCGCTGAAC	24360
Db	129200	GGATGTTAGTGGCGCAACCAAGCATTAACGTTCGGGGCGGGAGCTGGAGCGCTGAAC	12925
QY	24361	CCAGAGATGTCACCTGTTGAGGCAATGACAACTACCTCCGAAAGTGTCTCT	24420

Db	129260		129319
Qy	24421	TGGATGTTTTGTGATTAGGTAAACAGAAAGTTGTGAGAGAAAGTAACTTATAGATGAC	24480
Db	129320	TGGATGTTTTGTGATTAGGTAAACAGAAAGTTGTGAGAGAAAGTAACTTATAGATGAC	129379
Qy	24481	CTCCGTGCGGGCGGTGGGTGGGTGACAGCTGTGTGATGATGAACACTTCTCGGGC	24540
Db	129380	CTCCGTGCGGGCGGTGGGTGGGTGACAGCTGTGTGATGATGAACACTTCTCGGGC	129439
Qy	24541	GTTCCGTGGGGTGTGGGTGTGGTCTCACTAAGACGGCCAACTCAACACTACCTCTCC	24600
Db	129440	GTTCCGTGGGGTGTGGGTGTGGTCTCACTAAGACGGCCAACTCAACACTACCTCTCC	129499
Qy	24601	CGTTCCAGACCGTGAAGCGGTTTCGTCGTAGCGTCTGTGGAGGGGTGGCTCAACCTT	24660
Db	129500	CGTTCCAGACCGTGAAGCGGTTTCGTCGTAGCGTCTGTGGAGGGGTGGCTCAACCTT	129559
Qy	24661	GTTGGTGTAAACATCCACGGTAACCCGGTAAATGACGGCGGTCAAGGCAATTTGTAA	24720
Db	129560	GTTGGTGTAAACATCCACGGTAACCCGGTAAATGACGGCGGTCAAGGCAATTTGTAA	129619
Qy	24721	CGTAAACAGCATATAAGCTTACAAACGCAATTTTGTGAACGTTGTATATTTAGCC	24780
Db	129620	CGTAAACAGCATATAAGCTTACAAACGCAATTTTGTGAACGTTGTATATTTAGCC	129679
Qy	24781	CCAAAGTTTATACAAAGCAAACTACTTACGATTAATAATGCAACCGCAAGAAAGA	24840
Db	129680	CCAAAGTTTATACAAAGCAAACTACTTACGATTAATAATGCAACCGCAAGAAAGA	129739
Qy	24841	TAACTACTACGATTTCTGTTCCTAATTTGGTTCGAAATTTAAGATGAGAGATTAATTTGCC	24900
Db	129740	TAACTACTACGATTTCTGTTCCTAATTTGGTTCGAAATTTAAGATGAGAGATTAATTTGCC	129799
Qy	24901	CGCTGAGAAATGCTCGGAAATTAAGAGGGCGGCTATTTTCATGTGTACAGGGTGAACAC	24960
Db	129800	CGCTGAGAAATGCTCGGAAATTAAGAGGGCGGCTATTTTCATGTGTGTACAGGGTGAACAC	129859
Qy	24961	TTGTGAGTTTCAGTTGAGTCAACCTGCGACGTAACCCGCTAGAGTGCACAGCGGTC	25020
Db	129860	TTGTGAGTTTCAGTTGAGTCAACCTGCGACGTAACCCGCTAGAGTGCACAGCGGTC	129919
Qy	25021	TTGGTTCGAGAGAGTACATCTTAATTTTAACTGTAAGAGGGTCTCTGTAAATTAATTT	25080
Db	129920	TTGGTTCGAGAGAGTACATCTTAATTTTAACTGTAAGAGGGTCTCTGTAAATTAATTT	129979
Qy	25081	AAGTTATGCTACTTCAATATATCAATGAGAGTTACATCCAAAAAGATACCTCGAT	25140
Db	129980	AAGTTATGCTACTTCAATATATCAATGAGAGTTACATCCAAAAAGATACCTCGAT	130039
Qy	25141	AAAAATGCTGATAGTGAAGTTTTCACAACAATGACAGGGGTGATAGGCCCAAAATATGA	25200
Db	130040	AAAAATGCTGATAGTGAAGTTTTCACAACAATGACAGGGGTGATAGGCCCAAAATATGA	130099
Qy	25201	TAAACCTATATGAGAAATTTTATAGTACGTTTGTGTACATGCAAAATTAATTTTAA	25260
Db	130100	TAAACCTATATGAGAAATTTTATAGTACGTTTGTGTACATGCAAAATTAATTTTAA	130159
Qy	25261	ATTAATACTTATATATCATGTGTACCAAGTTTAATTTTGTGTGTCTTGAATTAAT	25320
Db	130160	ATTAATACTTATATATCATGTGTGTACCAAGTTTAATTTTGTGTGTCTTGAATTAAT	130219
Qy	25321	GTATCCGATGTTGAGAGCAACGTATGTAGTGAAGCAACGGGCTGTGAACATTAACCA	25380
Db	130220	GTATCCGATGTTGAGAGCAACGTATGTAGTGAAGCAACGGGCTGTGAACATTAACCA	130279
Qy	25381	ATAGGCAATGTTCCATGATTCGATATTCGCCATGCAATTTTAAGTGCACGCAATTTGCAG	25440
Db	130280	ATAGGCAATGTTCCATGATTCGATATTCGCCATGCAATTTTAAGTGCACGCAATTTGCAG	130339
Qy	25441	CAATAGCTATTAATAAAACAAAGTATGTATATAGTCTATTAAGTATTAACATTTAAACA	25500
Db	130340	CAATAGCTATTAATAAAACAAAGTATGTATATAGTCTATTAAGTATTAACATTTAAACA	130399
Qy	25501	AAATTAATAAATTAATAATCTGTATATTTGCGTAACATATAGAGTATGTATATAGGTG	25560
Db	130400	AAATTAATAAATTAATAATCTGTATATTTGCGTAACATATAGAGTATGTATATAGGTG	130459
Qy	25561	TAAAGCTGTGTGTAGTTTGTGTATATGCAATTAAGTCCCAAGTGTAAATTAATA	25620
Db	130460	TAAAGCTGTGTGTAGTTTGTGTATATGCAATTAAGTCCCAAGTGTAAATTAATA	130519
Qy	25621	AAATTAATGTAGTATTAATTTTAAAGTTTATATCTATATCAAGTAATTTCAAGTGT	25680
Db	130520	AAATTAATGTAGTATTAATTTTAAAGTTTATATCTATATCTATTTCAAGTAATTTCAAGTGT	130579
Qy	25681	GTCATACCTGGCTAAATTTGCAACCAAGATCCAAATTAATCTGTATGTATGTTTGTTC	25740
Db	130580	GTCATACCTGGCTAAATTTGCAACCAAGATCCAAATTAATCTGTATGTATGTTTGTTC	130639
Qy	25741	CATAGCCACATTAACATTAACACAAATGGGCAATTAATTTACTGGCAACGCGCAT	25800
Db	130640	CATAGCCACATTAACATTAACACAAATGGGCAATTAATTTACTGGCAACGCGCAT	130699
Qy	25801	ACTTTGTATTTGGAGTCCACATTAAGAAATCCGTAAAGTAAACAGTCCATCCATGTT	25860
Db	130700	ACTTTGTATTTGGAGTCCACATTAAGAAATCCGTAAAGTAAACAGTCCATCCATGTT	130759
Qy	25861	GGTCCACAGAGACATGATGTTGTTTACTAGAAACAAATTTTCGGTGTATTAACA	25920
Db	130760	GGTCCACAGAGACATGATGTTTACTAGAAACAAATTTTCGGTGTATTAACA	130819
Qy	25921	AATATTAATATGCTTGAAATTAATTAACAAACATTAATTTAAGGCCAATATCATAGTA	25980
Db	130820	AATATTAATATGCTTGAAATTAATTAACAAACATTAATTTAAGGCCAATATCATAGTA	130879
Qy	25981	AACAACCTTTAAACAGTAAAGATGTCGTCTCTATGTAATTAATGATATCGCATGC	26040
Db	130880	AACAACCTTTAAACAGTAAAGATGTCGTCTCTATGTAATTAATGATATCGCATGC	130939
Qy	26041	AATGACACTACAGCTGTGTACCAAAATTAATTCGTTGTCGAAGGCCAATGCGATAGTA	26100
Db	130940	AATGACACTACAGCTGTGTGTACCAAAATTAATTCGTTGTCGAAGGCCAATGCGATAGTA	130999
Qy	26101	AACACACATGCTGCAACAAATGTAACAAATTAATTAATTTGCTAATTAATTAATTA	26160
Db	131000	AACACACATGCTGCAACAAATGTAACAAATTAATTAATTTGCTAATTAATTAATTA	131059
Qy	26161	TATTTCAATGATTAATTAATTAATCTACTCTGTAATCCATGGGAAAAAATGAAGGCAAG	26220
Db	131060	TATTTCAATGATTAATTAATTAATCTACTCTGTAATCCATGGGAAAAAATGAAGGCAAG	131119
Qy	26221	GAGTTAATTTGACCTGCTCTGCTTGATTAACATTAACAACTAATAGTTTTCATTAAGAAG	26280
Db	131120	GAGTTAATTTGACCTGCTCTGCTTGATTAACATTAACAACTAATAGTTTTCATTAAGAAG	131179
Qy	26281	AACAACAGTAAACAAATGAAACAAATTAATGTGACTGCTGATTAAGAAGTCCCTGGCAT	26340
Db	131180	AACAACAGTAAACAAATGAAACAAATTAATGTGACTGCTGATTAAGAAGTCCCTGGCAT	131239
Qy	26341	GTTGTACCAAGGCTATTAATCCAAACGTTAATGTAAGAAGTTTGTAAAGTAACCACTAC	26400
Db	131240	GTTGTACCAAGGCTATTAATCCAAACGTTAATGTAAGAAGTTTGTAAAGTAACCACTAC	131299
Qy	26401	TCCAAATTAATAAAGGTATAGTACAGCCCAATTTTAAATATCAAAAAGTATATTAACAAG	26460
Db	131300	TCCAAATTAATAAAGGTATAGTACAGCCCAATTTTAAATATATCAAAAAGTATATTAACAAG	131359
Qy	26461	TTAAGGGGAGTTTGACCTTTAAAGGTTGTTATACATCGTTTCCAGGCAAACTCCACACT	26520
Db	131360	TTAAGGGGAGTTTGACCTTTAAAGGTTGTTATACATCGTTTCCAGGCAAACTCCACACT	131419
Qy	26521	GAGTCCACAAAGGTTTCTGTGTGCCCCCTGACGGGAATCTGCCCTTAATGTGATTTTGT	26580
Db	131420	GAGTCCACAAAGGTTTCTGTGTGCCCCCTGACGGGAATCTGCCCTTAATGTGATTTTGT	131479

OY	26561	TGGCACCACCAAGAAATCATGTGAAAGACAGAGTGGGAATATTTGTTTGTTCGTTG	26640
Db	131480	TGGCAACCAACCAAGAAATCATGTGAAAGACAGAGTGGGAATATTTGTTTGTTCGTTG	131539
OY	26641	GCGTGAATGCTTGGAAACATTCCTGTTATTTGATGTATGGCCAACTGTGGAAACATT	26700
Db	131540	GCGTGAATGCTTGGAAACATTCCTGTTATTTGATGTATGGCCAACTGTGGAAACATT	131599
OY	26701	AAGAGTTGTATTTGAAATATTTTTTGGTAACAAAACATGTTTTAGTCCCAAGAGAA	26760
Db	131600	AAGAGTTGTATTTGAAATATTTTTTGGTAACAAAACATGTTTTAGTCCCAAGAGAA	131659
OY	26761	CATAAAAATGTTTAAATAGAACATCGCTTAGTACAGAACATTTTGTGTGTAGCTAACTA	26820
Db	131660	CATAAAAATGTTTAAATAGAACATCGCTTAGTACAGAACATTTTGTGTGTAGCTAACTA	131719
OY	26821	AAAAATATGTATGTAAAGGGCTTAAGGGGTAAAGGCAAGGGGTAAAGGGCTTAAGGGCA	26880
Db	131720	AAAAATATGTATGTAAAGGGCTTAAGGGGTAAAGGCAAGGGGTAAAGGGCTTAAGGGCA	131779
OY	26881	AGGGGTAAAGGGCAAGGGGTAAAGGCAAGGGGTAAAGGGGTAAAGGGCAAGGGGTAA	26940
Db	131780	AGGGGTAAAGGGCAAGGGGTAAAGGCAAGGGGTAAAGGGGTAAAGGGGTAAAGGGGTAA	131839
OY	26941	GGGCAAGGGGTAAAGGCAAGGGGTAAAGGCAAGGGGTAAAGGGGTAAAGGGCTTAGG	27000
Db	131840	GGGCAAGGGGTAAAGGCAAGGGGTAAAGGCAAGGGGTAAAGGGGTAAAGGGCTTAGG	131899
OY	27001	GGTAAAGGCTTAAGGGGTAAAGGGGTAAAGGGGTAAAGGGGTAAAGGGGTAAAGGTATAG	27060
Db	131900	GGTAAAGGCTTAAGGGGTAAAGGGGTAAAGGGGTAAAGGGGTAAAGGGGTAAAGGTATAG	131959
OY	27061	GTAAATATATAGCCCTACGATAAAAATGTCACATATATTTTAAATTTGTGTTCACTAA	27120
Db	131960	GTAAATATATAGCCCTACGATAAAAATGTCACATATATTTTAAATTTGTGTTCACTAA	132019
OY	27121	CAGCCATGCTGATATATAGATTAAGGTTAAAGCTTCAATATCAATATACAGTAAAGTAA	27180
Db	132020	CAGCCATGCTGATATATAGATTAAGGTTAAAGCTTCAATATCAATATACAGTAAAGTAA	132079
OY	27181	CCACACGAATTTATACATATTTTACAAAAAGCAACCAACTGGCACAATGTAACCTACGC	27240
Db	132080	CCACACGAATTTATACATATTTTACAAAAAGCAACCAACTGGCACAATGTAACCTACGC	132139
OY	27241	TACCTTAAACGTACATATCTGGGACTAGAACCCAGAGGTAGTTAGATATATACGGTAGTTA	27300
Db	132140	TACCTTAAACGTACATATCTGGGACTAGAACCCAGAGGTAGTTAGATATATACGGTAGTTA	132199
OY	27301	CAGAACTTGCAGTTCCTTACAGCCAGCAGAGGGCTCTGCGCGTTAATTAACAAAGTTTAA	27360
Db	132200	CAGAACTTGCAGTTCCTTACAGCCAGCAGAGGGCTCTGCGCGTTAATTAACAAAGTTTAA	132259
OY	27361	GATTACTGAATTTTAGAAGTGGCGATATGGTATGTTTCCAAATATAGGCAAGGGTT	27420
Db	132260	GATTACTGAATTTTAGAAGTGGCGATATGGTATGTTTCCAAATATAGGCAAGGGTT	132319
OY	27421	ACATAAACTGTTGCTTAGCGGCGCCGAGGCGCCGCGCGCGCGCGCGCGCGCGCGG	27480
Db	132320	ACATAAACTGTTGCTTAGCGGCGCCGAGGCGCCGCGCGCGCGCGCGCGCGCGCGG	132379
OY	27481	GGGGCGCGCATTTTGGCGCCCGGGGGCGAGGGTCCCGCGCGCGCCCGCGCGCGCG	27540
Db	132380	GGGGCGCGCATTTTGGCGCCCGGGGGCGAGGGTCCCGCGCGCGCCCGCGCGCGCG	132439
OY	27541	GGGGCGCGCGCGCTCCCGCGGCTCCCGGCTCCCGCGCCCGCGCGCGCGCGCGCGG	27600
Db	132440	GGGGCGCGCGCGCTCCCGCGGCTCCCGGCTCCCGCGCCCGCGCGCGCGCGCGCGG	132499
OY	27601	GCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCTTTCGGTTTCGCGGCGCGGGGT	27660
Db	132500	GCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCTTTCGGTTTCGCGGCGCGGGGT	132559

QY	27661	CCCGCGGGGGCGGGGGCGCGCCCGCGGGTGCCTCTCCCGGGGCCCGGACACTCCGGG	27720
Db	132560	CCCCCGGGGGGGCGGGGGCGCCCCCGGGTGCCTCTCCCGGGGCCCGGACACTCCCGGG	132611
QY	27721	AGCGCCCCGGTCCGGCGGAGACCCCGGGGGGGCGCGCCCCGAGCGCCCGCGGGGCCGGGGC	27780
Db	132620	AGCGCCCCGGTCCGGCGGAGACCCCGGGGGGGCGCGCCCCGAGCGCCCGCGGGGCCGGGGC	132677
QY	27781	CCGCAAGCCGCGCGCGCGGGCTCCGATGCGGGGCGCGCCCGCGCGGCAATGCGGGTCC	27840
Db	132680	CCGCAAGCGCGGGCGCGGGGGTCCGAGATCCGGGGGGCGCGCCCGCGGCAATGCGGGTCC	132733
QY	27841	TCGCGCGGGCTCCCCCTCCCGACGCGCCCGCCGAAAGTGTCTCCGCGCGCCCGGAGAGG	27900
Db	132740	TCGCGCGGGCTCCCCCTCCCGACGCGCCCGCCGAAAGTGTCTCCGCGCGCCCGGAGAGG	132799
QY	27901	GGGCGGGGGGCGGGGGGGCGCTCGGGGGGGCGCGCGCGGGGGGGGACCGAGGGGCCCGGG	27960
Db	132800	GGGCGGGGGGCGGGGGGGCGCTCGGGGGGGCGCGCGCGGGGGGGGACCGAGGGGCCCGGG	132855
QY	27961	AGAACGGGGGATCGGGAAAAACGGAGGGGAGCGGGGACAGGGGAGCGGCGTTCGGTCT	28020
Db	132860	AGAACGGGGGATCGGGAAAAACGGAGGGGAGCGGGGACAGGGGAGCGGCGTTCGGTCT	132921
QY	28021	TGTGAGACACCGGGGTACGGCTGCTTCCTGCTGCTGCGCTCTCTTGTGAGGGGACACTA	28080
Db	132920	TGTGAGACACCGGGGTACGGCTGCTTCCTGCTGCTGCGCTCTCTTGTGAGGGGACACTA	132977
QY	28081	GGCGTGTTCCTCGCGTGGCGCTGCTTCTGTAGGGGACAGTAGGCGCTGTTGCTGAGGGGAC	28140
Db	132980	GGCGTGTTCCTCGCGTGGCGCTGCTTCTGTAGGGGACAGTAGGCGCTGTTGCTGAGGGGAC	133033
QY	28141	AGTAGGCGCTCTTGCTCGTGGCGCTGCTTGTGTAGAGGGGAGCACTAGAGGCGTGGCTTGTCT	28200
Db	133040	AGTAGGCGCTCTTGCTCGTGGCGCTGCTTGTGTAGAGGGGAGCACTAGAGGCGTGGCTTGTCT	133099
QY	28201	AGTAGGCGCTCTGCGTGGCGCTGCTTGTGTCTGCTGCTGCGCTCTTGTGCTCCGTGGCC	28260
Db	133100	AGTAGGCGCTCTGCGTGGCGCTGCTTGTGTCTGCTGCTGCGCTCTTGTGCTCCGTGGCC	133155
QY	28261	TGCTATGCTTCCTCGCGTGGCGCTGCTTGTGTGTGCTGCGCGCTGTTGCTTGGTGGCG	28320
Db	133160	TGCTATGCTTCCTCGCGTGGCGCTGCTTGTGTGTGCTGCGCGCTGTTGCTTGGTGGCG	133211
QY	28321	TGCTATGCTTCCTCGCGTGGCGCTGCTTGTGTGTGCTGCGCGCTGTTGCTGAGGGGACACTA	28380
Db	133220	TGCTATGCTTCCTCGCGTGGCGCTGCTTGTGTGTGCTGCGCGCTGTTGCTGAGGGGACACTA	133277
QY	28381	GGGCTGCTTCGTTGCTTAGGGGAGCGTAGCGCTCGCTGATAGGCTTGTAGTAGGGCTCTCT	28440
Db	133280	GGGCTGCTTCGTTGCTTAGGGGAGCGTAGCGCTCGCTGATAGGCTTGTAGTAGGGCTCTCT	133333
QY	28441	GGGCTGCTTAGTAGGGGCTGCTGGGCGCTGTAGTAGGCGTCTGGGGCGTGTAGTAGGGCTCT	28500
Db	133340	GGGCTGCTTAGTAGGGGCTGCTGGGCGCTGTAGTAGGCGTCTGGGGCGTGTAGTAGGGCTCT	133399
QY	28501	GGGCTGCTTAGTAGGGGCTCGTGGGCGCTGTAGTAGGCGTCTGGGCGTGTAGTAGGGCTCT	28560
Db	133400	GGGCTGCTTAGTAGGGGCTCGTGGGCGCTGTAGTAGGCGTCTGGGCGTGTAGTAGGGCTCT	133455
QY	28561	GGGCTGCTTAGTAGGGGCTGCTGGGCGCTGTAGTAGGCGTCTGGGCGTGTAGTAGGGCTCT	28620
Db	133460	GGGCTGCTTAGTAGGGGCTGCTGGGCGCTGTAGTAGGCGTCTGGGCGTGTAGTAGGGCTCT	133511
QY	28621	GGGCTGCTTAGTAGGGGCTGCTGGGCTGTGCTTGTGCTGTAGTAGGGGCGCGCTTGGC	28680
Db	133520	GGGCTGCTTAGTAGGGGCTGCTGGGCTGTGCTTGTGCTGTAGTAGGGGCGCGCTTGGC	133577
QY	28681	TGTGACTAGAGGGCTGTGACGTGGGAGAAAGATAGGGCGCGCGGCACTCTCGTGC	28740
Db	133580	TGTGACTAGAGGGCTGTGACGTGGGAGAAAGATAGGGCGCGCGGCACTCTCGTGC	133633
QY	28741	GAGGGCGCTCGAGGGGCGAGACGAGGACACGGGACCCGGGCGCTCTCCCGCGCGGACCGC	28800

```

Db      133640 GAGGGGCTCCGAGGGCCAGACGAGACCGGGGCTCTCCCGCCGCGACCGC 133699
QY      28801 CGGGCACCCGCCAGATCT 28820
Db      133700 CGGGCACCCGCCAGATCT 133719

RESULT 3
AAI64291/c
ID      AAI64291 standard; DNA; 128139 BP.
XX
AC      AAI64291;
XX
DT      22-APR-2002 (first entry)
XX
DE      RRV genome nucleotide sequence.
XX
KM      RRV; rhesus rhadinovirus; japanese macaque virus; multiple sclerosis;
KM      JMHV; cytosolic; antiaesthetic; antiallergic; dermatological;
KM      vulnary; gene therapy; leucopenia; thrombocytopenia;
KM      inflammatory disease; asthma; allergy; dermatitis; virus; ds.
XX
XX      Macaca mulatta rhadinovirus 17577.
XX
FH      Key
FT      CDS
FT      1353..2674
FT      /tag= a
FT      /product= "RRV R1"
FT      complement (2692..3258)
FT      /tag= b
FT      /product= "dihydrofolate reductase"
FT      /label= RRV_ORF2
FT      /note= "has similarity to Kaposi's sarcoma-associated
FT      virus (KSHV) open reading frame (ORF) 2"
FT      3676..5613
FT      /tag= c
FT      /product= "complement binding protein"
FT      /label= RRV_ORF4
FT      /note= "has similarity to KSHV ORF4"
FT      6045..9443
FT      /tag= d
FT      /product= "ssDNA binding protein"
FT      /label= RRV_ORF6
FT      /note= "has similarity to KSHV ORF6"
FT      9468..11528
FT      /tag= e
FT      /product= "transport protein"
FT      /label= RRV_ORF7
FT      /note= "has similarity to KSHV ORF7"
FT      11515..14004
FT      /tag= f
FT      /product= "glycoprotein B"
FT      /label= RRV_ORF8
FT      /note= "has similarity to KSHV ORF8"
FT      14122..17166
FT      /tag= g
FT      /product= "DNA polymerase protein"
FT      /label= RRV_ORF9
FT      /note= "has similarity to KSHV ORF9"
FT      17261..18511
FT      /tag= h
FT      /label= RRV_ORF10
FT      /note= "has similarity to KSHV ORF10"
FT      18520..19749
FT      /tag= i
FT      /label= RRV_ORF11
FT      /note= "has similarity to KSHV ORF11"
FT      complement (19921..20544)
FT      /tag= j
FT      /product= "RRV R2"
FT      /label= RRV_ORF
FT      /note= "has similarity to KSHV interleukin (IL)-6 gene"

```

```

FT      CDS
FT      complement (20777..21778)
FT      /tag= k
FT      /product= "thymidylate synthase"
FT      /label= RRV_ORF70
FT      /note= "has similarity to KSHV ORF70"
FT      complement (22245..22592)
FT      /tag= l
FT      /product= "RRV R3"
FT      /note= "has similarity to KSHV R4 viral MIP gene"
FT      26846..27409
FT      /tag= m
FT      /product= "Bcl2-homologue"
FT      /label= RRV_ORF16
FT      /note= "has similarity to KSHV ORF16"
FT      complement (27515..29125)
FT      /tag= n
FT      /label= RRV_ORF17
FT      /note= "has similarity to KSHV ORF17"
FT      28998..29897
FT      /tag= o
FT      /label= RRV_ORF18
FT      /note= "has similarity to KSHV ORF18"
FT      complement (29905..31548)
FT      /tag= p
FT      /product= "tegument protein"
FT      /label= RRV_ORF19
FT      /note= "has similarity to KSHV ORF19"
FT      complement (31043..32095)
FT      /tag= q
FT      /label= RRV_ORF20
FT      /note= "has similarity to KSHV ORF20"
FT      32094..33767
FT      /tag= r
FT      /product= "thymidine kinase"
FT      /label= RRV_ORF21
FT      /note= "has similarity to KSHV ORF21"
FT      33754..35868
FT      /tag= s
FT      /product= "glycoprotein H"
FT      /label= RRV_ORF22
FT      /note= "has similarity to KSHV ORF22"
FT      complement (35865..37073)
FT      /tag= t
FT      /label= RRV_ORF23
FT      /note= "has similarity to KSHV ORF23"
FT      complement (37123..39321)
FT      /tag= u
FT      /label= RRV_ORF24
FT      /note= "has similarity to KSHV ORF24"
FT      39323..43459
FT      /tag= v
FT      /product= "major capsid protein"
FT      /label= RRV_ORF25
FT      /note= "has similarity to KSHV ORF25"
FT      43491..44408
FT      /tag= w
FT      /product= "capsid protein"
FT      /label= RRV_ORF26
FT      /note= "has similarity to KSHV ORF26"
FT      44433..45242
FT      /tag= x
FT      /label= RRV_ORF27
FT      /note= "has similarity to KSHV ORF27"
FT      45408..45683
FT      /tag= y
FT      /label= RRV_ORF28
FT      /note= "has similarity to KSHV ORF28"
FT      complement (45733..46779)
FT      /tag= z
FT      /label= RRV_ORF29b
FT      /note= "has similarity to KSHV ORF29b"
FT      46905..47135
FT      /tag= aa
FT      CDS

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FT /label- RRV_ORF30
FT /note- "has similarity to KSHV ORF30"
FT CDS 47093..47746
FT /tag- ab
FT /label- RRV_ORF31
FT /note- "has similarity to KSHV ORF31"
FT CDS 47683..49077
FT /tag- ac
FT /label- RRV_ORF32
FT /note- "has similarity to KSHV ORF32"
FT CDS 49049..50059
FT /tag- ad
FT /label- RRV_ORF33
FT /note- "has similarity to KSHV ORF33"
FT CDS complement (49977..50960)
FT /tag- ae
FT /label- RRV_ORF29a
FT /note- "has similarity to KSHV ORF29a"
FT CDS 50959..51942
FT /tag- af
FT /label- RRV_ORF34
FT /note- "has similarity to KSHV ORF34"
FT CDS 51923..52372
FT /tag- ag
FT /label- RRV_ORF35
FT /note- "has similarity to KSHV ORF35"
FT CDS 52278..53585
FT /tag- ah
FT /product- "kinase"
FT /label- RRV_ORF36
FT /note- "has similarity to KSHV ORF36"
FT CDS 53566..55008
FT /tag- ai
FT /product- "alkaline exonuclease"
FT /label- RRV_ORF37
FT /note- "has similarity to KSHV ORF37"
FT CDS 54963..55172
FT /tag- aj
FT /label- RRV_ORF38
FT /note- "has similarity to KSHV ORF38"
FT CDS complement (55255..56391)
FT /tag- ak
FT /product- "glycoprotein M"
FT /label- RRV_ORF39
FT /note- "has similarity to KSHV ORF39"
FT CDS 56526..57932
FT /tag- al
FT /product- "helicase/primase"
FT /label- RRV_ORF40
FT /note- "has similarity to KSHV ORF40"
FT CDS 57917..58528
FT /tag- am
FT /product- "helicase/primase"
FT /label- RRV_ORF41
FT /note- "has similarity to KSHV ORF41"
FT CDS complement (58525..59343)
FT /tag- an
FT /label- RRV_ORF42
FT /note- "has similarity to KSHV ORF42"
FT CDS complement (59297..61027)
FT /tag- ao
FT /product- "capsid protein"
FT /label- RRV_ORF43
FT /note- "has similarity to KSHV ORF43"

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Query Match 0.1%; Score 33; DB 24; Length 128139;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12644 ATATATATAGGAAGCTGTAAACAACCCCAAC 12676
 DB 18331 ATATATATAGGAAGCTGTAAACAACCCCAAC 18299

```

RESULT 4
AAC64754/C
ID AAC64754 standard; DNA; 133719 BP.
XX
XX AAC64754;
AC
XX 28-FEB-2001 (first entry)
DE
XX Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1.
XX
XX Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
XX genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;
XX IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
XX cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
XX lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
XX splenomegaly; hypergammaglobulinemia; autoimmune haemolytic anaemia;
XX ds.
XX
XX Macaca mulatta rhadinovirus 17577.
XX
XX WO200028040-A2.
XX
XX 18-MAY-2000.
XX
XX 05-NOV-1999; 99WO-US26260.
XX
XX 06-NOV-1998; 98US-0107507.
XX 20-NOV-1998; 98US-0109409.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Wong SW, Axthelm MK, Searles RP;
XX WPI. 2000-376552/32.
XX
XX New rhesus rhadno virus for producing non-human primate model useful
XX for testing potential treatments and efficacy of the candidate vaccine
XX for conditions associated with RRV infection
XX
XX Claim 2; Page 83-122; 141pp; English.
XX
XX The present invention describes a novel rhesus macaque rhadinovirus
XX called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
XX RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
XX encoded by the genome sequence. The present invention also specifically
XX claims the individual open reading frame (ORF) nucleotide sequences from
XX the genome which encode the individual proteins, but these sequences are
XX not given. A non-human animal infected with RRV can be used for testing
XX the efficacy of drug in the treatment of condition associated with
XX infection with RRV such as Kaposi's sarcoma, lymphoproliferative
XX disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
XX hypergammaglobulinemia or autoimmune haemolytic anaemia, by
XX administering the drug to a immuno-compromised non-human primate
XX preferably Rhesus macaque monkey obtained by as a result of infection
XX by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
XX non-human primate model for testing potential treatments for conditions
XX associated with RRV infection. It is also useful for testing the
XX efficacy of the candidate vaccine against RRV infection or conditions
XX associated with its infection by administering the vaccine to the
XX CC subject capable of infection with RRV, inoculating the subject with RRV
XX CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
XX CC to AAB53213 represent sequence used in the exemplification of the
XX CC present invention.
XX
XX Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;
SQ

```

Query Match 0.1%; Score 33; DB 21; Length 133719;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12644 ATATATATAGGAAGCTGTAAACAACCCCAAC 12676

DB 23911 ATATATATAGGAGACTTGTAACAAACCCAC 23879

RESULT 5
AAC81583/c
ID AAC81583 standard; DNA; 3571 BP.
XX
XX AAC81583;
XX
XX 09-MAR-2001 (first entry)
XX
XX Mouse zvegfg3 DNA, SEQ ID NO:34.
DE
XX
XX Mouse; zvegfg3; zvegfg4 fusion; growth factor homologue; VEGF/PDGF family;
KM murine; CUB domain; PDGF-like activity; mitogenic; osteogenic;
KM neovascularisation; tissue repair; proliferation; differentiation;
KM liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KM periodontal disease; bone fracture; wound healing; vulnerrary; ischaemia;
KM immunomodulation; hepatic; ds.
XX
XX Mus musculus.
XX
XX WO200066736-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US40047.
XX
XX 03-MAY-1999; 99US-0304216.
XX 10-NOV-1999; 99US-0164463.
XX 04-FEB-2000; 2000US-0180169.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI
PI WPI: 2000-687541/67.
DR P-PSDB; AAB48658.
XX
XX Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -
XX
XX Disclosure; Page 127-130; 143pp; English.

The invention relates to the human growth factor homologue zvegfg4 (AAB48653), and nucleic acids encoding it (AAC81555). zvegfg4 is a member of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial growth factor) family. zvegfg4 has a growth factor domain (AAB48654) characterised by a PDGF cystine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. zvegfg4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3 fusions; expression constructs and host cells comprising human zvegfg4 nucleic acids; the recombinant expression of human zvegfg4; an antibody which binds to human zvegfg4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zvegfg4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegfg4 gene of a patient. zvegfg4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischemia, in wound healing, and in the modulation of the immune system. The present sequence represents DNA encoding mouse

CC zvegfg3.
XX
XX Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
SQ
Query Match 0.1%; Score 28; DB 21; Length 3571;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16376 GCGCGCGCGCGCGCGCGCGCGCGCG 16403
DB 184 GCGCGCGCGCGCGCGCGCGCGCGCGCG 157

RESULT 6
AAA51527/c
ID AAA51527 standard; cDNA; 3571 BP.
XX
XX AAA51527;
AC
XX 26-SEP-2000 (first entry)
DT
XX
XX Murine vascular endothelial growth factor homologue, ZVEGF3 DNA.
DE
XX
XX Vascular endothelial growth factor; homologue; zvegfg3; CUB domain;
KM Cystine knot; platelet-derived growth factor; PDGF; neuropilin;
KM chromosome 4q28.3; cytosstatic; anti-psoriatic; anti-inflammatory;
KM anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
KM vulnerrary; ss.
XX
XX Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT CDS 1049..2086
FT /tag= a
FT /product= ZVEGF3
XX
XX WO200034474-A2.
XX
XX 15-JUN-2000.
XX
XX 07-DEC-1999; 99WO-US28968.
XX
XX 07-DEC-1998; 98US-0207120.
XX 06-JUL-1999; 99US-0142576.
XX 21-OCT-1999; 99US-0161653.
XX 12-NOV-1999; 99US-0165255.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
PI Gilbertson DG, West JW;
PI
XX
XX WPI: 2000-423420/36.
DR P-PSDB; AAY96861.
XX
XX Novel zvegfg3 polypeptides and nucleotides encoding them useful for
PT stimulating growth of smooth muscle cells and fibroblasts comprising an
PT epitope bearing portion of a specific amino acid sequence
PT
XX
PS Claim 30; Page 166-169; 173pp; English.

This DNA encodes murine ZVEGF3 a novel vascular endothelial growth factor homologue. Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3 are claimed. The growth factors comprise a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY96859 and AAY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta-strands that is characteristic of the "cystine knot" structure of the platelet-derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in neuropilins, human bone morphogenetic protein-1, porcine seminal plasma protein, bovine acidic seminal fluid protein and Xenopus laevis tolloid-like protein. Structural analysis and homology to form multimeric ZVEGF3 polypeptides complex with a second polypeptide to form multimeric

CC proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3.
 CC ZVGF3 is useful for stimulating the growth of fibroblasts or smooth
 CC muscle cells, for activating cell surface PDGF- α receptor and for
 CC inhibiting PDGF- α receptor mediated cellular processes. ZVEGF3 is
 CC useful for regulating (post-development) organ growth, regeneration and
 CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3
 CC antagonists are useful for treating cancer, rheumatoid arthritis,
 CC diabetic retinopathy, ischemic limb disease, peripheral vascular
 CC disease, myocardial ischemia, vascular intimal hyperplasia,
 CC atherosclerosis, wound healing, chronic liver disease and haemangioma
 CC formation. ZVEGF3 can also be used to modulate neurite growth and
 CC development of the nervous system, and for treating neurodegenerative
 CC diseases.
 CC XX

SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;

Query Match 0.1%; Score 28; DB 21; Length 3571;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16376 GCGGGCGCGGGGGCGGGGGCGCG 16403
 ||||||||||||||||||||||||||||
 Db 184 GCGGGCGCGGGGGCGGGGGCGCGCG 157

RESULT 7
 AD04650/C
 ID AD04650 standard; DNA: 3571 BP.
 AC AD04650;
 XX 04-JUL-2001 (first entry)
 DT
 DE Mouse zvegf3 DNA.
 XX

Mouse; zvegf3 antagonist; cell proliferation; stellate cell activation;
 KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
 KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;
 KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
 KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
 KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
 KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
 KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
 KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
 KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
 KW fibropoliferative disorder; ds.
 KW XX

OS Mus musculus.
 XX

Key Location/Qualifiers
 FH CDS 1049..2086
 FT /*tag= a
 FT /product= "Mouse zvegf3 protein"
 FT XX

W0200128586-A1.
 PN
 XX 26-APR-2001.
 PD
 XX 23-OCT-2000; 2000WO-US29270.
 PF
 XX 21-OCT-1999; 99US-0161653.
 PR 12-NOV-1999; 99US-0165255.
 PR 01-AUG-2000; 2000US-0222223.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Glibertson DG;
 PI
 XX WPI: 2001-300278/31.
 DR P-PSDB; AAE00998.
 DR
 XX Use of zvegf3 antagonist for reducing fibropoliferative disorder of
 PT kidney, liver and bone, reducing extracellular matrix production,

PT treating fibrosis or reducing stellate cell activation in mammal -
 XX
 XX Example 2; Page 58-61; 70pp; English.
 XX

CC The patent discloses materials and methods for reducing cell
 CC proliferation or extracellular matrix production, treating fibrosis and
 CC reducing stellate cell activation in a mammal. The method comprises
 CC administering a composition containing a zvegf3 antagonist in combination
 CC with a delivery vehicle. The zvegf3 is a protein that is structurally
 CC related to platelet-derived growth factor (PDGF) and the vascular
 CC endothelial growth factors (VEGF). The zvegf3 protein is also designated
 CC as "VEGF-R" and "PDGF-C". The zvegf3 antagonist is useful to block the
 CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
 CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
 CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and
 CC alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as
 CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
 CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
 CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
 CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
 CC fibrotic disorders of pancreas, fibropoliferative disorders of the
 CC vasculature such as transplant vasculopathy and fibropoliferative
 CC disorders of the bone such as osteopetrosis and hyperostosis.
 CC The present sequence is mouse zvegf3 DNA.
 CC XX

SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;

Query Match 0.1%; Score 28; DB 22; Length 3571;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16376 GCGGGCGCGGGGGCGGGGGCGCGCG 16403
 ||||||||||||||||||||||||||||
 Db 184 GCGGGCGCGGGGGCGGGGGCGCGCGCG 157

RESULT 8
 ABS68648/C
 ID ABS68648 standard; cDNA: 3571 BP.
 AC ABS68648;
 XX 19-NOV-2002 (first entry)
 DT
 DE Mouse cDNA encoding VEGF-like protein zvegf 3.
 XX

ss; gene; VEGF; vascular endothelial growth factor; zvegf 3;
 KW chromosome 3; cell proliferation; differentiation; metabolism;
 KW migration; revascularisation; solid tumour; diabetic retinopathy;
 KW psoriasis; rheumatoid arthritis; cancer; autoimmune disease;
 KW inflammation; myocardial ischaemia; scleroderma; fibrosis; mouse;
 KW glomerulosclerosis; atherosclerosis; skin wound; ulcer; burn;
 KW skin grafting; female reproductive tract disorder; chronic liver disease;
 KW circulatory disorder; heart failure; neurodegenerative disease;
 KW multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;
 KW neurite outgrowth.
 KW XX

OS Mus musculus.
 XX

US6432673-B1.
 FN
 XX 13-AUG-2002.
 PD
 XX 07-DEC-1999; 99US-0457066.
 PF
 XX 07-DEC-1998; 98US-111173P.
 PR 06-JUL-1999; 99US-142576P.
 PR 21-OCT-1999; 99US-161653P.
 PR 12-NOV-1999; 99US-165255P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Gao Z, Hart CE, Piddington GS, Sheppard PO, Shoemaker KE;
 PI

PI Gilbertson DG, West JW;
 XX WPI, 2002-689759/74.
 DR P-PSDB; ABG92894.
 XX Novel polypeptide, designated zvegf3 useful for treating skin wounds,
 PT ulcers, burns, skin grafting, female reproductive tract disorders,
 PT Parkinson's disease, and Alzheimer's disease -
 XX Example 4; Column 97-104; 68pp; English.
 XX
 CC The invention relates to an isolated polypeptide, designated zvegf3
 CC (a vascular endothelial growth factor-like protein) of 111-136 amino acid
 CC residues in length and comprises the sequence appearing as ABG92889
 CC from amino acid residues 235-345. Also included are an isolated
 CC protein comprising a first polypeptide disulphide bonded to a second
 CC polypeptide, where each of the first and second polypeptides is from
 CC zvegf 3, and where the protein modulates cell proliferation,
 CC differentiation, metabolism or migration, the zvegf 3 encoding
 CC polynucleotides and zvegf 3 expression vectors and host cells.
 CC Zvegf 3 is useful as additives in tissue adhesives for promoting
 CC revascularisation of the healing tissue, for designing molecules that
 CC antagonise semaphorin-stimulated activities, including neurite growth,
 CC cardiovascular development, cartilage and limb development, and T and
 CC B-cell function, and for imaging tumours or other sites of abnormal cell
 CC proliferation and in gene therapy applications. The proteins are useful
 CC therapeutically to stimulate tissue development or repair, or cellular
 CC differentiation or proliferation, for stimulating the growth of
 CC fibroblast or smooth muscle cells, as molecular weight standards, as
 CC reagents in assays for determining circulatory level of the protein or as
 CC standards in the analysis of cell phenotype, for identifying inhibitors
 CC of their activity which are useful for reducing the growth of solid
 CC tumours, for treating diabetic retinopathy, psoriasis, rheumatoid
 CC arthritis, various forms of cancers, autoimmune disease, inflammation,
 CC myocardial ischaemia, scleroderma, and reducing fibrosis, including scar
 CC formation, keloids, liver fibrosis, lung fibrosis (e.g. silicosis,
 CC asbestosis), kidney fibrosis (including diabetic nephropathy),
 CC glomerulosclerosis, atherosclerosis, skin wounds, ulcers, burns, skin
 CC grafting, and female reproductive tract disorders, chronic liver disease
 CC (hepatitis), cirrhosis, Reye's syndrome, Wilson's disease, circulatory
 CC disorders e.g. heart failure, hepatic or portal vein thrombosis, cardiac
 CC sclerosis, neurodegenerative diseases such as multiple sclerosis,
 CC Parkinson's disease, Alzheimer's disease, and for regenerating neurite
 CC outgrowths following strokes. The gene for mouse zvegf3 is located on
 CC chromosome 3. The present sequence encodes zvegf 3.
 XX
 XX Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
 SQ
 CC Query Match 0.1%; Score 28; DB 24; Length 3571;
 CC Best Local Similarity 100.0%; Pred. No. 0.081;
 CC Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16376 GCGGGGCGGGGGCGGGGGCGCG 16403
 DB 184 GCGGGGCGGGGGCGGGGGCGCGCG 157
 RESULT 9
 AA172444/c
 ID AA172444 standard; cDNA; 3571 BP.
 XX
 AC AA172444;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Mouse zvegf3 coding sequence.
 XX
 KW Gene; human; mouse; zvegf3; zvegf4; platelet derived growth factor;
 KW PDGF; homolog; growth; bone; ligament; cartilage; proliferation;
 KW osteoblast; chondrocyte; bony defect; fracture; bone graft;
 KW implant; periodontal pocket; osteoclast; bone marrow stem cell;
 KW osteoporosis; ss.
 XX

OS Mus musculus.
 FH Key Location/Qualifiers
 FT CDS 1049..2086
 FT /*tag= a
 FT /product= "zvegf3"
 XX
 XX US2002004225-A1.
 XX
 XX 10-JAN-2002.
 PD
 XX
 PF 29-MAR-2001; 2001US-0823033.
 XX
 PR 07-DEC-1998; 98US-111173P.
 PR 06-JUL-1999; 99US-142576P.
 PR 21-OCT-1999; 99US-161653P.
 PR 12-NOV-1999; 99US-165255P.
 PR 31-MAR-2000; 2000US-193723P.
 PR 07-DEC-1999; 99US-0457066.
 XX
 PA (HART/) HART C E.
 PA (GILB/) GILBERTSON D G.
 XX
 PI Hart CE, Gilbertson DG;
 XX
 DR WPI, 2002-171026/22.
 DR P-PSDB; AAB47890.
 XX
 XX Promoting growth of bone, ligament or cartilage in a mammal, involves
 PT administering to the mammal a protein which comprises growth factor
 PT domain of zvegf3 protein, a homolog of platelet-derived growth factor
 PT -
 XX
 PS Disclosure; Page 16-19; 31pp; English.
 XX
 CC The sequences given in AA172443-44 encode human and mouse zvegf3,
 CC respectively. zvegf3 is a platelet derived growth factor (PDGF) homolog
 CC and it was used in the method of the invention for promoting growth of
 CC bone, ligament or cartilage and stimulating proliferation of osteoblasts
 CC or chondrocytes in a mammal. The proteins used were preferably a dimeric
 CC protein of residues 235-345 of human zvegf3 or all of the mouse zvegf3
 CC protein, with a delivery vehicle. The method of the invention is useful
 CC for promoting growth of bone, ligament or cartilage in a mammal, where
 CC the composition is administered at a site of a bony defect, preferably
 CC a fracture, bone graft site, implant site, or periodontal pocket, and
 CC for stimulating proliferation of osteoblasts or chondrocytes in a
 CC mammal. It is further useful for promoting proliferation of osteoblasts,
 CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
 CC marrow stem cells are harvested from a patient prior to culture. The
 CC method is therefore useful for treating osteoporosis.
 CC
 XX
 XX Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
 SQ
 CC Query Match 0.1%; Score 28; DB 24; Length 3571;
 CC Best Local Similarity 100.0%; Pred. No. 0.081;
 CC Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16376 GCGGGGCGGGGGCGGGGGCGCG 16403
 DB 184 GCGGGGCGGGGGCGGGGGCGCGCG 157
 RESULT 10
 ABX93182/c
 ID ABX93182 standard; DNA; 3571 BP.
 XX
 AC ABX93182;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE DNA encoding mouse growth factor homologue, zvegf3.
 XX
 KW Mouse; growth factor homologue; zvegf3; fibroblast; smooth muscle cell;
 XX

CC phenylmethyl sulphonyl fluoride. PACE 4 and 4.1 convert prorenin to
 CC renin in the human kidney, causing elevation of blood pressure.
 CC They can therefore be used to identify other inhibitors of their
 CC action and may also be used to inhibit blood coagulation.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 2218 BP; 534 A; 623 C; 623 G; 438 T; 0 other;

Query Match 0.1%; Score 27; DB 14; Length 2218;
 Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16377 GCGGGCGGGGGCGGGGGCGGG 16403
 |||||

Db 242 GCGGGCGGGGGCGGGGGCGGG 268

RESULT 12

AA594758
 ID AA594758 standard; DNA; 4361 BP.

XX
 AC AA594758;

DT 14-FEB-2002 (first entry)

XX Human DNA sequence #13 expressed during foam cell differentiation.

XX Human; foam cell differentiation; atherosclerosis; cerebral stroke;

KW cardiovascular disorder; coronary artery disease; gene therapy; ds.

XX Homo sapiens.

XX WO200177389-A2.

PD 18-OCT-2001.

PF 04-APR-2001; 2001WO-US11128.

PR 05-APR-2000; 2000US-195106P.

PA (INCY-) INCYTE GENOMICS INC.

XX Shiffman D, Somogyi R, Lawn R, Selhamer JJ, Porter GJ, Mikita T;
 PI Tai J;

DR WPI; 2002-010925/01.

XX Composition useful for diagnosis of conditions, disorders or diseases
 PT associated with atherosclerosis, comprises several polynucleotides that
 PT are differentially expressed in foam cell development -

XX Claim 1; Page 70-71; 315pp; English.

XX The present invention relates to the isolation of human polynucleotide
 CC sequences that are differentially expressed during foam cell
 CC differentiation. The polynucleotide sequences of the invention or a
 CC composition comprising these polynucleotides are useful as a high
 CC throughput method for detecting altered expression of one or more
 CC polynucleotides in a sample. The polynucleotides can be used in the
 CC diagnosis of disorders associated with foam cell development such as
 CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
 CC coronary artery disease. The polynucleotide sequences can also be used
 CC as PCR primers and probes. The polynucleotides of the invention are also
 CC useful in gene therapy. AA594746-AA595021 represent the human
 CC polynucleotide sequences of the invention which are differentially
 CC expressed during foam cell differentiation.

SQ Sequence 4361 BP; 1013 A; 1229 C; 1203 G; 916 T; 0 other;

Query Match 0.1%; Score 27; DB 24; Length 4361;
 Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16377 GCGGGCGGGGGCGGGGGCGGG 16403
 |||||

Db 200 GCGGGCGGGGGCGGGGGCGGG 226

RESULT 13

AA047927
 ID AA047927 standard; cDNA; 4403 BP.

XX
 AC AA047927;

DT 25-MAR-2003 (updated)

DT 24-MAR-1994 (first entry)

XX Paired basic amino acid converting enzyme (PACE) 4 gene.

XX Paired basic amino acid converting enzyme; PACE; prorenin; renin;
 KW hypertension; blood; coagulation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 170..3079
 FT /*tag= a
 FT /product= PACE 4.

XX WO9318159-A2.

PN 16-SEP-1993.

PF 09-MAR-1993; 93WO-US02147.

PR 09-MAR-1992; 92US-0848629.

PA (CHIR) CHIRON CORP.

XX Barr PJ, Kiefer MC;

XX WPI; 1993-303473/38.

DR P-PSDB; AAR41662.

XX New polynucleotide encoding PACE endo-peptidase - used for e.g.
 PT reducing blood pressure

XX Claim 1; Figure 1; 81pp; English.

XX The mammalian endopeptidases PACE 4 and PACE 4.1 (an alternative
 CC form of PACE 4) are involved in the production of mature
 CC polypeptides from precursor polypeptides by cleavage at pairs of
 CC basic amino acids e.g. Lys-Arg, Lys-Lys and Arg-Arg. The enzymes
 CC are stimulated by the presence of calcium ions and inhibited by
 CC phenylmethyl sulphonyl fluoride. PACE 4 and 4.1 convert prorenin to
 CC renin in the human kidney, causing elevation of blood pressure.
 CC They can therefore be used to identify other inhibitors of their
 CC action and may also be used to inhibit blood coagulation.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 4403 BP; 1016 A; 1253 C; 1214 G; 920 T; 0 other;

Query Match 0.1%; Score 27; DB 14; Length 4403;
 Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16377 GCGGGCGGGGGCGGGGGCGGG 16403
 |||||

Db 242 GCGGGCGGGGGCGGGGGCGGG 268

RESULT 14

ABN95905
 ID ABN95905 standard; DNA; 4403 BP.

XX
 AC ABN95905;

XX 13-AUG-2002 (first entry)
 DT XX
 XX Gene #2403 used to diagnose liver cancer.
 DE XX
 XX
 KW Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX
 OS Homo sapiens.
 XX
 PN WO200229103-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US30589.
 XX
 PR 02-OCT-2000; 2000US-237054P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 XX
 DR WPI; 2002-426119/45.
 XX
 PT Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample -
 PS Claim 1: SEQ ID NO 2403; 298pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumor in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 4403 BP; 1016 A; 1252 C; 1214 G; 921 T; 0 other;
 XX
 Query Match 0.1%; Score 27; DB 24; Length 4403;
 Best local Similarity 100.0%; Pred. No. 0.23;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16377 GCGGGCGGGGGGGCGGGGGCGCG 16403
 DB 242 GCGGGCGGGGGGGCGGGGGCGCG 268
 XX
 RESULT 15
 AAS94759/c
 ID AAS94759 standard; DNA; 3132 BP.
 XX
 AC AAS94759;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human DNA sequence #14 expressed during foam cell differentiation.
 KW Human: foam cell differentiation; atherosclerosis; cerebral stroke;
 KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
 XX
 OS Homo sapiens.

XX WO200177389-A2.
 PN XX
 XX 18-OCT-2001.
 PD XX
 XX
 PF 04-APR-2001; 2001WO-US11128..
 XX
 PR 05-APR-2000; 2000US-195106P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Shiffman D, Somogyi R, Lawn R, Sellhammer JJ, Porter GJ, Mikita T;
 PI Tai J;
 XX
 DR WPI; 2002-010925/01.
 XX
 PT Composition useful for diagnosis of conditions, disorders or diseases
 PT associated with atherosclerosis, comprises several polynucleotides that
 PT are differentially expressed in foam cell development -
 PS Claim 1: Page 71-72; 315pp; English.
 XX
 CC The present invention relates to the isolation of human polynucleotide
 CC sequences that are differentially expressed during foam cell
 CC differentiation. The polynucleotide sequences of the invention or a
 CC composition comprising these polynucleotides are useful as a high
 CC throughput method for detecting altered expression of one or more
 CC polynucleotides in a sample. The polynucleotides can be used in the
 CC diagnosis of disorders associated with foam cell development such as
 CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
 CC coronary artery disease. The polynucleotide sequences can also be used
 CC as PCR primers and probes. The polynucleotide sequences of the invention
 CC useful in gene therapy. AAS94746-AAS95021 represent the human
 CC polynucleotide sequences of the invention which are differentially
 CC expressed during foam cell differentiation.
 XX
 SQ Sequence 3132 BP; 578 A; 924 C; 885 G; 700 T; 45 other;
 XX
 Query Match 0.1%; Score 26; DB 24; Length 3132;
 Best local Similarity 100.0%; Pred. No. 0.68;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16378 CGGGCGGGGGGGCGGGGGCGCG 16403
 DB 2985 CGGGCGGGGGGGCGGGGGCGCG 2960
 XX
 RESULT 16
 ABV94750/c
 ID ABV94750 standard; cDNA; 2870 BP.
 XX
 AC ABV94750;
 XX
 DT 14-JAN-2003 (first entry)
 XX
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 131.
 KW Human: pancreas; cancer; gene therapy; vaccine; immunostimulant;
 KW cytostatic; tumour; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200260317-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 30-JAN-2002; 2002WO-US02781.
 XX
 PR 30-JAN-2001; 2001US-265305P.
 PR 31-JAN-2001; 2001US-265682P.
 PR 09-FEB-2001; 2001US-267568P.
 PR 21-MAR-2001; 2001US-278651P.
 PR 28-APR-2001; 2001US-287112P.

PR 16-MAY-2001; 2001US-291631P.
 PR 12-JUL-2001; 2001US-305484P.
 PR 20-AUG-2001; 2001US-313999P.
 PR 27-NOV-2001; 2001US-333626P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX
 DR WPI: 2002-627435/67.
 DR P-PSDB: ABP68605.
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful
 PT for diagnosing, preventing and/or treating cancer, particularly
 PT pancreatic cancer
 XX
 PS Claim 1; SEQ ID NO 131; 300pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);
 CC (b) complements of (a); (c) sequences consisting of at least 20
 CC contiguous residues of (a); (d) sequences that hybridize to (a), under
 CC moderately stringent conditions; (e) sequences having at least 75% or 90%
 CC identity to (a); or (f) degenerate variants of (a). Polypeptides
 CC (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to
 CC detect cancer in a patient and compositions comprising polypeptides and
 CC polynucleotides, antibodies, fusion proteins, T cell populations and
 CC antigen presenting cells expressing the polypeptide are useful in
 CC treating pancreatic cancer and stimulating an immune response. The
 CC polynucleotides can be used as probes or primers for nucleic acid
 CC hybridisation, in the design and preparation of ribozyme molecules for
 CC inhibiting expression of the tumor polypeptides and proteins in the
 CC tumour cells, in vaccines and for gene therapy.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 2870 BP; 704 A; 792 C; 725 G; 649 T; 0 other;
 XX
 QY Query Match 0.1%; Score 25; DB 24; Length 2870;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 16379 GGGCGCGGGGGCGGGGGCGCG 16403
 2291 GGGCGCGGGGGCGGGGGCGCG 2267
 XX
 RESULT 17
 AAT97303/C
 ID AAT97303 standard; DNA; 2876 BP.
 XX
 AC AAT97303;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Human plasminogen activator inhibitor DNA.
 XX
 KW plasminogen activator inhibitor type 1; PAI-1; human;
 KW elastase inhibitor; vitronectin; cell attachment;
 KW cell proliferation; emphysema; adult respiratory distress syndrome;
 KW acute lung inflammation; alpha 1-antitrypsin deficiency;
 KW cystic fibrosis; atopic dermatitis; pancreatitis;
 KW periodontal disease; arthritis; HIV; atherosclerosis; restenosis;
 KW neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
 KW thrombosis; angiogenesis; therapy; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 76..1284
 FT /tag- a
 FT sig_peptide 76..144

FT mat_peptide /*tag- b
 FT 145..1281
 FT /tag- c
 XX
 XX WO9739028-A1.
 XX
 XX 23-OCT-1997.
 XX
 XX 11-APR-1997; 97WO-US06071.
 XX
 XX 12-APR-1996; 96US-0015299.
 XX
 PA (AMNA-) AMERICAN NAT RED CROSS.
 PA Lawrence DA, Stefansson SP;
 PI
 DR WPI: 1997-526399/48.
 DR P-PSDB: AAM31587.
 XX
 DR
 XX
 PT Plasminogen activator-inhibitor type I mutant inhibits elastase - or
 PT has high affinity for vitronectin, for therapeutic inhibition of
 PT elastase or vitronectin-mediated cell attachment, migration etc.
 XX
 PS Disclosure; Page 91-95; 144pp; English.
 XX
 CC This nucleotide sequence codes for wild-type human plasminogen
 CC activator inhibitor type (PAI-1) (see AAM31587). Novel mutants
 CC (see AAM26710-25) of the PAI-1 mature protein are claimed that
 CC inhibit elastase or other elastase-like proteases, or are
 CC inhibitors of vitronectin-dependent cell migration. The mutants
 CC are obtained by site-directed mutagenesis of the PAI-1 DNA sequence
 CC and expression in host cells, and have a range of therapeutic uses.
 CC
 SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 other;
 XX
 QY Query Match 0.1%; Score 25; DB 18; Length 2876;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 16379 GGGCGCGGGGGCGGGGGCGCG 16403
 2297 GGGCGCGGGGGCGGGGGCGCG 2273
 XX
 RESULT 18
 AAS09460/C
 ID AAS09460 standard; CDNA; 2876 BP.
 XX
 AC AAS09460;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Human cDNA encoding Plasminogen activator inhibitor-1, PAI-1.
 XX
 KW Human; Plasminogen activator inhibitor-1; PAI-1; serpin;
 KW immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome;
 KW ARDS; HIV infection; Human immunodeficiency virus; prostate cancer;
 KW TNF-mediated inflammation; benign prostatic hypertrophy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 76..1284
 FT /tag- a
 FT /product= "PAI-1"
 FT sig_peptide 76..138
 FT /tag- b
 FT /note= "Alternative signal peptide"
 FT sig_peptide 76..143
 FT /tag- c
 FT /note= "Alternative signal peptide"
 FT mat_peptide 139..1281
 FT /tag- d

```
FT FT /label= Mature_PAI-1 #1
FT FT /note= "Both forms of the protein are detected in vivo"
FT FT 144..1281
FT FT /**tag=
FT FT /label= Mature_PAI-1 #2
FT FT /note= "Both forms of the protein are detected in vivo"
XX XX
XX XX WO200138560-A2.
XX XX
XX XX 31-MAY-2001.
XX XX
XX XX 22-NOV-2000; 2000WO-US32315.
XX XX
XX XX 22-NOV-1999; 99US-0167553.
XX XX
XX XX (AMNA-) AMERICAN NAT RED CROSS.
XX XX
XX XX Lawrence DA, Day D;
XX XX
XX XX WPI; 2001-441438/47.
XX XX
XX XX P-PSDB; AAU04913.
XX XX
XX XX Detecting a functionally active form of an enzyme in a biological
XX XX sample comprises contacting an enzyme inhibitor immobilised on a solid
XX XX substrate -
XX XX
XX XX Disclosure: Flg 3; 69pp; English.
XX XX
XX XX The sequence encodes human plasminogen activator inhibitor-1,
XX XX PAI-1, a serine proteinase inhibitor or serpin. The protein
XX XX is used to demonstrate the method of the invention which comprises
XX XX detecting a functionally active form of an enzyme in a biological
XX XX sample by contacting an enzyme inhibitor immobilised on a
XX XX solid substrate with the biological sample and measuring the binding of
XX XX the enzyme inhibitor to the active form of the enzyme by a detectable
XX XX label, where the enzyme inhibitor specifically forms a covalent bond or
XX XX binds with a dissociation constant of 1 x 10-9M or less with the active
XX XX form of the enzyme. The present invention provides a sensitive method for
XX XX the detection of a functionally active form of an enzyme in a biological
XX XX sample. Human PAI-1 can be used to detect a number of enzymes including
XX XX tissue plasminogen activator, urokinase, thrombin, plasmin, neutrophil
XX XX elastase, pancreatic elastase, trypsin, chymotrypsin, cathepsin G and
XX XX prostate specific antigen and as such can be used in methods to diagnose
XX XX diseases such as cystic fibrosis, acute respiratory distress syndrome
XX XX (ARDS), HIV infection, TNF-mediated inflammation, prostate cancer and
XX XX benign prostatic hypertrophy.
XX XX
XX XX Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 other:
XX XX
XX XX Query Match 0.1%; Score 25; DB 22; Length 2876;
XX XX Best Local Similarity 100.0%; Pred. No. 2;
XX XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16379 GGGCGCGGGGGCGGGCGGGCGCG 16403
DB 2297 GGGCGCGGGGGCGGGCGGGCGCG 2273
XX XX
XX XX RESULT 19
XX XX AAH02917/c
XX XX ID AAH02917 standard; DNA; 2876 BP.
XX XX
XX XX AAH02917;
XX XX
XX XX 15-JUN-2001 (first entry)
XX XX
XX XX Human shear stress-response coding sequence SEQ ID NO: 87.
XX XX
XX XX Human: shear stress-response protein; vascular disease;
XX XX arteriosclerosis; ds.
XX XX
XX XX Homo sapiens.
XX XX
XX XX
```

```
PN WO200125427-A1.
XX 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-JP06840.
XX
XX 01-OCT-1999; 99JP-0280976.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX (NOJI/) NOJIMA H.
XX
XX Nojima H, Yoshisue H, Odayashi M, Ota T, Kawabata A, Sakurada K;
XX Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
XX WPI; 2001-266308/27.
XX
XX P-PSDB; AAB90794.
XX
XX DNA sequences, proteins encoded by them and antibodies against them
XX useful in diagnosis and treatment of vascular disease caused by
XX arteriosclerosis -
XX
XX Claim 20; Page 472-476; 678pp; Japanese.
XX
XX The present invention provides the protein and coding sequences of a
XX number of human shear stress response proteins. These are useful in the
XX diagnosis, treatment and screening of vascular diseases caused by
XX arteriosclerosis, including heart failure, post-PTCA restenosis and
XX hypertension.
XX
XX Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 other:
XX
XX Query Match 0.1%; Score 25; DB 22; Length 2876;
XX XX Best Local Similarity 100.0%; Pred. No. 2;
XX XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16379 GGGCGCGGGGGCGGGCGGGCGCG 16403
DB 2297 GGGCGCGGGGGCGGGCGGGCGCG 2273
XX XX
XX XX RESULT 20
XX XX ABV77991/c
XX XX ID ABV77991 standard; DNA; 2876 BP.
XX XX
XX XX ABV77991;
XX XX
XX XX 12-NOV-2002 (first entry)
XX XX
XX XX Hypoxia-regulated protein coding sequence #11.
XX XX
XX XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
XX XX antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine;
XX XX hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
XX XX ischemic condition; reperfusion injury; retinopathy; neonatal stress;
XX XX preclampsia; atherosclerosis; inflammatory condition; wound healing;
XX XX inflammation; erythropoiesis; hair loss; human; gene; ds.
XX XX
XX XX Homo sapiens.
XX XX
XX XX WO200246465-A2.
XX XX
XX XX 13-JUN-2002.
XX XX
XX XX 10-DEC-2001; 2001WO-GB05458.
XX XX
XX XX 08-DEC-2000; 2000GB-0030076.
XX XX
XX XX 08-FEB-2001; 2001GB-0003156.
XX XX
XX XX 25-OCT-2001; 2001GB-0025666.
XX XX
XX XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX XX
XX XX White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
XX XX Rayner WN;
XX XX
```


[illegible]

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FR 19-AUG-1986; 86US-0897990.
XX
XX (SCRI ) SCRIPPS CLINIC & RES FOUND.
PA (LOSK/) LOSKUTOFF D J.
XX
XX ..
PI Loskutoff DJ, Ny T, Sawdey M;
XX
XX
DR WPI: 1988-063992/09.
DR P-PSDB; AAP82007.
XX
XX Diagnostic assays for tissue - and urokinase-type plasminogen
PT inhibitor - and pure, recombinant human endothelial plasminogen
PT activator inhibitor.
XX
XX
PS Claim 1; Fig 22; 100pp; English.
XX
XX The lambda 3 clone DNA or plasmid pPA13 can be used to produce the
CC t-PA inhibitor by recombinant DNA technology. The protein can
CC be used in a solid phase assay for detection of endothelial PAI,
CC and as an immunogen to raise antibodies for use as receptor molecules
CC in other assay systems.
CC See also AAP80252-54.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 2944 BP; 734 A; 784 C; 728 G; 698 T; 0 other;
SQ
Query Match 0.1%; Score 25; DB 9; Length 2944;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16379 GGGCGGGGGGGCGCGGGGGCGCG 16403
DB 2165 GGGCGCGGGGGCGCGCGGGGGCGCG 2141
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
RESULT 22
AAS94905/c
ID AAS94905 standard; DNA; 3171 BP.
XX
XX AAS94905;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Human DNA sequence #160 expressed during foam cell differentiation.
DE
XX
XX Human: foam cell differentiation; atherosclerosis; cerebral stroke;
KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200177389-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 04-APR-2001; 2001WO-US11128.
PF
XX
XX 05-APR-2000; 2000US-195106P.
PR
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX
XX Shiffman D, Somogyi R, Lawn R, Sellhammer J, Porter GJ, Mikita T;
PI Tai J;
PI
XX
XX WPI: 2002-010925/01.
DR
XX
XX Composition useful for diagnosis of conditions, disorders or diseases
PT associated with atherosclerosis, comprises several polynucleotides that
PT are differentially expressed in foam cell development -
XX
XX Claim 1; Page 215; 315pp; English.
XX
XX The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell
CC

```


CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and
 CC oncogenes having a sequence taken from 536 (actually 533 since
 CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
 CC (5s) and sequences complementary to (5s). The nucleic acid may be a
 CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
 CC form part of a set of probes for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms and also to be used in an
 CC array for analysing diseases associated with CPG dinucleotides e.g.
 CC cancers and tumours. The probes can also be used in a method for
 CC ascertaining genetic and/or epigenetic parameters for the diagnosis
 CC and/or therapy of existing diseases or the predisposition to specific
 CC diseases, by analysing cytosine methylations. The parameters may be
 CC compared to another set of genetic and/or epigenetic parameters, the
 CC differences serving as basis for diagnosis and/or prognosis events which
 CC are disadvantageous to patients. The present sequence is one of the
 CC 533 genomic sequences derived from tumour suppressor genes and
 CC oncogenes. Sequences with even numbered Seq ID numbers are the
 CC complementary sequence of the corresponding odd numbered sequence (e.g.
 CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
 CC is missing).

CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 7309 BP; 1739 A; 181 C; 1806 G; 3583 T; 0 other;

CC Query Match 0.1%; Score 25; DB 22; Length 7309;

CC Best Local Similarity 100.0%; Pred. No. 1.9;
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25487 AAAACATTAACCAAAATTAATAAA 25511

DB 7011 AAAACATTAACCAAAATTAATAAA 6987

RESULT 25

ABK34011/C

ID ABK34011 standard; DNA: 7309 BP.

AC ABK34011;

DT 18-JUN-2002 (first entry)

XX Human DNA for staging of Astrocytomas, complement, #49.

KW Human; ds; astrocytoma; cytostatic; staging; cytosine methylation; CPG;
 KM bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry;
 KM matrix assisted laser desorption/ionization mass spectrometry.

XX Homo sapiens.

OS WO200202808-A2.

PN 10-JAN-2002.

PD 02-JUL-2001; 2001WO-EP05738.

PF 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.

PA Olek A, Plepenbrock C, Berlin K;

PI WPI; 2002-171649/22.

DR Novel chemically modified genomic DNA sequences, useful in the

XX characterisation, classification, differentiation, grading, staging,
 PT treatment and/or diagnosis of astrocytomas or predisposition to
 PT astrocytomas

PS Claim 1; SEQ ID No 98; 37bp; English.

XX The invention relates to a nucleic acid comprising a sequence (I) of at
 CC least 18 bases in length of a segment of chemically pre-treated genomic
 CC DNA which has any one of the sequences of (ABK33919-ABK34032) or its
 CC complement. Also included are an oligonucleotide or peptide nucleic
 CC acid (or set thereof) of at least 9 nucleotides which hybridises to (I),
 CC primers for (I), probes for detecting cytosine methylation or single-
 CC nucleotide polymorphisms (SNP) in (I), an array of oligomers
 CC or peptide nucleic acids for analysing diseases associated with the
 CC methylation states of the Cpg dinucleotides of (I). The array is useful
 CC for determining genetic and/or epigenetic parameters, classification,
 CC differentiation, grading, staging, treatment and/or diagnosis of
 CC astrocytomas, or the predisposition to astrocytomas by analysing cytosine
 CC methylations, involves obtaining a biological sample containing genomic
 CC DNA, extracting the genomic DNA, converting cytosine bases which are
 CC unmethylated at the 5-position, in the genomic DNA sample, to uracil or
 CC another base which is dissimilar to cytosine in terms of hybridisation
 CC behaviour, by chemical treatment and amplifying chemically pre-treated
 CC genomic DNA fragments using the array and a polymerase, where the
 CC amplification carries a detectable label. The method further involves
 CC identifying methylation status of one or more cytosine positions, and
 CC analysing methylation status of the cytosine positions by reference to
 CC one or more data sets. The genomic DNA is chemically treated by using a
 CC bisulphite, hydrogen sulphide or disulphite. The amplification
 CC step amplifies DNA which is of particular interest in astrocytoma or
 CC brain tissue, based on the specific genomic methylation status of brain
 CC tissues, as opposed to background DNA. The amplification carries a
 CC fluorescent label or radionuclide. Optionally, the labels of the
 CC which are detected in a mass spectrometer. The fragments of chemically
 CC pre-treated genomic DNA to be amplified, have a single positive or
 CC negative charge for a better detectability in the mass spectrometer.
 CC Preferably, the amplification or fragments of the amplification are
 CC detected by matrix assisted laser desorption/ionization mass spectrometry
 CC (MALDI) or using electron spray mass spectrometry (ESI). The
 CC present sequence is one of the chemically pre-treated reference DNA
 CC samples of the invention.

CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 7309 BP; 1739 A; 181 C; 1806 G; 3583 T; 0 other;

CC Query Match 0.1%; Score 25; DB 24; Length 7309;

CC Best Local Similarity 100.0%; Pred. No. 1.9;
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25487 AAAACATTAACCAAAATTAATAAA 25511

DB 7011 AAAACATTAACCAAAATTAATAAA 6987

RESULT 26

ABL33817/C

ID ABL33817 standard; DNA: 7309 BP.

AC ABL33817;

DT 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 1790.

KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; anti-naemic; cytosine; neotropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmologic;
 KW antineumatic; antiarthritis; antidiabetic; antipsoriatic;
 KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.

OS Homo sapiens.
 XX WO200200928-A2.
 XX
 XX 03-JAN-2002.
 XX
 XX 02-JUL-2001; 2001WO-EP07537.
 XX
 XX 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 XX (EPIC-) EPIDENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI: 2002-130909/17.
 DR
 XX
 XX Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation -
 PS
 XX Claim 1; SEQ ID NO 1790; 32pp + Sequence listing; German.
 CC
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 CC
 XX
 SQ Sequence 7309 BP; 1739 A; 181 C; 1806 G; 3583 T; 0 other;

Query Match 0.1%; Score 25; DB 24; Length 7309;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 25487 AAACATTAAACAAATTATAAAA 25511
 ||||||||||||||||||||||||||||
 Db 7011 AAACATTAAACAAATTATAAAA 6987

RESULT 27
 ABN95599/C
 ID ABN95599 standard; DNA: 17509 BP.
 XX
 AC ABN95599;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Gene #2097 used to diagnose liver cancer.
 XX
 KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytosolic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX
 OS Homo sapiens.
 XX
 XX WO200229103-A2.
 XX
 XX 11-APR-2002.
 XX
 XX 02-OCT-2001; 2001WO-US30589.
 PF
 XX 02-OCT-2000; 2000US-237054P.
 PR
 XX (GENE-) GENE LOGIC INC.
 XX
 XX Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 XX WPI: 2002-426119/45.
 DR
 XX

PT Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample -
 PS
 XX Claim 1; SEQ ID NO 2097; 298pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumour in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytosolic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX
 SQ Sequence 17509 BP; 4974 A; 4406 C; 4386 G; 3743 T; 0 other;

Query Match 0.1%; Score 25; DB 24; Length 17509;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 16379 GGGCGGGGGGGGGGGGGGGCGG 16403
 ||||||||||||||||||||||||||||
 Db 14507 GGGCGGGGGGGGGGGGGGGCGG 14483

RESULT 28
 ABK32842/C
 ID ABK32842 standard; DNA: 2307 BP.
 XX
 AC ABK32842;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE DNA encoding human homologue of MPT1 antifungal target.
 XX
 KW antifungal; fungal gene transcription; RPB34; POP3; TFA2; NAB2;
 KW MPT1; MTR2; BOS1; POL30; RSA2; SOR1; MTW1; TFB1; SPC98; BPR2; RAN1;
 KW GCD7; SKI6; NRP1; LCP5; NCE103; ECO1; ORC2; CNS1; YPD1; TIM10; SRB4;
 KW yeast; fungus; ds; gene.
 XX
 OS Homo sapiens.
 XX
 XX WO200202055-A2.
 XX
 XX 10-JAN-2002.
 XX
 XX 28-JUN-2001; 2001WO-US20592.
 PF
 XX 29-JUN-2000; 2000US-215164P.
 PR 10-AUG-2000; 2000US-224457P.
 XX
 XX (ANAD-) ANADYS PHARM INC.
 XX
 XX Moore J, Buurman ET, Desilva T, Harris S, Komarnitsky S;
 PI Mendillo M, Moore D, McCoy M, Sanderson K, Haq T, Zhu S, Long F;
 PI Davidov E, Thompson CM;
 XX
 XX WPI: 2002-147962/19.
 DR P-PSDB; AAU82954.
 DR
 XX
 XX Screening candidate antifungal compound for interaction with essential
 PT protein, modulation of essential protein activity, binding to essential
 PT protein, by contacting protein with test compound and determining
 PT effects -
 PT

XX		
PS	Disclosure; Figure 80; 522pp; English.	
XX		
CC	The invention describes a method of screening a candidate antifungal	
CC	compound for interaction with essential proteins (EP) or for modulation	
CC	of EP activity e.g fungal gene transcription. The proteins tested in the	
CC	invention include Rpe344, POP3, TFA2, NAB3, MPT1, MTR2, BOS1, POL30, RSA2,	
CC	SORT1, MTW1, TPB1, SPC98, BPR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103,	
CC	ECOI, ORC2, CNS1, YPO1, TIM10 and SRB4 from S. cerevisiae; C. albicans	
CC	and human homologues. The method involves contacting a culture with one	
CC	or more test compounds and determining the effects on the growth or	
CC	viability of the culture of cells which preferably comprises fungal cells	
CC	or yeast cells. Preferably the identified compounds interact with, or	
CC	modulate (preferably inhibit) the activity of C. albicans EP. The inhibitor	
CC	compounds identified by the method are useful for preventing or	
CC	inhibiting fungal, particularly C. albicans growth in culture or in a	
CC	mammal. The antifungal agents interact with essential fungal elements	
CC	that can be used to treat fungal infection by preventing the growth and	
CC	preferentially killing the fungi, but does not inhibit the biological	
CC	activity of mammalian homologues. This sequence encodes a target protein	
CC	to test the antifungal compounds, described in the method of the	
CC	invention.	
XX		
XX		
SQ	Sequence 2307 BP; 359 A; 969 C; 724 G; 255 T; 0 other;	
	Query Match 0.1%; Score 23; DB 24; Length 2307;	
	Best Local Similarity 100.0%; Pred. No. 16;	
	Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	16373 CGCGGCGGGCGCGGGCGGCGGCGG 16395	
DB	756 CGCGGCGGGCGCGGGCGGCGGCGG 734	
RESULT 29		
ABX08754		
ID	ABX08754 standard; CDNA; 6816 BP.	
XX		
AC	ABX08754;	
XX		
DT	21-JAN-2003 (first entry)	
XX		
DE	Angiogenesis-associated human polynucleotide sequence #16.	
XX		
KM	Human; angiogenesis-associated transcript; angiogenesis;	
KM	angiogenesis-associated disease; cancer; cytostatic; gene therapy;	
KW	gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200279492-A2.	
XX		
PD	10-OCT-2002.	
XX		
PF	14-FEB-2002; 2002WO-US04915.	
XX		
XX		
PR	14-FEB-2001; 2001US-0784356.	
PR	22-FEB-2001; 2001US-0791390.	
PR	19-APR-2001; 2001US-285475P.	
PR	03-AUG-2001; 2001US-310025P.	
PR	13-NOV-2001; 2001US-350666P.	
PR	29-NOV-2001; 2001US-334244P.	
XX		
PA	(EOSB-) EOS BIOTECHNOLOGY INC.	
XX		
PI	Murray R, Glynn R, Watson SR, Aziz N;	
XX		
DR	WP1; 2003-040681/O3.	
DR	P-PSDB; ABU03471.	
XX		
XX	Detecting angiogenesis-associated transcript in a cell for diagnosing	
PT	and treating cancer by contacting a sample with a polynucleotide that	
PT	exhibits changes in expression level as a function of time in tissue	

PT		undergoing angiogenesis -
XX		
PS	Example 2; Page 193-195; 291pp;	English.
CC		
XX		The present invention relates to methods and compositions for
CC		detecting an angiogenesis-associated transcript in a cell in
CC		a patient. The method involves contacting a biological sample from
CC		the patient with a polynucleotide that selectively hybridises to a
CC		sequence at least 80% identical to any of the angiogenesis-associated
CC		human polynucleotide sequences given in the specification. These
CC		angiogenesis-associated polynucleotide sequences comprise genes that
CC		exhibit changes in expression levels as a function of time in tissue
CC		undergoing angiogenesis. The method and the polynucleotide sequences
CC		of the invention are useful for diagnosing and treating angiogenesis
CC		and angiogenesis-associated diseases e.g. cancer. The polynucleotide
CC		sequences are also useful in the gene therapy of such disorders. The
CC		angiogenesis-associated proteins encoded by the polynucleotide
CC		sequences are useful as a vaccine for therapeutic and prophylactic
CC		immunisation. ABX08739-ABX08853 represent angiogenesis-associated
CC		polynucleotide sequences.
XX		
SQ	Sequence 6816 BP; 1852 A; 1702 C; 1736 G; 1526 T; 0 other;	
	Query Match	0.1%; Score 23; DB 25; Length 6816;
	Best Local Similarity	100.0%; Pred. No. 16;
	Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	16379 GGGCGGCGGGCGCGGGCGG 16401 	
DB	2802 GGGCGCGGGCGCGGGCGG 2824	
RESULT 30		
ID	ABL70224/C	
ID	ABL70224 standard; DNA; 7752 BP.	
XX		
AC	ABL70224;	
XX		
DT	01-JUL-2002 (first entry)	
XX		
DE	Chemically treated cell signalling DNA sequence complementary to#57.	
XX		
KW	Cell signalling; cytosine methylation; cell signalling disease;	
KW	cancer; tumour; cytostatic; ds.	
XX		
OS	Unidentified.	
XX		
PN	WO200202807-A2.	
PD	10-JAN-2002.	
XX		
PF	29-JUN-2001; 2001WO-EP07471.	
XX		
PR	30-JUN-2000; 2000DE-1032529.	
PR	01-SEP-2000; 2000DE-1043826.	
XX		
PA	(EPIG-) EPIGENOMICS AG.	
XX		
PI	Olek A, Piepenbrock C, Berlin K;	
DR	WPI; 2002-154758/20.	
XX		
PT	Nucleic acid, useful for diagnosis and therapy of diseases associated	
PT	with cell signalling e.g. cancer, comprises chemically modified genomic	
PT	sequences of genes associated with cell signalling -	
XX		
PS	Claim 1; SEQ ID NO 114; 24pp+sequence listing; English.	
CC		
CC	The invention relates to a nucleic acid comprising a sequence of at least	
CC	18 bases of a segment of chemically pretreated DNA of genes associated	
CC	with cell signalling. The activity of the modified sequences of the	
CC	invention may be described as cytostatic. The object of the invention is	
CC	to provide the chemically modified DNA of genes associated with cell	

CC signalling, as well as oligonucleotides and/or PNA-oligomers for
CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL/70111-ABL/70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.

SQ Sequence 7752 BP; 1847 A; 113 C; 1696 G; 4096 T; 0 other;

Query Match	23;	Score	23;	DB	24;	length	7752;
Best Local Similarity	100.0%;	Pred. No.	16;				
Matches	23;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

Qy	25494	TAAACCAAAATTAAAAATTAAA	25516
Db	4024	TAAACCAAAATTAAAAATTAAA	4002

RESULT 31
AAV73805
ID AAV73805 standard; DNA; 32207 BP.

AC AAV73805;

DT 25-FEB-1999 (first entry)

DE KSHV LUR DNA (nucleotides 105,301-137,507)

KM Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2
KM dihydropyolate reductase; LUR; long unique region; vaccine; prophylaxis;
KM diagnosis; treatment; HHV8; capsid protein IV; tegument protein IV;
KM glycoprotein; Kaposin; cyclin D; immediate early protein; IEB; OX-2;
KM v-abl; G-protein coupled receptor; FGFR4T; ds.

OS Kaposi's sarcoma-associated herpesvirus.

PN US5849564-A.

PD 15-DEC-1998.

PF 29-NOV-1996; 96US-0770379.

PR 29-NOV-1996; 96US-0770379.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;

WPI; 1999-069741/06.

PT Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
PT dihydrofolate reductase and is useful for treatment, prophylaxis
PT or diagnosis of Kaposi's sarcoma

PS Disclosure; Column 155-182; 109pp; English.

CC This sentence is a fragment of the Kaposi's sarcoma-associated
CC hepersvirus (KSHV) LUR (long unique region). This fragment contains
CC coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67
CC which encodes tegument protein IV, ORF68 which encodes a glycoprotein,
CC ORF69, K12 which encodes Kaposin, K13, ORF72 which encodes cyclin D,
CC ORF73 which encodes immediate early protein (IEP), K14 which encodes
CC OX-2 (V-abh), ORF74 which encodes G-protein coupled receptor, ORF75
CC which encodes tegument protein/FCGR4R, K15. KSHV is a new human
CC Hepevirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the
CC most common form of neoplasm occurring in persons with acquired immune
CC deficiency syndrome (AIDS). The DHFR protein is useful for vaccination,
CC prophylaxis diagnosis and treatment of a subject with Kaposi's sarcomam

CC and for detecting expression of a DNA virus associated with Kaposi's
CC sarcoma in a cell.

SQ Sequence 32207 BP; 7229 A; 9156 C; 8713 G; 7109 T; 0 other;

Query Match	0.1%	Score 23	DB 20	Length 32207
Best Local Similarity	100.0%	Pred. No. 15		
Matches 23	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	5460	GT	TTTT	TA	AT	ACTG	AC	AG	TAG	TT	5482
Db	9402	GT <td>TTTT <td>TA <td>AT <td>ACTG <td>AC <td>AG <td>TAG <td>TT</td> <td>9424</td> </td></td></td></td></td></td></td>	TTTT <td>TA <td>AT <td>ACTG <td>AC <td>AG <td>TAG <td>TT</td> <td>9424</td> </td></td></td></td></td></td>	TA <td>AT <td>ACTG <td>AC <td>AG <td>TAG <td>TT</td> <td>9424</td> </td></td></td></td></td>	AT <td>ACTG <td>AC <td>AG <td>TAG <td>TT</td> <td>9424</td> </td></td></td></td>	ACTG <td>AC <td>AG <td>TAG <td>TT</td> <td>9424</td> </td></td></td>	AC <td>AG <td>TAG <td>TT</td> <td>9424</td> </td></td>	AG <td>TAG <td>TT</td> <td>9424</td> </td>	TAG <td>TT</td> <td>9424</td>	TT	9424

RESULT	32
AAV19941	
ID	AAV19941 standard; DNA; 137507 BP

AC AAV19941

DT 03-AUG-1998 (first entry)

DE KSHV long unique coding region and terminal repeat

KW KSHV; H8: human herpes virus 8; macrophage inflammatory protein II;
interleukin-6; IL-6: interferon regulatory factor; rheumatoid arthritis;
complement-binding protein; glycoprotein; capsid protein IV; infection;
immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
lymphoproliferative disease; leukemia; splenomegaly; mycosis fungoides;
HIV immune status; anti-inflammatory agent; therapy; ds.

OS Kaposi's sarcoma-associated herpes virus.

FH	Key	Location/Qualifiers
ET	CDS	1142..2794

```

CDS      complement (111931..112443)
FT       /*tag= m
FT       /product= capsid protein IV
FT

```

```

FT CDS complement (123808..127296)
ET /*tag= n
EE /product= immediate early protein
PN MO9804576-AI.
XX
XX PD 05-FEB-1998.
XX PE 22-JUL-1997; 97WO-USL3346.
XX PR 29-NOV-1996; 96US-0757669.
XX PR 25-JUL-1996; 96US-0686243.
PR 25-JUL-1996; 96US-0686349.
PR 25-JUL-1996; 96US-0686350.
PR 25-JUL-1996; 96US-0687253.
PR 25-JUL-1996; 96US-0688814.
PR 05-SEP-1996; 96US-0708678.
PR 10-OCT-1996; 96US-0728323.
PR 13-NOV-1996; 96US-0747877.
PR 13-NOV-1996; 96US-0748640.
XX PA (UWCO ) UNIV COLUMBIA NEW YORK.
XX PI Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
DR WPI; 1998-130615/12.
XX PT New nucleic acid encoding Kaposi's sarcoma associated herpes virus
PT proteins - useful for, e.g. detecting levels of HHV8 in, and
PT preparation of vaccines for treatment of, HIV patients
PS Example 2; page 135-203; 230pp; English.
XX
XX This sequence represents the long unique region and terminal repeat of
CC the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known
CC as human herpes virus 8 (HHV8). This sequence contains the DNAs of the
CC invention which encode KSHV polypeptides selected from: (a) viral
CC macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6);
CC (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;
CC (e) capsid protein IV encoded by ORF5; and (f) Immediate early protein
CC encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded
CC by it, and antibodies (Ab) specific for the proteins are useful for
CC detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body
CC fluids or tissue samples. HHV8 infections can be treated with antisense
CC or triplex forming molecules or agents that bind specifically to the
CC protein. Ab may be used for prophylaxis or treatment of HHV8 infection,
CC while the protein can be used in protective vaccines. Ab may also be used
CC to differentiate between lymphomas, and HHV8 may be implicated in many
CC other lymphoproliferative diseases such as lymphomas, leukaemia,
CC splenomegaly and mycosis fungoides. Cells and animals containing the
CC nucleic acid are useful for drug screening. HHV8-derived peptides can be
CC used as targets for antiviral drugs, e.g. dihydrofolate reductase gene
CC can be inhibited with methotrexate. These can also be used to determine
CC the immune status of a patient infected with HIV. HHV8 derived protein
CC viral MIP III may be used as an anti-inflammatory agent for,
CC e.g., treating rheumatoid arthritis. This sequence is stated as containing
CC 81 open reading frames.
XX
SQ Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
Query Match 0.1%; Score 23; DB 19; Length 137507;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY 5460 GTTTTAATACTGACAGTACTGT 5482
DB 114702 GTTTTAATACTGACAGTAGT 114724

```

AC	ABK97604;	
XX		
DT	07-OCT-2002	(first entry)
XX		
DE	Human prostate specific nucleic acid DEX0293_31.	
XX		
KW	Human; prostate specific nucleic acid; PSNA; prostate cancer; PSP;	
KW	prostate specific protein; cytosolic; non-cancerous prostate disease;	
KW	gene therapy; cancer; immunostimulant; vaccine; ss; gene.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200255735-A2.	
XX		
PD	18-JUL-2002.	
XX		
PF	27-NOV-2001; 2001WO-US44363.	
XX		
PR	27-NOV-2000; 2000US-253176P.	
XX		
PA	(DIAD-) DIADEXUS INC.	
PI	Salceda S, Machua RA, Recipon H, Cafferey R, Ali S, Sun Y;	
PI	Liu C, Chen S;	
XX		
DR	WPI; 2002-557831/59.	
XX		
XX	New prostate specific genes, useful for treating or diagnosing cancer,	
PT	or useful as vaccines for treating cancer, particularly prostate	
PT	cancer, in a patient	
XX		
XX	Claim 1; Page 160; 212pp; English.	
PS		
XX		
CC	The invention relates to a new isolated prostate-specific nucleic acid	
CC	(PSNA) molecule comprising the cDNA sequences appearing as ABK97574-	
CC	ABK97642 which encode prostate specific proteins appearing as	
CC	ABG68701-ABG68746, or a sequence hybridising to a PSNA or which has 60%	
CC	sequence homology with a PSNA. Also included are a method of determining	
CC	the presence of a PSNA in a sample, a vector comprising the PSNA,	
CC	a host cell comprising the vector, producing the polypeptide encoded by	
CC	the PSNA, a method of determining the presence of a PSP in a sample,	
CC	diagnosing and monitoring the presence and metastases of prostate cancer	
CC	in a patient, a kit for detecting a risk of cancer or presence of cancer	
CC	in a patient (the kit comprising a means for determining the presence of	
CC	the PSNA or PSP in a sample of a patient) and a vaccine comprising the	
CC	polypeptide or the nucleic acid encoding the polypeptide. The PSNA, PSP	
CC	and anti-PSP antibody are useful for diagnosing and treating cancer in a	
CC	patient (e.g. by gene therapy). The nucleic acid molecule and polypeptide	
CC	are also useful as vaccines for treating cancer, particularly prostate	
CC	cancer and non-cancerous prostate diseases. The present sequence is	
CC	a PSNA of the invention.	
XX		
XX	Sequence 1044 BP; 344 A; 161 C; 260 G; 279 T; 0 other:	
SO		
XX		
Query Match	0.1%; Score 22; DB 24; Length 1044;	
Best Local Similarity	100.0%; Pred. No. 48;	
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	25633 GTATTTAATTTTAAAGTTT 25654	
DB	751 GTATTTAATTTTAAAGTTT 772	
XX		
RESULT 34		
ID	AAK90497/C	
XX	AAK90497 standard; DNA; 3024 BP.	
XX	AAK90497;	
XX		
DT	05-NOV-2001 (first entry)	
XX		
DE	Human digestive system antigen sequence SEQ ID NO: 4073.	
XX		

KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX Homo sapiens.
XX WO200155314-A2.
XX 02-AUG-2001.
PD 17-JAN-2001; 2001WO-US01324.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
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PR 14-AUG-2000; 2000US-0224518.
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PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.

PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-502630/55.
DR
XX
PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases -
XX
PS Disclosure; SEQ ID NO 4073; 986bp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention.
XX
SQ Sequence 3024 BP; 765 A; 751 C; 761 G; 747 T; 0 other;
Query Match 0.1%; Score 22; DB 22; Length 3024;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9722 CAAAGGCACATATTTT 9743
Db 927 CAAAGGCACATATTTT 906
RESULT 35
AAK90501/C
ID AAK90501 standard; DNA: 3024 BP.
XX
AC AAK90501;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4077.
XX
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
XX
PN WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01324.
XX
XX 31-JAN-2000; 2000US-0179065.
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PR 05-JAN-2001; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI: 2001-502630/55.
XX
XX Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases -
XX
XX disclosure; SEQ ID NO 4077; 986pp; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention.
XX
XX Sequence 3024 BP; 760 A; 753 C; 763 G; 748 T; 0 other;
SQ
Query Match 0.1%; Score 22; DB 22; Length 3024;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9722 CAAAGGCACATATTTT 9743
DB 928 CAAAGGCACATATTTT 907
RESULT 36
AA157831
ID AA157831 standard; cDNA; 4176 BP.
XX
XX AA157831;
XX
XX 22-OCT-2001 (first entry)
DE Human polynucleotide SEQ ID NO 34.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
XX Homo sapiens.
OS
PN WO200153312-A1.
XX
XX 26-JUL-2001.
PD
XX 26-DEC-2000; 2000WO-US34263.
PF
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0635450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HSE-) HSEQ INC.
XX
XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR P-PSDB; AAM38675.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Claim 1; SEQ ID NO 34; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX Sequence 4176 BP; 668 A; 1320 C; 1591 G; 597 T; 0 other;
SQ
Query Match 0.1%; Score 22; DB 22; Length 4176;

Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27465 GCGCCGCGCGCGCGCGCGCC 27486
DB 1749 GCGCCGCGCGCGCGCGCGCC 1770
RESULT 37
ABAI5786/c
ID ABAI5786 standard; DNA: 13334 BP.
XX
AC ABAI5786;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 8117.
XX
KW Human; neurotropic; neuroprotective; cytoskeletal; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnereary;
KW antiparkinsonian; antistroke; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiac; infection; immune disorder; cardiovascular disorder;
KW neurological disease; infection; neurotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0186874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234423.
PR 21-SEP-2000; 2000US-0234474.
PR 25-SEP-2000; 2000US-0234497.
PR 25-SEP-2000; 2000US-0234498.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235634.
PR 27-SEP-2000; 2000US-0235636.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.

XX Ryan JM;
PI WPI; 2002-394128/42.
DR P-PSDB; AAE22737.
XX
PT Novel genomic polynucleotide from human chromosome-7 encoding snare
PT YKT6, liver glucokinase, adipocyte enhancer binding protein polynase
PT delta small subunit useful in gene therapy for treating e.g. diabetes,
PT cancer.
PS Claim 1; Page 5-21; 94pp; English.
XX
CC The present invention relates to novel genomic polynucleotide from human
CC chromosome 7 encoding human snare YKT6, liver glucokinase (ATP: D-hexose
CC 6-phosphotransferase), adipocyte enhancer binding protein (ABEP1) and DNA
CC directed 50 kpa regulatory subunit (POLD2). Sequences of the invention
CC are used to prevent, treat or ameliorate a medical condition. Antisense
CC oligonucleotides specific for snare YKT6 are useful for inhibiting cell
CC growth and in particular to treat or prevent tumour growth. Glucokinase
CC and ABEP are useful for treating hyperglycaemia. Genomic sequences of
CC the invention are useful for gene therapy e.g., SNARE YKT6 is useful to
CC modulate or prevent cell apoptosis and treat disorder such as virus-
CC induced lymphocyte depletion (AIDS-acquired immune deficiency syndrome),
CC cell death in neurodegenerative disorders (e.g., Alzheimer's disease,
CC Parkinson's disease, ALS (amyotrophic lateral sclerosis), retinitis
CC pigmentosa, spinal muscular atrophy and various forms of cerebellar
CC degeneration), cell death in blood cell disorders resulting from the
CC deprivation of growth factors (anaemia associated with chronic disease,
CC aplastic anaemia, chronic neutropenia and myelodysplastic syndromes)
CC and disorders arising from acute loss of blood flow such as stroke and
CC myocardial infarctions. Glucokinase gene is useful for treating diabetes
CC mellitus. ABEP is useful in modulating or inhibiting adipogenesis and
CC in treating obesity, diabetes mellitus or osteopenic disorders. POLD2 is
CC useful in treating defects in DNA repair such as xeroderma pigmentosum,
CC progeria and ataxia telangiectasia. The present sequence is human snare
CC YKT6 genomic DNA.
XX
SQ Sequence 38997 BP; 10813 A; 9678 C; 9403 G; 9103 T; 0 other;
Query Match 0.1%; Score 22; DB 24; Length 38997;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2543 GAGTACCCCAATCCTCCAC 2564
DB 14535 GAGTACCCCAATCCTCCAC 14556
RESULT 39
ABK99972
ID ABK99972 standard; DNA; 157875 BP.
XX
AC ABK99972;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human CADPKL genomic DNA.
XX
KW Human; calcium/calmodulin-dependent protein kinase-like gene; CADPKL; ds;
KW gene; neuropsychiatric disorder; attention deficit disorder; ADD;
KW schizoaffective disorder; bipolar disorder; unipolar affective disorder;
KW schizophrenia; adolescent conduct disorder; pharmacogenomics;
KW fingerprinting; paternity testing; antidepressant; neuroleptic.
XX
OS Homo sapiens.
XX
PN WO200254939-A2.
XX
PD 18-JUL-2002.
XX
PF 07-JAN-2002; 2002WO-US00367.
XX

PR 09-JAN-2001; 2001US-0757300.
PR 23-AUG-2001; 2001US-0935464.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyer JM, Barrington-Martin R, Parker A;
XX WPI; 2002-590643/63.
XX
DR New variants of calcium/calmodulin-dependent protein kinase-like
XX PT nucleic acids and polypeptides, useful for diagnosing and treating
PT neuropsychiatric disorders, e.g. schizophrenia, schizoaffective
PT disorder, and bipolar disorder.
PS Claim 1; Page 119-200; 223pp; English.
XX
CC The invention relates to a nucleic acid comprising a polymorphic region
CC of a Calcium/calmodulin-dependent protein kinase-like gene (CADPKL)
CC allelic variant, and the polypeptide it encodes. CADPKL allelic variants
CC are useful in determining whether a subject has or is at risk of
CC developing a neuropsychiatric disorder, such as schizophrenia, attention
CC deficit disorder (ADD), schizoaffective disorder, bipolar disorder,
CC unipolar affective disorder and adolescent conduct disorder. The
CC polypeptides, polynucleotides, antibodies and modulators of the CADPKL
CC allelic variants are useful for diagnosing or treating these
CC neuropsychiatric disorders. The polypeptides may be used to raise
CC antibodies to a CADPKL polypeptide. The nucleic acids may be used as
CC probes or primers, in pharmacogenomics for designing therapies for the
CC disorders, and in fingerprinting for detection of different individuals
CC with the same species (e.g. paternity testing). This sequence represents
CC human CADPKL genomic DNA of the invention.
XX
SQ Sequence 157875 BP; 44403 A; 35734 C; 34322 G; 43416 T; 0 other;
Query Match 0.1%; Score 22; DB 24; Length 157875;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28643 CTGGCTGCTGCTGCTGCT 28664
DB 80030 CTGGCTGCTGCTGCTGCT 80051
RESULT 40
ABZ23704
ID ABZ23704 standard; CDNA; 254366 BP.
XX
AC ABZ23704;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human phosphatase genomic DNA #SEQ ID 3.
XX
KW Human; phosphatase; enzyme; chromosome 12; colon adenocarcinoma;
KW placenta; gene therapy; single nucleotide polymorphism; SNP;
KW gene; ds.
XX
OS Homo sapiens.
XX
FH Key
FH variation
FT location/Qualifiers
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FT /standard_name= "single nucleotide polymorphism"
FT replace(1414, A,C)
FT /tag= b
FT /standard_name= "single nucleotide polymorphism"
FT replace(1743,C)
FT /tag= c
FT /standard_name= "single nucleotide polymorphism"
FT replace(2766,A)
FT /tag= d
FT /standard_name= "single nucleotide polymorphism"
FT replace(3155,T)
FT variation

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FT      replace(6074,T)
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FT      replace(9550,C)
FT      /*tag- h
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FT      replace(9644,G)
FT      /*tag- i
FT      /standard_name= "single nucleotide polymorphism"
FT      replace(16630,G)
FT      /*tag- j
FT      /standard_name= "single nucleotide polymorphism"
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FT      /standard_name= "single nucleotide polymorphism"
FT      replace(18299,G)
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FT      replace(23521,G)
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FT      /standard_name= "single nucleotide polymorphism"
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FT      /standard_name= "single nucleotide polymorphism"
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FT      /standard_name= "single nucleotide polymorphism"
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FT      /*tag- ac

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FT      replace(82930,C)
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FT      /*tag- an
FT      /standard_name= "single nucleotide polymorphism"
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FT      replace(129447,A)
FT      /*tag- ba
FT      /standard_name= "single nucleotide polymorphism"
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FT /standard_name= "single nucleotide polymorphism"
FT variation replace(148111,T)
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FT /standard_name= "single nucleotide polymorphism"
FT variation replace(200822,G)
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FT variation replace(207967,G)
FT /*tag= be
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(213624,C)
FT /*tag= bf
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(215753,G)
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FT /standard_name= "single nucleotide polymorphism"
FT variation replace(216081,A)
FT /*tag= bh
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(218692,T)
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FT /standard_name= "single nucleotide polymorphism"
FT variation replace(218705,G)
FT /*tag= bj
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Query Match 0.1%; Score 22; DB 25; Length 254366;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25240 AACGCAAAATTAATTTAA 25261
Db 244415 AACGCAAAATTAATTTAA 244436

RESULT 41

```
AAF22305
ID AAF22305 standard; DNA; 1082138 BP.
XX
AC AAF22305;
XX
DT 20-MAR-2001 (first entry)
XX
DE Arabidopsis thaliana chromosome 4 centromere.
XX
KW Centromere; michromosome; vector; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200055325-A2.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US07392.
XX
PR 18-MAR-1999; 99US-0125219.
PR 01-APR-1999; 99US-0127409.
PR 18-MAY-1999; 99US-0134770.
PR 13-SEP-1999; 99US-0153584.
PR 17-SEP-1999; 99US-0154603.
XX
PA (UYCH-) UNIV CHICAGO.
PI Preuss D, Copenhaver G, Keith K;
XX
DR WPI; 2000-587529/55.
XX
PT Recombinant DNA construct comprising a plant centromere, useful for
PT producing stably inherited michrosomes which can serve as vectors for
PT the construction of transgenic plant and animal cells.
PS Claim 68; Page 977-1388; 1449pp; English.
```

XX The present invention relates to a recombinant DNA construct of a plant
CC (Arabidopsis thaliana) centromere. The constructs are useful for
CC producing stably inherited michrosomes which can serve as vectors for
CC the construction of transgenic plant and animal cells expressing
CC selected proteins such as hormones, enzymes, interleukins, clotting
CC factors, cytokines, antibodies, and growth factors.
XX

SQ Sequence 1082138 BP; 348775 A; 194404 C; 195515 G; 343444 T; 0 other;

Query Match 0.1%; Score 22; DB 21; Length 1082138;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25246 AAAATTAATTTAAATAATA 25267
Db 637773 AAAATTAATTTAAATAATA 637794

RESULT 42

```
AAH42781/C
ID AAH42781 standard; cDNA; 414 BP.
XX
AC AAH42781;
XX
DT 01-OCT-2001 (first entry)
XX
DE Nucleotide sequence of cancer associated gene KIA0160.
XX
KW Cancer associated gene; prostate cancer; stomach cancer;
KW oesophageal cancer; cancer; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200153524-A2.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-GB00188.
XX
PR 18-JAN-2000; 2000GB-0000993.
XX
PA (UYNO-) UNIV NOTTINGHAM TRENT.
XX
PI Rees RC, Li G, Mian S;
XX
DR WPI; 2001-476121/51.
XX
PT Use of cancer-associated genes and their products in detecting,
PT monitoring, treating or preventing cancer, specifically prostate
PT cancer, and in developing DNA-based vaccines that promote anti-tumor
PT responses
```

PS Claim 1; Page 18; 43pp; English.

CC AAH42781-AAH42846 represent the nucleotide sequences of cancer
CC associated genes, identified using SEREX (Serological Identification of
CC Antigens by Recombinant Expression Cloning). The genes are overexpressed
CC in prostate cancer, and some are overexpressed in other cancers such as
CC stomach cancer and oesophageal cancer. The nucleic acids are useful for
CC detecting and monitoring cancer, particularly prostate cancer. They are
CC particularly useful in the treatment or prevention of cancer. In
CC producing DNA-based vaccines against prostate cancer or that promote
CC anti-tumor immune responses, and to raise antibodies. The expression of
CC genes and detection of their protein products and/or peptides may be
CC used to monitor disease progression during therapy, or as a prognostic
CC indicator of initial disease status of the patient.

XX SQ Sequence 414 BP; 101 A; 102 C; 132 G; 79 T; 0 other;

Query Match 0.1%; Score 21; DB 22; Length 414;
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 12956 GCCACCGCGCGCGACCCCG 12976
|||||
DB 62 GCCACCGCGCGCGACCCCG 42

RESULT 43
ABQ41636
ID ABQ41636 standard; DNA: 597 BP.
XX
AC ABQ41636:
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28227.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001MO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12: 56bp + Sequence Listing; 56bp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 597 BP: 48 A; 87 C; 217 G; 245 T; 0 other;

Query Match 0.1%; Score 21; DB 24; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 16383 GCGGGGCGCGCGCGCGCG 16403
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DB 413 GCGGGGCGCGCGCGCGCGCG 433

RESULT 44
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XX
AC ABQ41637:
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28228.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001MO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
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PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12: 56bp + Sequence Listing; 56bp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 597 BP: 245 A; 217 C; 87 G; 48 T; 0 other;

Query Match 0.1%; Score 21; DB 24; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 16383 GCGGGGCGCGCGCGCGCGCG 16403
|||||

DB 185 GCGGGGCGCGCGCGCGCGCG 165

RESULT 45
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ID AAK77708 standard; DNA; 607 BP.
XX
AC AAK77708;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:32520.
XX
KW Human; Immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0188874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
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PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225447.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
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PR 01-SEP-2000; 2000US-0229345.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0232080.
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PR 21-SEP-2000; 2000US-0234223.
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PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236327.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 17-NOV-2000; 2000US-0249300.
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PR 01-DEC-2000; 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure: SEQ ID NO 32520; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 607 BP: 192 A; 127 C; 123 G; 165 T; 0 other;
SO

Query Match 0.1%; Score 21; DB 22; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12632 AATGAAATATATATATATA 12652
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Db 60 AATGAAATATATATATATA 80

Search completed: September 30, 2003, 03:05:17
Job time : 6377 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2003, 10:19:43 ; Search time 7579 Seconds
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12466.068 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

word size :

Total number of hits satisfying chosen parameters: 5105512

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SUMMARIES

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2	29420	84.1	128139	24	AA164291	RRV genome nucleot
3	624	1.8	624	21	AAC64764	RRV interl leukin 6
4	348	1.0	348	21	AAC64765	RRV macrophage in
5	201	0.6	630	24	AA164294	JMNV nucleotide se
6	107	0.3	406	24	AA164295	JMNV ORF1 nucleo
7	107	0.3	497	24	AA897190	JMNV ORF2 nucleo
8	74	0.2	358	24	AA164298	JMNV OR7 nucleo

C	9	71	0.2	426	24	AA164292	JMH Orf21 nucleot
C	10	71	0.2	524	24	AA164293	JMH Orf21 nucleot
C	11	70	0.2	314	24	ABA97191	JMH cosmid 3 ECOR
C	12	58	0.2	330	24	ABA97194	JMH cosmid 3 ECOR
C	13	59	0.2	681	24	ABA97192	JMH cosmid 3 ECOR
C	14	50	0.1	438	24	AA164300	JMH cosmid 3 ECOR
C	15	41	0.1	389	24	ABA97193	JMH cosmid 3 ECOR
C	16	40	0.1	630	24	AA164296	JMH Orf21 nucleot
C	17	37	0.1	524	24	AA164299	JMH nucleotide se
C	18	33	0.1	128139	24	AA164291	RRV genome nucleot
C	19	33	0.1	133719	21	AA164754	Macca multia rha
C	20	29	0.1	2511	18	AAC65153	Herpes virus DNA p
C	21	29	0.1	35100	20	AAV37802	KSHV LTR DNA (nucl
C	22	29	0.1	137507	19	AAV13941	KSHV long unique c
C	23	26	0.1	536	18	AA151545	Herpes virus DNA p
C	24	26	0.1	651	23	AA584956	DNA encoding novel
C	25	26	0.1	1024	25	AB283296	Toxicologically re
C	26	26	0.1	1536	24	ABO82701	Human thymidylate
C	27	26	0.1	1536	24	ABK90458	Human thymidylate
C	28	26	0.1	1536	24	ABK43335	Human Thymidylate
C	29	26	0.1	3056	18	AA184648	KSHV capsid matura
C	30	26	0.1	3598	24	AA594945	Human DNA sequence
C	31	26	0.1	3612	18	AA184697	KSHV capsid matura
C	32	26	0.1	18596	22	AAF31109	Thymidylate synth
C	33	26	0.1	18596	22	AA191215	Human thymidylate
C	34	26	0.1	18596	24	ABN95092	Gene #1590 used to
C	35	26	0.1	18596	24	ABK43334	Human Thymidylate
C	36	26	0.1	18596	24	ABL62854	Breast cancer rela
C	37	26	0.1	18596	24	ABL63078	Breast cancer rela
C	38	26	0.1	18596	24	ABL67927	Ovary cancer relat
C	39	24	0.1	535	24	ABL38539	Human colon tumour
C	40	24	0.1	1539	23	AA584960	DNA encoding novel
C	41	24	0.1	1692	22	ABA09660	Human bone marrow
C	42	24	0.1	3422	23	AA584959	DNA encoding novel
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C	44	23	0.1	542	24	ABO30240	Oligonucleotide fo
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ALIGNMENTS

RESULT 1
AAC64754

AC AAC64754;

DT 28-FEB-2001 (first entry)

Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1

KW	Macaca mullata rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
KW	genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;
KW	IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
KW	cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
KW	lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
KW	splenoomegaly; hypergammaglobulinlaemia; autoimmune haemolytic anaemia;
ds.	

OS Macaca mulatta rhadinovirus 17577.

PN WO200028040-A2

PD 18-MAY-2000.
XY

PF 05-NOV-1999; 99W0-0526260.

PR	08-NOV-1998;	98US-0107307.
PR	20-NOV-1998;	98US-0109409.

PA (UYOR-) UNIV OREGON HEALTH SCI.

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OY	2221	ACAGAAATGCTCATCAGAGAGAGATTTGAAGAATACCAACCAACACACAGTGA	2280
Db	2221	ACAGAAATGCTCATCAGAGAGAGATTTGAAGAATACCAACCAACACACAGTGA	2280
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OY	2461	ATTTTAAATTTACTACAGTGAATTAATTTGGAAGAGTAGATGAAGTTTTTTTACATGAC	2520
Db	2461	ATTTTAAATTTACTACAGTGAATTAATTTGGAAGAGTAGATGAAGTTTTTTTACATGAC	2520
OY	2521	TAGAAAATCAATATCATGCGATTTAATACGGAGATTTAGATCACAAATGAGTACATCAT	2580
Db	2521	TAGAAAATCAATATCATGCGATTTAATACGGAGATTTAGATCACAAATGAGTACATCAT	2580
OY	2581	TAAATGAATTAACATGATAGAACATATGATGTGTTAGATTAATTAATCTGTGGTTAT	2640
Db	2581	TAAATGAATTAACATGATAGAACATATGATGTGTTAGATTAATTAATCTGTGGTTAT	2640
OY	2641	TTTTTAATTAATAACATTAACAACATTTAAGCAGCATTTTGTGTAAATCCTTTATTTAT	2700
Db	2641	TTTTTAATTAATAACATTAACAACATTTAAGCAGCATTTTGTGTAAATCCTTTATTTAT	2700

QY	2701	AAAAATTTTTCATATACCTGAAACTATATTTAAATTCATTTTCCCTCAAGTTTGTATC	2760
Db	2701	AAAAATTTTTCATATACCTGAAACTATATTTAAATTCATTTTCCCTCAAGTTTGTATC	2760
QY	2761	TTTGGCCGGTATCCTGATTAACATGAGTATATTCGGTAAATTAATTAATGATGAAAAAATAC	2820
Db	2761	TTTGGCCGGTATCCTGATTAACATGAGTATATTCGGTAAATTAATTAATGATGAAAAAATAC	2820
QY	2821	ATCAACAACAAACCTCTCATATATGCGCGTAAATATATAGTTTAAAGGACACTTATAGTT	2880
Db	2821	ATCAACAACAAACCTCTCATATATGCGCGTAAATATATAGTTTAAAGGACACTTATAGTT	2880
QY	2881	AAGAACTCTCATTAACAGATTTTTCCTCAATAAACCCAGACCGTATTAAATGTCCTTT	2940
Db	2881	AAGAACTCTCATTAACAGATTTTTCCTCAATAAACCCAGACCGTATTAAATGTCCTTT	2940
QY	2941	TAGTTGTATGTCTATAGAAATTAACAGCATGCTATGCGTCTCGCTACAAAGTGGC	3000
Db	2941	TAGTTGTATGTCTATAGAAATTAACAGCATGCTATGCGTCTCGCTACAAAGTGGC	3000
QY	3001	TCCGCGCGGTGGTTCACGTAATTTCTGCTCAAAAATATATTAATTTGTTCTGTCACACAGAG	3060
Db	3001	TCCGCGCGGTGGTTCACGTAATTTCTGCTCAAAAATATATTAATTTGTTCTGTCACACAGAG	3060
QY	3061	GCGCTTCTTTTCAAGGATGAAAAACCATGTTCTTTTCCCATTAATTAACACATTTCTTTTC	3120
Db	3061	GCGCTTCTTTTCAAGGATGAAAAACCATGTTCTTTTCCCATTAATTAACACATTTCTTTTC	3120
QY	3121	ACCTTAACACCGATGGCGGTAGACGTCATTTTCTGAAAAATACATTCATTTGTTCTTAAGSTA	3180
Db	3121	ACCTTAACACCGATGGCGGTAGACGTCATTTTCTGAAAAATACATTCATTTGTTCTTAAGSTA	3180
QY	3181	CGGCGAAGGCAATGTTCGCTTTTAAACAAATTCCTTAATTCATTCACATCACTGCAACAGATGCA	3240
Db	3181	CGGCGAAGGCAATGTTCGCTTTTAAACAAATTCCTTAATTCATTCACATCACTGCAACAGATGCA	3240
QY	3241	GTTAACTGTAAATGTCATGTTAGTTAGTGGCACTGACGGGTTTAAACAGAGTATTTTCA	3300
Db	3241	GTTAACTGTAAATGTCATGTTAGTTAGTGGCACTGACGGGTTTAAACAGAGTATTTTCA	3300
QY	3301	CAATTATTAACAAATAAACCCACGACGACATGACTTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA	3360
Db	3301	CAATTATTAACAAATAAACCCACGACGACATGACTTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA	3360
QY	3361	TAGTAAATCATATTCGCTTTCACATTAATGAGCAAAAACGAAAAAATGTTACTGTTTAAAG	3420
Db	3361	TAGTAAATCATATTCGCTTTCACATTAATGAGCAAAAACGAAAAAATGTTACTGTTTAAAG	3420
QY	3421	CCTACCTTGTTGGATGGATTTATGTTTACAATGAAAAATATAATATATATTAACGTT	3480
Db	3421	CCTACCTTGTTGGATGGATTTATGTTTACAATGAAAAATATAATATATATTAACGTT	3480
QY	3481	TTTTACGTAAAAACATATGTATTTAATACAGTGTATTTATGTTGGCTACTTAACACACA	3540
Db	3481	TTTTACGTAAAAACATATGTATTTAATACAGTGTATTTATGTTGGCTACTTAACACACA	3540
QY	3541	ATGTTTGCATTAAGCACTTAATGTTAGAGCTTCAATCTTATATTTTAAATTTATTTCAAAATGT	3600
Db	3541	ATGTTTGCATTAAGCACTTAATGTTAGAGCTTCAATCTTATATTTTAAATTTTATTTCAAAATGT	3600
QY	3601	TTTAAAGAGCATGTGAATATATTTAAACAGCATTCAGAAATAGGCGCAACGCTGCGCT	3660
Db	3601	TTTAAAGAGCATGTGAATATATTTAAACAGCATTCAGAAATAGGCGCAACGCTGCGCT	3660
QY	3661	ATAACTGGTAAAAACATGACGTTTAAACCTTTTCTCTGTTTAAATTAACAGCATATATG	3720
Db	3661	ATAACTGGTAAAAACATGACGTTTAAACCTTTTCTCTGTTTAAATTAACAGCATATATG	3720
QY	3721	TACGTCCACTGGATGAAGCAATGTTAAACCTCACATTTACAGGAATATGCGGTCAAGCT	3780
Db	3721	TACGTCCACTGGATGAAGCAATGTTAAACCTCACATTTACAGGAATATGCGGTCAAGCT	3780
QY	3781	AACACAGAAAGCACTTATATAGTGTGGAGAAACAGCTGATTAATTTGTCTGCTGGT	3840

Db 3781 AACACGAAAAAGACTTATATAGTGTGGAGAAACAGCTGAATTAATTTGTCCTCGT 3940
QY 3841 TATGTACAAATACAAAAATATATACAAACAGATGTTTACAAAATGGTACGTGTACACA 3900
Db 3841 TATGTACAAATACAAAAATATATACAAACAGATGTTTACAAAATGGTACGTGTACACA 3900
QY 3901 CCAAAATTTTCATCGACACAGAAAAAGATGCCACACCTGCTGACTGCTGAATGAGCC 3960
Db 3901 CCAAAATTTTCATCGACACAGAAAAAGATGCCACACCTGCTGACTGCTGAATGAGCC 3960
QY 3961 GTGCACATTCACGGGGGAGATATGCTTAATTTGATGCCAATTTTCCTGTGAGTGT 4020
Db 3961 GTGCACATTCACGGGGGAGATATGCTTAATTTGATGCCAATTTTCCTGTGAGTGT 4020
QY 4021 AATGAAGTTATGATTTAATTTGTTAGTAAATGTTGCTTTTGTATTTTACAGACACAGAA 4080
Db 4021 AATGAAGTTATGATTTAATTTGTTAGTAAATGTTGCTTTTGTATTTTACAGACACAGAA 4080
QY 4081 AACGTAAATTTGGGATTCAAAATGACACAGCTGTGAAATTCAGAAATGATTTAAACGACCG 4140
Db 4081 AACGTAAATTTGGGATTCAAAATGACACAGCTGTGAAATTCAGAAATGATTTAAACGACCG 4140
QY 4141 GCAGTGAACATGGGGAGTACTACCTACCTAACCAAGATGTTTATTAAGTATGAGATGCAATT 4200
Db 4141 GCAGTGAACATGGGGAGTACTACCTACCTAACCAAGATGTTTATTAAGTATGAGATGCAATT 4200
QY 4201 ACATTTAAATGTTTCAATTTGCTATACACTGTTGATCAACAACATTAATGATGACAGTCA 4260
Db 4201 ACATTTAAATGTTTCAATTTGCTATACACTGTTGATCAACAACATTAATGATGACAGTCA 4260
QY 4261 AACAAAAATGGTCAAACTCTTCCCAAGCTGTTTAATGCTGATGTAAGTGAAGTCCACAA 4320
Db 4261 AACAAAAATGGTCAAACTCTTCCCAAGCTGTTTAATGCTGATGTAAGTGAAGTCCACAA 4320
QY 4321 ATAGACAATGGGTACATACATGATGCTGTCAGAAAGATACAAACATGAGACATCAATT 4380
Db 4321 ATAGACAATGGGTACATACATGATGCTGTCAGAAAGATACAAACATGAGACATCAATT 4380
QY 4381 ACTGTAAAGTGTAGCAGCGGATACAACTGTTGGGCTGAAAACATTTAACGTGACACAAC 4440
Db 4381 ACTGTAAAGTGTAGCAGCGGATACAACTGTTGGGCTGAAAACATTTAACGTGACACAAC 4440
QY 4441 ACAACTTGGGTTCCACATTAAGTATGCTGATGTTGATGTTTACAAATTAACCAACAGCACCC 4500
Db 4441 ACAACTTGGGTTCCACATTAAGTATGCTGATGTTGATGTTTACAAATTAACCAACAGCACCC 4500
QY 4501 ATGCCAGAAACACCCATGCCAGAAACACCCAGCCAGATTATCAAAAAATTAATTTGTCA 4560
Db 4501 ATGCCAGAAACACCCATGCCAGAAACACCCAGCCAGATTATCAAAAAATTAATTTGTCA 4560
QY 4561 ACCGCTAAATGTGCAACAACCAAAATGCGTTTGTATCAAACTGTTTCTCCAGAGAAA 4620
Db 4561 ACCGCTAAATGTGCAACAACCAAAATGCGTTTGTATCAAACTGTTTCTCCAGAGAAA 4620
QY 4621 GACGAGCTACTTGTGTAAAGCTCATTTTGAAGCCATTCATGTTAAAGGCTGAAAAATGAC 4680
Db 4621 GACGAGCTACTTGTGTAAAGCTCATTTTGAAGCCATTCATGTTAAAGGCTGAAAAATGAC 4680
QY 4681 AAGGAAAAATACAGTGTGTGAGAGCTGTTGAGCTAATATGTCGACAGAGATTTACTAAA 4740
Db 4681 AAGGAAAAATACAGTGTGTGAGAGCTGTTGAGCTAATATGTCGACAGAGATTTACTAAA 4740
QY 4741 ATGCACTTACAGTTTCTGTGAATGTTTGTCCAAAGCAATGCACTGCTCCAAATGCG 4800
Db 4741 ATGCACTTACAGTTTCTGTGAATGTTTGTCCAAAGCAATGCACTGCTCCAAATGCG 4800
QY 4801 AAGTGTACATGAAAAAATGTCCAAACCTTAAAGAACTTTTAAACGAGAGATATATAGTT 4860
Db 4801 AAGTGTACATGAAAAAATGTCCAAACCTTAAAGAACTTTTAAACGAGAGATATATAGTT 4860
QY 4861 ACAAGGGAGAGATGCTTTTAAGTACGAGAAATATTAACATTAATTAAGTATGAGGT 4920
Db 4861 ACAAGGGAGAGATGCTTTTAAGTACGAGAAATATTAACATTAATTAAGTATGAGGT 4920

Db 4861 ACAAGGGAGAGATGCTTTTAAGTACGAGAAATATTAACATTAATTAAGTATGAGGT 4920
QY 4921 TATCAACTTTTAGAAGTATGTCGCGAATTTGTATGCTTAAAGACGATTTAAACAGTT 4980
Db 4921 TATCAACTTTTAGAAGTATGTCGCGAATTTGTATGCTTAAAGACGATTTAAACAGTT 4980
QY 4981 GACTGGAGCCAAAGCGCTATATGTGATATTTGAAAAATGTAAAGCCACGACCAAAAT 5040
Db 4981 GACTGGAGCCAAAGCGCTATATGTGATATTTGAAAAATGTAAAGCCACGACCAAAAT 5040
QY 5041 ACAAGGAAAAATATCATCCGCTGTAAGAGACTTTATACATATTTGGACACCCGTAACATTT 5100
Db 5041 ACAAGGAAAAATATCATCCGCTGTAAGAGACTTTATACATATTTGGACACCCGTAACATTT 5100
QY 5101 TCGTGCATTCGTGACTTTTCTTATGTTGAGATGAATGACAACGTTATTAAGTAAATAGC 5160
Db 5101 TCGTGCATTCGTGACTTTTCTTATGTTGAGATGAATGACAACGTTATTAAGTAAATAGC 5160
QY 5161 TGGATTAACCCGTTTCCAAAGATGTGAACAATACCTTGCAGCGCTCTTAATATTGACAC 5220
Db 5161 TGGATTAACCCGTTTCCAAAGATGTGAACAATACCTTGCAGCGCTCTTAATATTGACAC 5220
QY 5221 GGAAGCTGCTAACAGTTCCTTCAACGCTTTTACAAATPACGGTCAATCTGTACATTTGGT 5280
Db 5221 GGAAGCTGCTAACAGTTCCTTCAACGCTTTTACAAATPACGGTCAATCTGTACATTTGGT 5280
QY 5281 TGTGAACGTGATTTACTTAATTTGGCAGTGAATTTCTACATGCAAGATTCATGCTGG 5340
Db 5281 TGTGAACGTGATTTACTTAATTTGGCAGTGAATTTCTACATGCAAGATTCATGCTGG 5340
QY 5341 GATCCACACTTCCTTACGTGCGTGCAGCTGTTTCAATGCTTCTGACACACTTAACCA 5400
Db 5341 GATCCACACTTCCTTACGTGCGTGCAGCTGTTTCAATGCTTCTGACACACTTAACCA 5400
QY 5401 GAAACCAAAAAACCAAAACAGCCACAGCCAGCAAGCAACCAACCAACCAACCAACGTT 5460
Db 5401 GAAACCAAAAAACCAAAACAGCCACAGCCAGCAAGCAACCAACCAACCAACCAACGTT 5460
QY 5461 GGAACACATACACCATTAACCAACCAACCAACCAACCAACCAACCAACCAACCAACGTT 5520
Db 5461 GGAACACATACACCATTAACCAACCAACCAACCAACCAACCAACCAACCAACCAACGTT 5520
QY 5521 AAATGAAAAAGGATGCTGTTGTTTGAAGTGTGCGCTGTTGTTATTCGTA 5580
Db 5521 AAATGAAAAAGGATGCTGTTGTTTGAAGTGTGCGCTGTTGTTATTCGTA 5580
QY 5581 CTTGCTGCCCTTATTTGTTTCTTAAATAACTGTTTCTTCTTACAGAGTTGCGC 5640
Db 5581 CTTGCTGCCCTTATTTGTTTCTTAAATAACTGTTTCTTCTTACAGAGTTGCGC 5640
QY 5641 AAGCAAACTGCGACGATTACCAATCTGCAACCCGCTGATTCGGAATTAAGTTTA 5700
Db 5641 AAGCAAACTGCGACGATTACCAATCTGCAACCCGCTGATTCGGAATTAAGTTTA 5700
QY 5701 CATTATTCAGAGTGTGCATTAAGGTTTAAATATTTCTATGTTGCTCATGTTT 5760
Db 5701 CATTATTCAGAGTGTGCATTAAGGTTTAAATATTTCTATGTTGCTCATGTTT 5760
QY 5761 ATGTTGACCCGTTTATAGTTATGCGCAGCTTGTGCTTACATTAATATAGCAAGATCACT 5820
Db 5761 ATGTTGACCCGTTTATAGTTATGCGCAGCTTGTGCTTACATTAATATAGCAAGATCACT 5820
QY 5821 TTCCACGTTTATCTTACGTTACTATGACTCATACGCTTAAAGCTGACGCTGCGTGCAT 5880
Db 5821 TTCCACGTTTATCTTACGTTACTATGACTCATACGCTTAAAGCTGACGCTGCGTGCAT 5880
QY 5881 TGTGCGCGGGGCTGAAAAATTAACAAGGGGTACATATTCATATCCAGCGGCAACATTAAG 5940
Db 5881 TGTGCGCGGGGCTGAAAAATTAACAAGGGGTACATATTCATATCCAGCGGCAACATTAAG 5940
QY 5941 ACACGGTTTATTAATATATGATGCGCCCAACATCACTGTGCTGCTACGACACTGATA 6000
Db 5941 ACACGGTTTATTAATATATGATGCGCCCAACATCACTGTGCTGCTACGACACTGATA 6000

QY	6001	GAATAACATTTTAAAGTTTGTATTAGCAACTGTAATAACATTAATGGCTTCCAAAGCA	6060
Db	6001	GAATAACATTTTAAAGTTTGTATTAGCAACTGTAATAACATTAATGGCTTCCAAAGCA	6060
QY	6061	ACGGCGGACAAACCCCTGGAGATATATCAGGGGTCTGTGCCCGATAGGTGGGTGGGAT	6120
Db	6061	ACGGCGGACAAACCCCTGGAGATATATCAGGGGTCTGTGCCCGATAGGTGGGTGGGAT	6120
QY	6121	ACGGTACGGGTATTGCAACAAAGACTTTTCCCTTGGCGAGGCGTCCATCTCGGCACAA	6180
Db	6121	ACGGTACGGGTATTGCAACAAAGACTTTTCCCTTGGCGAGGCGTCCATCTCGGCACAA	6180
QY	6181	GACCATCTGGATCTGGCGTTTTCCTCCGTACCAATCTTTACGGACTTACAGTTGAACAG	6240
Db	6181	GACCATCTGGATCTGGCGTTTTCCTCCGTACCAATCTTTACGGACTTACAGTTGAACAG	6240
QY	6241	AATTCCCTCTCACCCTTAAAGCCGATACAAAAGTTGACACACAGCTGTGCCCTTA	6300
Db	6241	AATTCCCTCTCACCCTTAAAGCCGATACAAAAGTTGACACACAGCTGTGCCCTTA	6300
QY	6301	AGGTGACGTGGCTTTCACAGAGAGGTATTTGTTGTTTCACAATGCAAGTTTATTCAGGCGG	6360
Db	6301	AGGTGACGTGGCTTTCACAGAGAGGTATTTGTTGTTTCACAATGCAAGTTTATTCAGGCGG	6360
QY	6361	TGTTTGAAGGTACCGGCTTAAACGAACATATGCGAGGAAGCCAGGCTCTCTTTGGGTACA	6420
Db	6361	TGTTTGAAGGTACCGGCTTAAACGAACATATGCGAGGAAGCCAGGCTCTCTTTGGGTACA	6420
QY	6421	CGCAGTTTATTAAGAACCGGGTCCACCTACACAGCATATGGAACCCCTGTGAATGTCCGAGT	6480
Db	6421	CGCAGTTTATTAAGAACCGGGTCCACCTACACAGCATATGGAACCCCTGTGAATGTCCGAGT	6480
QY	6481	TACCGGACAAAGATGAGATGTTTCTTGCGCTTGTGTTACGGAAGGGTTTAAAGAAAGAC	6540
Db	6481	TACCGGACAAAGATGAGATGTTTCTTGCGCTTGTGTTACGGAAGGGTTTAAAGAAAGAC	6540
QY	6541	TGTGGAGGGGCTGTCTCGTCCCGCGGTGTTCCAGACCACAGCAGGTCCAGATTGCCGAC	6600
Db	6541	TGTGGAGGGGCTGTCTCGTCCCGCGGTGTTCCAGACCACAGCAGGTCCAGATTGCCGAC	6600
QY	6601	GCCAGGCGTTTAAAGTGGCGTTGTACGACGAAAGACCTGTTGGACCTCAGGGTATTAAGAA	6660
Db	6601	GCCAGGCGTTTAAAGTGGCGTTGTACGACGAAAGACCTGTTGGACCTCAGGGTATTAAGAA	6660
QY	6661	TGCCAAGGTTTACCATTAAGACGTATAGCGGTACTCTACGACTCCCTCTTACACAGCA	6720
Db	6661	TGCCAAGGTTTACCATTAAGACGTATAGCGGTACTCTCTACGACTCCCTCTTACACAGCA	6720
QY	6721	TGCGCCAGGGCCTTGAGACTCAAAAGACGTGAGCGGCGTATCTCACGCCACAGAAAGCAAT	6780
Db	6721	TGCGCCAGGGCCTTGAGACTCAAAAGACGTGAGCGGCGTATCTCACGCCACAGAAAGCAAT	6780
QY	6781	TCATGCAAGGACCATTAACAAATTGCCAAGATAGTGCAGCAAAACAGTTTTCACAGCAGC	6840
Db	6781	TCATGCAAGGACCATTAACAAATTGCCAAGATAGTGCAGCAAAACAGTTTTCACAGCAGC	6840
QY	6841	TGCGGAAAGACAGAGAGGGGTGCGCCACATGATTTGGACAGAGGTGGTGGCGGAGCTCG	6900
Db	6841	TGCGGAAAGACAGAGAGGGGTGCGCCACATGATTTGGACAGAGGTGGTGGCGGAGCTCG	6900
QY	6901	CCCTTAGTTACGGCTGTATGTTTCTCGAGTGTCCCGAGAGCGCTGGCAGTTGCTGAACT	6960
Db	6901	CCCTTAGTTACGGCTGTATGTTTCTCGAGTGTCCCGAGAGCGCTGGCAGTTGCTGAACT	6960
QY	6961	ACGATAGCTGGCCCATATTTGATGTTGTGACTCACAGAGGCTTAGGGTTAACCGCTTAG	7020
Db	6961	ACGATAGCTGGCCCATATTTGATGTTGTGACTCACAGAGGCTTAGGGTTAACCGCTTAG	7020
QY	7021	AGCGCTGGTGGCGGGAACAGGCGGTTCACGTGGGGGGTCACTGTGTGCTGCCAATTCCG	7080
Db	7021	AGCGCTGGTGGCGGGAACAGGCGGTTCACGTGGGGGGTCACTGTGTGCTGCCAATTCCG	7080

QY	7081	1GCTGACTACTACCTAAAGTGTGAGAAACAAGGCGCCACGAGGACAAAAAGGAGAGCTAAAGC	7140
Db	7081	TGCTGTACTACTACCTAAAGTGTGAGAAAGGCGCCACGAGGACAAAAAGGAGAGCTAAAGC	7140
QY	7141	TGTCACACTCCTTTTCTCTCCACACAGGACTGGGGGTTTAAATGAGAGCCACGATCAAG	7200
Db	7141	TGTACACTCCTTTTCTCTCCACACAGGACTGGGGGTTTAAATGAGAGCCACGATCAAG	7200
QY	7201	AAACGGCAGCGAAGCCCTTAAAGGGCGTACCCTCAACGCCCCGATGCTTCTTCGTTCA	7260
Db	7201	AAAAGGGAGGAGAAAGCCTTAAAGGGCGTACCCTCAACGCCCCGATGCTTCTTCGTTCA	7260
QY	7261	CGCGGTATCACCTGGCTACGCGCGCTTCTGCCCCATCTCTGGCCAGATTATGTT	7320
Db	7261	CGCGGTATCACCTGGCTACGCGCGCTTCTGCCCCATCTCTGGCCAGATTATGTT	7320
QY	7321	ATTACATGCACTTTCTTGCAACACCAAAAGCTCCAGAACCAAGGCTTAACTAGGATCC	7380
Db	7321	ATTACATGCACTTTCTTGCAACACCAAAAGCTCCAGAACCAAGGCTTAACTAGGATCC	7380
QY	7381	ATTATGTCGACCGCGCCGCAACTCAGAGATGTGACAGCTATGTACAGGCAACGCGCG	7440
Db	7381	ATTATGTCGACCGCGCCGCAACTCAGAGATGTGACAGCTATGTACAGGCAACGCGCG	7440
QY	7441	CAAGTCGCTTAACACACGCTGTTCTATATGACTGAAAGATAGTTTCCGCGCTAAACACCC	7500
Db	7441	CAAGTCGCTTAACACACGCTGTTCTATATGACTGAAAGATAGTTTCCGCGCTAAACACCC	7500
QY	7501	CTCAGCGGAGGAGGACCCCTACGTGGTGGAGCGGAAACAGCCGGAGCCTTAAACGACTGGAGA	7560
Db	7501	CTCAGCGGAGGAGGACCCCTACGTGGTGGAGCGGAAACAGCCGGAGCCTTAAACGACTGGAGA	7560
QY	7561	TTCTGGGCACTTGCGCGAGCTTATGAGACCGCGAAGAGGAGGAAACCCGGCGAGCAGC	7620
Db	7561	TTCTGGGCACTTGCGCGAGCTTATGAGACCGCGAAGAGGAGGAAACCCGGCGAGCAGC	7620
QY	7621	ACCCAAAGTACACGACTCTGGCAGCTATGTACAGCCGTGACAGAAAAGCTATCCGCGATTG	7680
Db	7621	ACCCAAAGTACACGACTCTGGCAGCTATGTACAGCCGTGACAGAAAAGCTATCCGCGATTG	7680
QY	7681	GAATCACCAGAGACAGCATATATACGAGCACTCATACCAACATCCAAAGTTTTCGA	7740
Db	7681	GAATCACCAGAGACAGCATATATACGAGCACTCATACCAACATCCAAAGTTTTCGA	7740
QY	7741	GGGTGTTCAAGGATCGACTCAATTTGTGACGAGGAGAGTCAAGTTTCCTTAATTCGA	7800
Db	7741	GGGTGTTCAAGGATCGACTCAATTTGTGACGAGGAGAGTCAAGTTTCCTTAATTCGA	7800
QY	7801	TGATTTAAATAATTACTTAAATTTCCGCGAGCACGTCAAATTCGGTCCATCATACTCCAGT	7860
Db	7801	TGATTTAAATAATTACTTAAATTTCCGCGAGCACGTCAAATTCGGTCCATCATACTCCAGT	7860
QY	7861	TCTGTGCAAGCTGATATGAGGAGCGCGCTCGCGGTTCTGTAACTGATACAAAT	7920
Db	7861	TCTGTGCAAGCTGATATGAGGAGCGCGCTCGCGGTTCTGTAACTGATACAAAT	7920
QY	7921	CCCTGCTGTGATCATTTAGGATATCTGCCCTGACGATGATATCTAGCAACAAGATA	7980
Db	7921	CCCTGCTGTGATCATTTAGGATATCTGCCCTGACGATGATATCTAGCAACAAGATA	7980
QY	7981	ATCCGGCGATGGGCACTCCCTCCCTCCGAGTGGCTAAAGATGCATTTTCAGACGTTGTGA	8040
Db	7981	ATCCGGCGATGGGCACTCCCTCCCTCCGAGTGGCTAAAGATGCATTTTCAGACGTTGTGA	8040
QY	8041	CGAACTTTAAAGCGGCGGTCTCGACCGCGGGGTCTCTACGGGGTGCACACTGAAAAATCG	8100
Db	8041	CGAACTTTAAAGCGGCGGTCTCGACCGCGGGGTCTCTACGGGGTGCACACTGAAAAATCG	8100
QY	8101	TACACCGGAGATGTTTGCACACTTCTTCGACACGAGCGGAGGTCACAAGGCTTAATG	8160
Db	8101	TACACCGGAGATGTTTGCACACTTCTTCGACACGAGCGGAGGTCACAAGGCTTAATG	8160
QY	8161	CCCCCTTTAAATGCAAGCTTAGAATAGCCGAGGCGATGATGTCGTTCCGAATTCATTA	8220

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Db 8161 CCCCCCTTAATGATGAGTTAGAAATAGCCGAGCCATGATGTGTTCCGAATCAATTA 8220
QY 8221 AAAAAAAAAATGATCATTTTTTTCACACCGCGGGATCCGAGGCGGTGCGAGTGGGGT 8280
Db 8221 AAAAAAAAAATGATCATTTTTTTCACACCGCGGGATCCGAGGCGGTGCGAGTGGGGT 8280
QY 8281 TCGTCAAAACGAGCGGAACACGAGACACTTACGTGTGGCGGACCGCTGATGAAAGTTTC 8340
Db 8281 TCGTCAAAACGAGCGGAACACGAGACACTTACGTGTGGCGGACCGCTGATGAAAGTTTC 8340
QY 8341 TCAACTGCTGATCGGCGGCTGTCCCGACACAGACCGCGCGTGTACCTGTGCGC 8400
Db 8341 TCAACTGCTGATCGGCGGCTGTCCCGACACAGACCGCGCGTGTACCTGTGCGC 8400
QY 8401 ACAAGATCTCCACAGACCAACAAAACCCAGTTCTGAAAAGAGTCCCGAGACGAGCTGG 8460
Db 8401 ACAAGATCTCCACAGACCAACAAAACCCAGTTCTGAAAAGAGTCCCGAGACGAGCTGG 8460
QY 8461 CGGAGCTGTGTCTGTACGTAAAGACACACAGCTCGCGTTGAGAAAACGAACTGCTGG 8520
Db 8461 CGGAGCTGTGTCTGTACGTAAAGACACACAGCTCGCGTTGAGAAAACGAACTGCTGG 8520
QY 8521 ACGTGTCCGAGTTCACTATGTCTGTACGCGAGAGATCAAACTGAACGCGGCCATTTCTAA 8580
Db 8521 ACGTGTCCGAGTTCACTATGTCTGTACGCGAGAGATCAAACTGAACGCGGCCATTTCTAA 8580
QY 8581 GGGCATGTGGCCAGATTCACTTCTACGCCACAGACGCTGCACTGCTCAGCGCGGTGTAC 8640
Db 8581 GGGCATGTGGCCAGATTCACTTCTACGCCACAGACGCTGCACTGCTCAGCGCGGTGTAC 8640
QY 8641 AGAGCATGATGCCGAGAGATACCCCAAGCTGTGGGCTCGCGGCAATGCCACACCGG 8700
Db 8641 AGAGCATGATGCCGAGAGATACCCCAAGCTGTGGGCTCGCGGCAATGCCACACCGG 8700
QY 8701 TGGCTTACCTGCGAGAATAGCGCGGCCGACCGCCCTACCGTCCACAGACGAGCGGCTC 8760
Db 8701 TGGCTTACCTGCGAGAATAGCGCGGCCGACCGCCCTACCGTCCACAGACGAGCGGCTC 8760
QY 8761 AGCGGTGCGCCGACAGGGCGCCTGCGTCCCGATTAACCGTTCATGATGATCAACA 8820
Db 8761 AGCGGTGCGCCGACAGGGCGCCTGCGTCCCGATTAACCGTTCATGATGATCAACA 8820
QY 8821 AATACAGGGGGGTCAACGGGAACAACAAGCTTTTCCACTGCGGAAACCTGGGTACTTCG 8880
Db 8821 AATACAGGGGGGTCAACGGGAACAACAAGCTTTTCCACTGCGGAAACCTGGGTACTTCG 8880
QY 8881 CGGGGCGCGGCTGTGACCGCAACTGTGGCGGAAAGCTCCCTTTAAGAAAACGGGCG 8940
Db 8881 CGGGGCGCGGCTGTGACCGCAACTGTGGCGGAAAGCTCCCTTTAAGAAAACGGGCG 8940
QY 8941 TCAAGCGCATGCTAAGAAAGACACGTGATGATGACCCCATTTATGACCGCCTAATAA 9000
Db 8941 TCAAGCGCATGCTAAGAAAGACACGTGATGATGACCCCATTTATGACCGCCTAATAA 9000
QY 9001 AGGAGCGCGGGGACACACATGACACGTTTCAGGCGGAAAGCGTTAAAGAGCGCTGC 9060
Db 9001 AGGAGCGCGGGGACACACATGACACGTTTCAGGCGGAAAGCGTTAAAGAGCGCTGC 9060
QY 9061 AGGCGCTGTAGAGATAGAGACAACCTTAACCTATTGAAGTGGGTATCTGGAGCTTA 9120
Db 9061 AGGCGCTGTAGAGATAGAGACAACCTTAACCTATTGAAGTGGGTATCTGGAGCTTA 9120
QY 9121 TACGACACCTGGGGAAGGGTGCAGAGCTTAAGCTCCGAGGACGTGCAATATTACTCG 9180
Db 9121 TACGACACCTGGGGAAGGGTGCAGAGCTTAAGCTCCGAGGACGTGCAATATTACTCG 9180
QY 9181 GTACACTATTGTATGTGACGAGAGGTTTATTTAGCTGTGATTAATATGACAGCTCAG 9240
Db 9181 GTACACTATTGTATGTGACGAGAGGTTTATTTAGCTGTGATTAATATGACAGCTCAG 9240
QY 9241 GCGTGCCTGTGACTATCGAGGACGCGGCTCCCTAATAGAGATGCGCAGAGACGACAGC 9300
Db 9241 GCGTGCCTGTGACTATCGAGGACGCGGCTCCCTAATAGAGATGCGCAGAGACGACAGC 9300

Db 9241 GCGTGCCTGTGACTATCGAGGACGCGGCTCCCTAATAGAGATGCCAGACGACAGC 9300
QY 9301 ATCTTCAAGTTCTGTAGACAGCAGCATATCGCCACCGTCTCTGTACGCCCCCGAGAAC 9360
Db 9301 ATCTTCAAGTTCTGTAGACAGCAGCATATCGCCACCGTCTCTGTACGCCCCCGAGAAC 9360
QY 9361 AGCTACCGACCCCTTAGCGCGCGGCGCTTACTGGCCGGGAGAGACGAAAATTAACGCGC 9420
Db 9361 AGCTACCGACCCCTTAGCGCGCGGCGCTTACTGGCCGGGAGAGACGAAAATTAACGCGC 9420
QY 9421 TGTGAGGAGATCTGACCTTTAGAAAACCGTGGCAGGCGGCAACATGGCCGAGGAGAC 9480
Db 9421 TGTGAGGAGATCTGACCTTTAGAAAACCGTGGCAGGCGGCAACATGGCCGAGGAGAC 9480
QY 9481 TCGCAGCATTTATACGCGAGCTGTGCGGCCCTGCGCGTGTGATGATGATGATGATGAT 9540
Db 9481 TCGCAGCATTTATACGCGAGCTGTGCGGCCCTGCGCGTGTGATGATGATGATGATGAT 9540
QY 9541 CGGACCGCGCAAGTATGACGCGTCCCGCATTTTAAACAAAACACAGATAGAGAAC 9600
Db 9541 CGGACCGCGCAAGTATGACGCGTCCCGCATTTTAAACAAAACACAGATAGAGAAC 9600
QY 9601 TGAACCGGACCTTCTGCGCGCTGTACGCGGCAAAACCTGCTGAGACGTCGACGCTGT 9660
Db 9601 TGAACCGGACCTTCTGCGCGCTGTACGCGGCAAAACCTGCTGAGACGTCGACGCTGT 9660
QY 9661 CGCTCGAAGTGTGAGACACCTGCGCAAAACATCGAGGACAACTCGGAGCTGTGAGGCA 9720
Db 9661 CGCTCGAAGTGTGAGACACCTGCGCAAAACATCGAGGACAACTCGGAGCTGTGAGGCA 9720
QY 9721 GTCTGCGGCGAGATATTCCAGCGCGAGACATTTTGAACACTACACTGAGACCCGAT 9780
Db 9721 GTCTGCGGCGAGATATTCCAGCGCGAGACATTTTGAACACTACACTGAGACCCGAT 9780
QY 9781 GTCACTATCACTGTACGTTACTTTTCACTTTTACGGGGGGGTTATGATGATTAACA 9840
Db 9781 GTCACTATCACTGTACGTTACTTTTCACTTTTACGGGGGGGTTATGATGATTAACA 9840
QY 9841 TGTGCTTAATTAACGATGTAGAACTGTGTATAAAGACTAGGAGTGTGTTTATGCA 9900
Db 9841 TGTGCTTAATTAACGATGTAGAACTGTGTATAAAGACTAGGAGTGTGTTTATGCA 9900
QY 9901 TCGGTGAAACGAAGCTGTGTGCGGATTTGAACCGGTTTGTAGCTTCTGTCAACACTGC 9960
Db 9901 TCGGTGAAACGAAGCTGTGTGCGGATTTGAACCGGTTTGTAGCTTCTGTCAACACTGC 9960
QY 9961 GGGGTATCTCCCGATCCCGACCCAGACCTAATGCTGACAGTCACTGCTGCTAGACT 10020
Db 9961 GGGGTATCTCCCGATCCCGACCCAGACCTAATGCTGACAGTCACTGCTGCTAGACT 10020
QY 10021 GCGTGAAGGAAATCGAACTGTACCAATCAGGGGTCAGTTTACTGCGGTGTGCGAG 10080
Db 10021 GCGTGAAGGAAATCGAACTGTACCAATCAGGGGTCAGTTTACTGCGGTGTGCGAG 10080
QY 10081 ACCGACACTGCGATCACTCTGTGTAAGAAAGTTAGGGGGGAGCCAAATACAGGCTGTTG 10140
Db 10081 ACCGACACTGCGATCACTCTGTGTAAGAAAGTTAGGGGGGAGCCAAATACAGGCTGTTG 10140
QY 10141 AGACAGAACTGAGCAGCTGGGTCTAATAAAGTTGAGAAACGTTGAGAGCCAGCAGAGC 10200
Db 10141 AGACAGAACTGAGCAGCTGGGTCTAATAAAGTTGAGAAACGTTGAGAGCCAGCAGAGC 10200
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Db 10201 GCGTCCGCTCTGTGAGATCACTTAAGGAGTGTGCTGCGCGCCATCAAGATACA 10260
QY 10261 ATATATTCAACGGGTTCCGCGTCAATGGAACATATCAATCTTAATTTATTTGAAAG 10320
Db 10261 ATATATTCAACGGGTTCCGCGTCAATGGAACATATCAATCTTAATTTATTTGAAAG 10320
QY 10321 CCGGGCAAAACCGGCTCCAGACGCGGACGAAACGAGTCTGCAAAATGGCCAGACTGC 10380
Db 10321 CCGGGCAAAACCGGCTCCAGACGCGGACGAAACGAGTCTGCAAAATGGCCAGACTGC 10380

QY	10381	TTAACACAGAGCCGATATGCAACAGACCCGTGCTTAATAACCCAAACTAAGCGCA	10440
Db	10381	TTAACACAGAGCCGATATGCAACAGACCCGTGCTTAATAACCCAAACTAAGCGCA	10440
QY	10441	CTCAGCTTCAAGCATGTTTCCGAGCGGATGCCATGAAATCCCTGTTTCCGGCGCTT	10500
Db	10441	CTCAGCTTCAAGCATGTTTCCGAGCGGATGCCATGAAATCCCTGTTTCCGGCGCTT	10500
QY	10501	TTTAACCTATAGACGACACCATTAAGCAGCACTGAGCCGGGATTTGTCGCCGAGCTTTTC	10560
Db	10501	TTTAACCTATAGAGAGACACCATTAAGCAGCACTGAGCCGGGATTTGTCGCCGAGCTTTTC	10560
QY	10561	AACAGGCAAACTATACCACGTTTATGCGAAAAACAAAGAGCTGTTCAACAGACTCAATA	10620
Db	10561	AACAGGCAAACTATACCACGTTTATGCGAAAAACAAAGAGCTGTTCAACAGACTCAATA	10620
QY	10621	GCATCCGTCGCTCAAGGGAGGCGGGGATGCGAAAAACCGGCCACCCCTCGGAGCCAGGGA	10680
Db	10621	GCATCCGTCGCTCAAGGGAGGCGGGGATGCGAAAAACCGGCCACCCCTCGGAGCCAGGGA	10680
QY	10681	CCACCAACCGTGGCGGCAACCGCGGCAAGGACGCTCATCAAAAGACGACAGTATGCCAAAG	10740
Db	10681	CCACCAACCGTGGCGGCAACCGCGGCAAGGACGCTCATCAAAAGACGACAGTATGCCAAAG	10740
QY	10741	AACAGTCAATGAAAAAAGGTGGCCAGGAGCGGCTTTAAAAAACTAACAGAGTCTGCGAGA	10800
Db	10741	AACAGTCAATGAAAAAAGGTGGCCAGGAGCGGCTTTAAAAAACTAACAGAGTCTGCGAGA	10800
QY	10801	CGCAGACCGCGGCTGTTGGCAAAAGCACTGCAATGCGCGCTATGCGGGGGCGTCGCTACG	10860
Db	10801	CGCAGACCGCGGCTGTTGGCAAAAGCACTGCAATGCGCGCTATGCGGGGGCGTCGCTACG	10860
QY	10861	GCAGAGCGTCCGAGCTGCTGTAACCATTTTCTCCTCAGGCGGCGCTTCTGCGCTTCCCT	10920
Db	10861	GCAGAGCGTCCGAGCTGCTGTAACCATTTTCTCCTCAGGCGGCGCTTCTGCGCTTCCCT	10920
QY	10921	GGGAGGGCGCTCCCGCTCGCGATCAATTTTATTCGAAAACTCAAGTACATTAATAACT	10980
Db	10921	GGGAGGGCGCTCCCGCTCGCGATCAATTTTATTCGAAAACTCAAGTACATTAATAACT	10980
QY	10981	CACATATTTTCCAGAGCGCTAGTACGGGAACAGCTAGAGATTTATCAAGCGTGCAGTTTACG	11040
Db	10981	CACATATTTTCCAGAGCGCTAGTACGGGAACAGCTAGAGATTTATCAAGCGTGCAGTTTACG	11040
QY	11041	GCCTGATTAACCGGCCCCCTGACGCGCCAGAGCATCTTTTCCGGCCCCCGCAACGTCG	11100
Db	11041	GCCTGATTAACCGGCCCCCTGACGCGCCAGAGCATCTTTTCCGGCCCCCGCAACGTCG	11100
QY	11101	CGCTGGCCCAAGTGTTCGAGAGCGCGCGGGAATGCTTCCGATACCAAGATGCTGGTGTAG	11160
Db	11101	CGCTGGCCCAAGTGTTCGAGAGCGCGCGGGAATGCTTCCGATACCAAGATGCTGGTGTAG	11160
QY	11161	AGATGATATGAGCCCAAGATTCAACCGCAAGAGCTGATTAACCAAGACATTTAATCTTTTT	11220
Db	11161	AGATGATATGAGCCCAAGATTCAACCGCAAGAGCTGATTAACCAAGACATTTAATCTTTTT	11220
QY	11221	ACCAACTTCCCGAAGGTGATCTCAACGCGGTACAAAAGTCCGCTGGTCTTTATAGAG	11280
Db	11221	ACCAACTTCCCGAAGGTGATCTCAACGCGGTACAAAAGTCCGCTGGTCTTTATAGAG	11280
QY	11281	AGCGCGTCCTCGTGGTGGCGCTTTATTAATGCGACGCGGGAAAAAGACGCTGGCGAATTTT	11340
Db	11281	AGCGCGTCCTCGTGGTGGCGCTTTATTAATGCGACGCGGGAAAAAGACGCTGGCGAATTTT	11340
QY	11341	CCCTAGGCGCGAGAAACTCTCCATCTCCAACCTTAAGCTTAAGGCGCTGAGCTCGGCGC	11400
Db	11341	CCCTAGGCGCGAGAAACTCTCCATCTCCAACCTTAAGCTTAAGGCGCTGAGCTCGGCGC	11400
QY	11401	TGATATTAAGGTACGAGCAAGACGCGCGCTGTTCTAATTTCTCAAAATACGGCTGGA	11460
Db	11401	TGATATTAAGGTACGAGCAAGACGCGCGCTGTTCTAATTTCTCAAAATACGGCTGGA	11460

QY	11461	TATTTAAAGACGTGTACGCTCTTCTGTACATACCTGTGCACTGTCTCCAGGGCCATGATG	11520
Dp	11461	TATTTAAAGACGTGTACGCTCTTCTGTACATACCTGTGCACTGTCTCCAGGGCCATGATG	11520
QY	11521	ATTAACCTAACCGAAGCGCTGCTCTCCTGCGGGGCGGTGGGTGTATATCCGATCCGACAG	11580
Dp	11521	ATTAACCTAACCGAAGCGCTGCTCTCCTGCGGGGCGGTGGGTGTATATCCGATCCGACAG	11580
QY	11581	GGCGTTGGCGAAAACGTCTACACACCCCCAAGGGCGCACACACACCGCCGAGCCAGCGCG	11640
Dp	11581	GGCGTTGGCGAAAACGTCTACACACCCCCAAGGGCGCACACACACCGCCGAGCCAGCGCG	11640
QY	11641	GGCCCGTCGACGCCACACTCCCGAGAACCCACTAGGGCGGAGGCGTTTAAATTGGC	11700
Dp	11641	GGCCCGTCGACGCCACACTCCCGAGAACCCACTAGGGCGGAGGCGTTTAAATTGGC	11700
QY	11701	GTTGTGACGGCGCTGGCGCACGGGGGAACCTTCAAGTTTAACTGTGAAAAAACGTGTCCG	11760
Dp	11701	GTTGTGACGGCGCTGGCGCACGGGGGAACCTTCAAGTTTAACTGTGAAAAAACGTGTCCG	11760
QY	11761	GGCACGAGGACAAGACGACACCAAGAAAGCATCGATGTTTAAAAAAATATTTGTC	11820
Dp	11761	GGCACGAGGACAAGACGACACCAAGAAAGCATCGATGTTTAAAAAAATATTTGTC	11820
QY	11821	CCGCACATCTTTAAAGTCTACAGCGTACCGCAAGGTGGCCACTCGGTGACCTGTATGCA	11880
Dp	11821	CCGCACATCTTTAAAGTCTACAGCGTACCGCAAGGTGGCCACTCGGTGACCTGTATGCA	11880
QY	11881	GGGTGACACCGGACCGCGCGTGTACCGGCAAGAGTCAATCCGACCGGTGGCGGAGTTC	11940
Dp	11881	GGGTGACACCGGACCGCGCGTGTACCGGCAAGAGTCAATCCGACCGGTGGCGGAGTTC	11940
QY	11941	GAGATCAACACCATGACACAGACCTTACCACTGTTTGAAGTCATGCGCTTAAACGTCAAC	12000
Dp	11941	GAGATCAACACCATGACACAGACCTTACCACTGTTTGAAGTCATGCGCTTAAACGTCAAC	12000
QY	12001	GGCATAGTAAACACTTACACGGACAGGACTTCACTAACAGACGCTGTTTTCGACACCG	12060
Dp	12001	GGCATAGTAAACACTTACACGGACAGGACTTCACTAACAGACGCTGTTTTCGACACCG	12060
QY	12061	GTCGAGGGGGCTCACAGGTAACATTCACAGCATCTTCAGTACAGCGGTGGCTGTACACAGCA	12120
Dp	12061	GTCGAGGGGGCTCACAGGTAACATTCACAGCATCTTCAGTACAGCGGTGGCTGTACACAGCA	12120
QY	12121	CCGGGATGCTTTCCGGGAATTTTACAGAGGTACAGAACACGGTCAACTGACAGATCGTGCAC	12180
Dp	12121	CCGGGATGCTTTCCGGGAATTTTACAGAGGTACAGAACACGGTCAACTGACAGATCGTGCAC	12180
QY	12181	ATGATTCGGGGCTTCGGCGGAACCGTACTCTATTTTGTACCCGCTCGGAGACACAGGTA	12240
Dp	12181	ATGATTCGGGGCTTCGGCGGAACCGTACTCTATTTTGTACCCGCTCGGAGACACAGGTA	12240
QY	12241	GAGGTTCGCCCTTCTCCACAAACGACTCAAGTGTCTGGTCCGGAGAAAACCGGAAAAC	12300
Dp	12241	GAGGTTCGCCCTTCTCCACAAACGACTCAAGTGTCTGGTCCGGAGAAAACCGGAAAAC	12300
QY	12301	GGCCTCGGGCGCGCTGTCTACAAAATTTACACCATGTGTGACTTCCGACCCGACAGCC	12360
Dp	12301	GGCCTCGGGCGCGCGCTGTCTACAAAATTTACACCATGTGTGACTTCCGACCCGACAGCC	12360
QY	12361	ACCAACCGAAGCGGGGCTTTCGCCGACTCGGAGAAATACACCGTATCTGTGAAGGCGGAG	12420
Dp	12361	ACCAACCGAAGCGGGGCTTTCGCCGACTCGGAGAAATACACCGTATCTGTGAAGGCGGAG	12420
QY	12421	GACCCCAAGTGTGGGGTCTCGGGCTGACACTCTGTGAAAACTTTCCCGAGGGCGATACAG	12480
Dp	12421	GACCCCAAGTGTGGGGTCTCGGGCTGACACTCTGTGAAAACTTTCCCGAGGGCGATACAG	12480
QY	12481	ACGACGACGAGGCGACCTTACCACTTGTGTGGCCAAAGACGATGACGGCGACCTTACAGTTC	12540
Dp	12481	ACGACGACGAGGCGACCTTACCACTTGTGTGGCCAAAGACGATGACGGCGACCTTACAGTTC	12540
QY	12541	CCGGTCTCCCAAGTAACTTTCACGGGACGATACCCTGCTCAATGATGTATTCAG	12600

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Db 12541 CGCTCTCCAGGTAATACTTACGTCACGGGACGTACCCCTGCTCATGATGTTATTCAG 12600
QY 12601 AAAACCTCAACGCCACCATCAAGAAGCTGTCCGATACCCACGCAACAAAGGATCGAG 12660
Db 12601 AAAACCTCAACGCCACCATCAAGAAGCTGTCCGATACCCACGCAACAAAGGATCGAG 12660
QY 12661 CAGTACTACGAACCGAGGGGGGTCTGTTTCTCTGTGGCAGCGTTAAAGCCGCTAAGC 12720
Db 12661 CAGTACTACGAACCGAGGGGGGTCTGTTTCTCTGTGGCAGCGTTAAAGCCGCTAAGC 12720
QY 12721 CTAGCTGACGAGATGCGCAATTAACGGGACACGCCACGCCACCCCAACCTCA 12780
Db 12721 CTAGCTGACGAGATGCGCAATTAACGGGACACGCCACGCCACCCCAACCTCA 12780
QY 12781 ACCGCCAACCGGTTTCGAAGAAGCGTGGGTACGACAGCAGGCAAGGCAAGCACTAAGC 12840
Db 12781 ACCGCCAACCGGTTTCGAAGAAGCGTGGGTACGACAGCAGGCAAGGCAAGCACTAAGC 12840
QY 12841 GCGCCCACTGACAGTTCGCTACGACAGCTCCGCGCAGCATCAAGAAGTGTGAG 12900
Db 12841 GCGCCCACTGACAGTTCGCTACGACAGCTCCGCGCAGCATCAAGAAGTGTGAG 12900
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Db 12901 GAGCTCTCCAGGGCGGTGGCGGAGAACAGGTGAGGGACACCTACATGTTGATCAGACAG 12960
QY 12961 AGCAAGATTAAACCCACACGAGCTAATGACGGGATATACGGGGCGCGGTGTCCGCAAG 13020
Db 12961 AGCAAGATTAAACCCACACGAGCTAATGACGGGATATACGGGGCGCGGTGTCCGCAAG 13020
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Db 13021 TTCGTGGGGAGAGCCATCTCCGTGACGAGCTGCTGGCGGTGAGCAGGCTCCGTACG 13080
QY 13081 ATCCACAAGAGCCTCGACAGCTCCACCCGGGGATGTGCTACTCGGCCCCCGGTACAG 13140
Db 13081 ATCCACAAGAGCCTCGACAGCTCCACCCGGGGATGTGCTACTCGGCCCCCGGTACAG 13140
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Db 13141 TTCAGGTTCTCAACAGCACAGCTGTTCAAGGGCCAGCTGGGACCCAGAAACGAGATC 13200
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Db 13321 AATATCCACCTCGGTACGTTCAATCGCCCTGAACCTGTCTGTTATAGAGAACATAGATTTC 13380
QY 13381 AAGGTCATGAGACTGTACAGCGCGCGGGAAGAAAGAGCTCCGGGAGCGTTTTCATATA 13440
Db 13381 AAGGTCATGAGACTGTACAGCGCGCGGGAAGAAAGAGCTCCGGGAGCGTTTTCATATA 13440
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Db 13621 TTCGATCAATGCTGACGGGGTTCATTAACTTATAAAGATCCGTTCCGGGGCATGCTC 13680
Db 13681 ATGATCTGGTGAATGTGGCGGTCTCTGATCGTGTGCGTAAACCGGCGCACCAAC 13740
QY 13681 ATGATCTGGTGAATGTGGCGGTCTCTGATCGTGTGCGTAAACCGGCGCACCAAC 13740
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QY 13741 GCCATGCCCGAGGCCCCCATCAGAGATGATCTACCCGACATAGACAAATTCAGACCTCT 13800
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QY 13801 GCGGCTAAAGTGCACAGAGCAGATTAATAAATCTTCGCGCGCATGACAGCATACAG 13860
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QY 13861 CAGGAAGAGCGTAGGCGGTAGACGAACAGCAGAGGTACGCGCTTTCGCGGC 13920
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QY 13921 GCGTCAAGAGCTAAACGCTGCTTACGGGATATAAACCGCTGGAAAAACGAAGGCT 13980
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QY 13981 CAAGATTAATGAATGACAAATTAACACACACACAGCCTGTACTTGCCCGCCAGAG 14040
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Db 14041 CCGCGCGGCAATTCGATTCGCGCACCCGCGGTCCCGACACCTTATAGCGCCCCGGG 14100
QY 14101 CGTCCGCGGTCTGTATCATATGATGATTTCTTTAAACCGCTACTGGGCCCTCGCGACCA 14160
Db 14101 CGTCCGCGGTCTGTATCATATGATGATTTCTTTAAACCGCTACTGGGCCCTCGCGACCA 14160
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QY 14581 CAACAGTATATTTCTACGGAAGTTCAGCGCGGCAATTAACGTCACCCATCTCTCAG 14640
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QY 14641 CAGGCGCTCAAAACAGACCGCGCGGTGCGCGGTCTTCACACGAAGAGTGAAC 14700
Db 14641 CAGGCGCTCAAAACAGACCGCGCGGTGCGCGGTCTTCACACGAAGAGTGAAC 14700
QY 14701 AAAAGATTTCTCAAAAGTACAGAGTGGGAGAGCATCCCGTACAGGAAATTCAGCTATG 14760
Db 14701 AAAAGATTTCTCAAAAGTACAGAGTGGGAGAGCATCCCGTACAGGAAATTCAGCTATG 14760
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[illegible]

QY	15841	AACCCATTCGGGGGTTTATACGACGAGCGGCTCTGCTGCTGATTTTGGCCAGCCTGTAC	15900
Db	15841	AACCCCATTCGGGGGTTTATACGACGAGCGGCTCTGCTGCTGATTTTGGCCAGCCTGTAC	15900
QY	15901	CCGAGCATTCATCCAGGCGGCACAACCTGTGCTACTCCACATATACACGAGACGACCTG	15960
Db	15901	CCGAGCATTCATCCAGGCGGCACAACCTGTGCTACTCCACATATACACGAGACGACCTG	15960
QY	15961	CACCTGCACCCCAACGTCGAGCGGCGAGACTACGAGACCTTGTGCTGAGCGGCGAGCG	16020
Db	15961	CACCTGCACCCCAACGTCGAGCGGCGAGACTACGAGACCTTGTGCTGAGCGGCGAGCG	16020
QY	16021	GTACATTTTGTAAAAAACAACAAGCGGGAGTCTGTGCTGGGAAGACTGCTACGCTGTGG	16080
Db	16021	GTACATTTTGTAAAAAACAACAAGCGGGAGTCTGTGCTGGGAAGACTGCTACGCTGTGG	16080
QY	16081	TTAGAAAAAGGAAGGCGATCCGGGCGCACCTTGGGGGCTGGGATGACCCGTCTGCTAAA	16140
Db	16081	TTAGAAAAAGGAAGGCGATCCGGGCGCACCTTGGGGGCTGGGATGACCCGTCTGCTAAA	16140
QY	16141	ACCATCTTACATTAACAACAAGCTGGGCATCAAGGTACACATTTGACGGGTTTACGGGTTT	16200
Db	16141	ACCATCTTACATTAACAACAAGCTGGGCATCAAGGTACACATTTGACGGGTTTACGGGTTT	16200
QY	16201	ACCGGGGTGGCCAGCGGCGCTCTCCCATGATTAACATAGCGGAAACCGTGAAGCTCGG	16260
Db	16201	ACCGGGGTGGCCAGCGGCGCTCTCCCATGATTAACATAGCGGAAACCGTGAAGCTCGG	16260
QY	16261	GGCGCGACGATGCTGCGAGATGTCAAAAGTCTTACGTGGAGCGCTGACGACGGAACCTG	16320
Db	16261	GGCGCGACGATGCTGCGAGATGTCAAAAGTCTTACGTGGAGCGCTGACGACGGAACCTG	16320
QY	16321	CGAAGCGGTCGCGTGGCGAGGATGACCGCCGTCAGGGGCGGGGTTTGCGCTGCTTAC	16380
Db	16321	CGAAGCGGTCGCGTGGCGAGGATGACCGCCGTCAGGGGCGGGGTTTGCGCTGCTTAC	16380
QY	16381	GGTATACACCGACTCCCTCTTATATCGGCGTGGAGGTTTATTCGCGGAGAACCGCTTTCGGT	16440
Db	16381	GGTATACACCGACTCCCTCTTATATCGGCGTGGAGGTTTATTCGCGGAGAACCGCTTTCGGT	16440
QY	16441	TTCTGTAGCATCTGCGCCGCCAGAGTACTGCGGAGCTGTTCGCCACCCATTAAAGCTA	16500
Db	16441	TTCTGTAGCATCTGCGCCGCCAGAGTACTGCGGAGCTGTTCGCCACCCATTAAAGCTA	16500
QY	16501	GAGCGGGAAGAAAGCGTCAAGTCTGCTGCTGCTGCTGACGAAAAAGCGTACATCGGGGTC	16560
Db	16501	GAGCGGGAAGAAAGCGTCAAGTCTGCTGCTGCTGCTGACGAAAAAGCGTACATCGGGGTC	16560
QY	16561	CTATTGAACGCAAAATGTCATGAAAGGGGTGAGCTCATTTGCGAAAAAGGCGCTGCAAG	16620
Db	16561	CTATTGAACGCAAAATGTCATGAAAGGGGTGAGCTCATTTGCGAAAAAGGCGCTGCAAG	16620
QY	16621	TTTGTCCAGGAGCGATGCCGCCATCTGTGACCTGTGCTCAGCATTCGGAGGTCAAG	16680
Db	16621	TTTGTCCAGGAGCGATGCCGCCATCTGTGACCTGTGCTCAGCATTCGGAGGTCAAG	16680
QY	16681	GCTCGGCGGGGCGTGTGTGCAAGCGGCGCGCCAGCGGGTATACGAGGAGGGGCTGGCG	16740
Db	16681	GCTCGGCGGGGCGTGTGTGCAAGCGGCGCGCCAGCGGGTATACGAGGAGGGGCTGGCG	16740
QY	16741	GCTGCGTTTATAAAAATCGTAGAGGTCCTCAAGCGCAGGTATCTGAGCTCCGAAACAGC	16800
Db	16741	GCTGCGTTTATAAAAATCGTAGAGGTCCTCAAGCGCAGGTATCTGAGCTCCGAAACAGC	16800
QY	16801	GTCGTGCCCATCGAGCAGTTAACGTTCTCCACCGAGCTACGCCGCCGCTGTGCGATTAC	16860
Db	16801	GTCGTGCCCATCGAGCAGTTAACGTTCTCCACCGAGCTACGCCGCCGCTGTGCGATTAC	16860
QY	16861	AAGACACACAAACCTGCCCCACCTGCGGGGTGTACCAAAACCTGCGGACGAGGTGCAAGG	16920
Db	16861	AAGACACACAAACCTGCCCCACCTGCGGGGTGTACCAAAACCTGCGGACGAGGTGCAAGG	16920
QY	16921	CTGCCCCAGGTGCAGATAGAAATCCCTTACGTGTTGTTGACGCGGCCGCGTCCCTTAAG	16980


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Db 16921 CTGCCCCAGGTGACATAGATCCCTTCGTTGTTGACGCGCCGGGTCTCTAAG 16980
QY 16981 TCGGACCTGGCCGAACCCGGATTACGTACAGACACACAGATTCCCGTCGGGTGCAG 17040
Db 16981 TCGGACCTGGCCGAACCCGGATTACGTACAGACACACAGATTCCCGTCGGGTGCAG 17040
QY 17041 CTTATTATTGACAACTGTGTGACAGCGCGCGCCACATCCTCCAGTGTCTGTTGGCAAC 17100
Db 17041 CTTATTATTGACAACTGTGTGACAGCGCGCGCCACATCCTCCAGTGTCTGTTGGCAAC 17100
QY 17101 AACGCGACACACCGGTGGCCATCTCTACATTTTCTCAAGCTCCCGATTAGAGTGTTC 17160
Db 17101 AACGCGACACACCGGTGGCCATCTCTACATTTTCTCAAGCTCCCGATTAGAGTGTTC 17160
QY 17161 TCGTGAAGCCCAATTGGAGAACGCCAATAGACGCCGCGCCAGCGAGTCCGACGGGA 17220
Db 17161 TCGTGAAGCCCAATTGGAGAACGCCAATAGACGCCGCGCGAGCGAGTCCGACGGGA 17220
QY 17221 GAGCTGAGCGCGGAGAGGACGACCAACGAGACCGCCACCATGTCTGTTAAGCACTGTC 17280
Db 17221 GAGCTGAGCGCGGAGAGGACGACCAACGAGACCGCCACCATGTCTGTTAAGCACTGTC 17280
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Db 17341 CACCCGCTGCAAAAGCTTCAAGGGCCACGCGGGGCTACGCCAGGGTCCGATCCCTTCTC 17400
QY 17401 GGTGCGACGATTACTCCACCAATTTCCGCTTCGAGCTGTCGACCGCGTCTCAAGAACT 17460
Db 17401 GGTGCGACGATTACTCCACCAATTTCCGCTTCGAGCTGTCGACCGCGTCTCAAGAACT 17460
QY 17461 GCCCCTCTCTCGAGTACGCTGGGCTTATCCGCCCGTGTGATTCCGCGGCGACCGGA 17520
Db 17461 GCCCCTCTCTCGAGTACGCTGGGCTTATCCGCCCGTGTGATTCCGCGGCGACCGGA 17520
QY 17521 CCGGCGCGCGTGGCCCCCGGGTTCGTGTGACCTCTCTCGCCGCTGACCGTGTGGGT 17580
Db 17521 CCGGCGCGCGTGGCCCCCGGGTTCGTGTGACCTCTCTCGCCGCTGACCGTGTGGGT 17580
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Db 17581 AAACGCGAGCGGCGGCGACACGATCCGCTTCGCTCTCTTTCTAAGCCGATCGACCT 17640
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Db 17701 AAAGCCACCTGCGGACCGAAAGCCCTGCCGCTGAGACCCCTGCGCTCTCGGCGAGGC 17760
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Db 18061 CGGCGGCGCGGATATTGGGGGTCTACGCGCGCAAGAAAAAACCATCAACTGGAAGCTC 18120
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Db 18901 TACGACTTAAGGATTTGCTGCGGATCGTTAGGAGTGTGCGCGCGCGCGGGGTCTTA 18960
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Db 18961 CACTTTCACAAGACCGGCTTCGATCGCGCTGACAGAGCGGTGACGAGGAGGCTCC 19020
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QY 19081 ACCGCGCACCACTTCTTAAACCCGAGAGACCAAGCCCTTAAACGAGGAAGTTTTC 19140
Db 19081 ACCGCGCACCACTTCTTAAACCCGAGAGACCAAGCCCTTAAACGAGGAAGTTTTC 19140
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QY	19141	CGCCTGATCATGGAACAACGACACGGCCAGGCGCGTCAACACCGTCTACCTGGGAAAGCAG	19200
Dp	19141	CGCCTGATCATGGAACAACGACACGGCCAGGCGCGTCAACACCGTCTACCTGGGAAAGCAG	19200
QY	19201	CAGGTGAGGGTGAACCGGACCGCGCCCGCGGAAACAAATGTCACGACGAGGGCCGCTGAGC	19260
Dp	19201	CAGGTGAGGGTGAACCGGACCGCGCCCGCGGAAACAAATGTCACGACGAGGGCCGCTGAGC	19260
QY	19361	GCGACCCCTGTCCCTCAACCGGTAAATGGCCAAATGCGCTTTCGGCACAAACCATACTTTGAA	19320
Dp	19261	GCGACCCCTGTCCCTCAACCGGTAAATGGCCAAATGCGCTTTCGGCACAAACCATACTTTGAA	19320
QY	19321	CTCCCGCTGGTCTGTCACACACGGCGATTTACAGCCCGCTGTGTAGTGGGCTGACCGTG	19380
Dp	19321	CTCCCGCTGGTCTGTCACACACGGCGATTTACAGCCCGCTGTGTAGTGGGCTGACCGTG	19380
QY	19381	TGCATCCCAACCACAACTGATAGCAAAATTCGTAAGGTACGTAAGACACCTACGTCGCGCATTT	19440
Dp	19381	TGCATCCCAACCACAACTGATAGCAAAATTCGTAAGGTACGTAAGACACCTACGTCGCGCATTT	19440
QY	19441	AACCGCAAGCTGACGGCGATTTATTAGCAATCACGCCACACAGCGCGGTTCCGGATTACG	19500
Dp	19441	AACCGCAAGCTGACGGCGATTTATTAGCAATCACGCCACACAGCGCGGTTCCGGATTACG	19500
QY	19501	GACGTGGAGTGGGACACCGAAACGGGGAGTATAGATTTGGTAAACAAAGCTGTCCAGAGCC	19560
Dp	19501	GACGTGGAGTGGGACACCGAAACGGGGAGTATAGATTTGGTAAACAAAGCTGTCCAGAGCC	19560
QY	19561	CCGGTGTACATCAGACACCGGAGCGACGTGGGGCAAGCCATCTGTTCTGTTCCGGCGGGG	19620
Dp	19561	CCGGTGTACATCAGACACCGGAGCGACGTGGGGCAAGCCATCTGTTCTGTTCCGGCGGGG	19620
QY	19621	TTGGGTGGCCCCCGGAGAACTGGCGGCAAGCTCTCGGCAACCGATGGCGCCCTGTGAAGCTG	19680
Dp	19621	TTGGGTGGCCCCCGGAGAACTGGCGGCAAGCTCTCGGCAACCGATGGCGCCCTGTGAAGCTG	19680
QY	19681	CCGGGCGGGGTGACAGTGGACACCCAAAAAAGTGTAGGTTTGAGACCATGTACCTGTTT	19740
Dp	19681	CCGGGCGGGGTGACAGTGGACACCCAAAAAAGTGTAGGTTTGAGACCATGTACCTGTTT	19740
QY	19741	TTCACAGTAATTTACTAATAAACCGTTTGCTCGTATGCTCACACAAACGCCAACCGTCTC	19800
Dp	19741	TTCACAGTAATTTACTAATAAACCGTTTGCTCGTATGCTCACACAAACGCCAACCGTCTC	19800
QY	19801	TCAATTCGGGGTTCGGCGCTCGGCAACACAAAGTGGTCTAAACACCCCGCTCCGCG	19860
Dp	19801	TCAATTCGGGGTTCGGCGCTCGGCAACACAAAGTGGTCTAAACACCCCGCTCCGCG	19860
QY	19861	ACCCTGGCCACACAAAAACAGTTAACGCCCTCCGTTAGATGCAAGTTATTATTATTTTA	19920
Dp	19861	ACCCTGGCCACACAAAAACAGTTAACGCCCTCCGTTAGATGCAAGTTATTATTATTTTA	19920
QY	19921	TTACATCATATGCTATTTGGGGGGCGCCGTCGCCGCAAAAACATCTGTAGATTTCCAGTAT	19980
Dp	19921	TTACATCATATGCTATTTGGGGGGCGCCGTCGCCGCAAAAACATCTGTAGATTTCCAGTAT	19980
QY	19981	GCGAAACGCGCTGAGAACACAGTCCCGGGGGCTCTCCCTCCCAAGCAGCAGCGGTTTT	20040
Dp	19981	GCGAAACGCGCTGAGAACACAGTCCCGGGGGCTCTCCCTCCCAAGCAGCAGCGGTTTT	20040
QY	20041	TTCTATTAGACTCCGCGCGACCTTATCTTGTATTATTACGGGAGGCTCTCAATTAGAGAGTC	20100
Dp	20041	TTCTATTAGACTCCGCGCGACCTTATCTTGTATTATTACGGGAGGCTCTCAATTAGAGAGTC	20100
QY	20101	GAGGGCGGAGACACACAGGTACACGGGGAGCCAAATGGCGGGGCTCCGCGCCCGGG	20160
Dp	20101	GAGGGCGGAGACACACAGGTACACGGGGAGCCAAATGGCGGGGCTCCGCGCCCGGG	20160
QY	20161	CGCGTGTTCACGACGACATCTCTCAGTGGCGGTCAAGTAACCTGCTAGAGCCCGGAGCCCGG	20220
Dp	20161	CGCGTGTTCACGACGACATCTCTCAGTGGCGGTCAAGTAACCTGCTAGAGCCCGGAGCCCGG	20220

QY	20221	AACCATGGCGTTCAATACACTGGCGCCCCGGGAAACTCGGGGCGCTGGCACTCAAGCTT	20280
Db	20221	AACCATGGCGTTCAATACACTGGCGCCCCGGGAAACTCGGGGCGCTGGCACTCAAGCTT	20280
QY	20281	CATCAAAATATGAGGAAGTGAACAACGACATGATGGCGGGTACTCCAGCACCCGACAGAG	20340
Db	20281	CATCAAAATATGAGGAAGTGAACAACGACATGATGGCGGGTACTCCAGCACCCGACAGAG	20340
QY	20341	AGTGGAGTGGTGGACAGGTAAACGAAACGACGCGTGTATGTTTAAACCCCACTTCAGACAG	20400
Db	20341	AGTGGAGTGGTGGACAGGTAAACGAAACGACGCGTGTATGTTTAAACCCCACTTCAGACAG	20400
QY	20401	GCGCCCCCTGGTCTGTCAAGAGAGGCGGCTTCCGCGCCACTGGGGGAGAACTGTAAT	20460
Db	20401	GCGCCCCCTGGTCTGTCAAGAGAGGCGGCTTCCGCGCCACTGGGGGAGAACTGTAAT	20460
QY	20461	TTCCAGGGGCAAGTGGGGGGAGGGCCCAAGCGTAAAGGGCGTGGCGGCCCAACAGCAGGTAA	20520
Db	20461	TTCCAGGGGCAAGTGGGGGGAGGGCCCAAGCGTAAAGGGCGTGGCGGCCCAACAGCAGGTAA	20520
QY	20521	CAAGACCAACACAGACAGAGGAACATGACCCGGTTAAATTACTCGCTTCAATTCGCGGCGCG	20580
Db	20521	CAAGACCAACACAGACAGAGGAACATGACCCGGTTAAATTACTCGCTTCAATTCGCGGCGCG	20580
QY	20581	GCGCGGTCAACGCCAGGTCCATTAAAAACACACCGGCGCCCAACCCCAACCGGGGCGCG	20640
Db	20581	GCGCGGTCAACGCCAGGTCCATTAAAAACACACCGGCGCCCAACCCCAACCGGGGCGCG	20640
QY	20641	CGCCCTTGGAAACGGGGTTCCTTCCAAATCGCAAAACACCGGCTCACAAAAGGGCTCGTTT	20700
Db	20641	CGCCCTTGGAAACGGGGTTCCTTCCAAATCGCAAAACACCGGCTCACAAAAGGGCTCGTTT	20700
QY	20701	GAACCCATTTTGTGGCCATCGGGTTTGGTTTTCAGATACGAAAGGCGCTGTCCAAAAACA	20760
Db	20701	GAACCCATTTTGTGGCCATCGGGTTTGGTTTTCAGATACGAAAGGCGCTGTCCAAAAACA	20760
QY	20761	CCCAACGGGGGTGTGCTCAAGAGGCCATCTCATCTCTATGTGGGATGGGGGTCTGTAC	20820
Db	20761	CCCAACGGGGGTGTGCTCAAGAGGCCATCTCATCTCTATGTGGGATGGGGGTCTGTAC	20820
QY	20821	CCCTGACACATCAATCCGGCGGGGTAAAGTCCACAGCGGCACTTTCACAAAATCT	20880
Db	20821	CCCTGACACATCAATCCGGCGGGGTAAAGTCCACAGCGGCACTTTCACAAAATCT	20880
QY	20881	TCAGCCCGCGGAAACGAGACGGGGGTCTCCGACGCTGAAGACAGCAGGGGATCAACGTGT	20940
Db	20881	TCAGCCCGCGGAAACGAGACGGGGGTCTCCGACGCTGAAGACAGCAGGGGATCAACGTGT	20940
QY	20941	TGTTGTAAACGTGGGGCTCACCCAAAGGTGTGCACAAAGTCTCCCGGGGTACAGCCCGTGA	21000
Db	20941	TGTTGTAAACGTGGGGCTCACCCAAAGGTGTGCACAAAGTCTCCCGGGGTACAGCCCGTGA	21000
QY	21001	CGTGAAGCATCAATACGTACGTACAGAGGGCGTACGTGGCGATGTTTAAACGGGACCCGAGGC	21060
Db	21001	CGTGAAGCATCAATACGTACGTACAGAGGGCGTACGTGGCGATGTTTAAACGGGACCCGAGGC	21060
QY	21061	CCATGTGGGGGAGACCTTGTGTACAGCTGGCAGGACAGCTCCCCCGGACAGCTGTAACCT	21120
Db	21061	CCATGTGGGGGAGACCTTGTGTACAGCTGGCAGGACAGCTCCCCCGGACAGCTGTAACCT	21120
QY	21121	GACACAAAACGTGACAAAGAGGAGAGACCATCCGCGCGAGAGTCCGCGGGGTTCCAGCGCG	21180
Db	21121	GACACAAAACGTGACAAAGAGGAGAGACCATCCGCGCGAGAGTCCGCGGGGTTCCAGCGCG	21180
QY	21181	ACATTAACGATGCGCGCATCTGTGGGGCGCTGTTAATTAGATCCACACAGTAAACGACCT	21240
Db	21181	ACATTAACGATGCGCGCATCTGTGGGGCGCTGTTAATTAGATCCACACAGTAAACGACCT	21240
QY	21241	GGTCCACCCCTGACCCCTGTAGTATGGCGTGGCGCCCGCTGTAATCTCGGCCCAAAATGTC	21300
Db	21241	GGTCCACCCCTGACCCCTGTAGTATGGCGTGGCGCCCGCTGTAATCTCGGCCCAAAATGTC	21300
QY	21301	TTCCACTGTGAACCCGTACACCGGCGCCAGATCGCGCTTGGGCGGGTCCCGGAAGCCCTGGG	21360


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Db 21541 CGAAGACGAGACCTGTGTGCGACGCCGCTCTCTCCCTCTGACAGCCGCTTTAAATA 21600
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[illegible]

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Qy 25861 GCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCC 25920
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Qy 25921 CCGCGAGGCTCCCGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCC 25980
Db 25921 CCGCGAGGCTCCCGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCC 25980
Qy 25981 CCGGAGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCC 26040
Db 25981 CCGGAGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCC 26040
Qy 26041 CCGTCCCGGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCG 26100
Db 26041 CCGTCCCGGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCG 26100
Qy 26101 AAGGTCCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCC 26160
Db 26101 AAGGTCCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCC 26160
Qy 26161 GCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCC 26220
Db 26161 GCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCC 26220
Qy 26221 CCGCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCT 26280
Db 26221 CCGCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCT 26280
Qy 26281 CCGGAGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCC 26340
Db 26281 CCGGAGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCC 26340
Qy 26341 CCGTCCCGGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCG 26400
Db 26341 CCGTCCCGGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCG 26400
Qy 26401 AAGGTCCTCCGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGG 26460
Db 26401 AAGGTCCTCCGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGG 26460
Qy 26461 GCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCCCGAGGCTCCGGGCTCCCGCTCC 26520
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Qy 26521 CCGCGATTCACGTTAAAGTGTATTATTAGCAACACAGTTTGTGGCGGCTTTGG 26580
Db 26521 CCGCGATTCACGTTAAAGTGTATTATTAGCAACACAGTTTGTGGCGGCTTTGG 26580
Qy 26581 TTGTACATACAGCGGCTGCGATTGGCCCGCCCATGCAAAAAATAAGTTGGGTTTCC 26640
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Db 26641 GAAACGCGTAGTGTCTTATAGTCTTATAGCACAGTTTGTGTCACAGTAGAGTGTAA 26700
Qy 26701 GTTTTGTGTAGCGAATGCAACAGTAGTCTGCTGACACCGGGAAGGAAAGTTTAA 26760
Db 26701 GTTTTGTGTAGCGAATGCAACAGTAGTCTGCTGACACCGGGAAGGAAAGTTTAA 26760
Qy 26761 CCGCAGTGTACCGGCTGCGCATACGTTTAACTGCAACTGCGGCTCCGCGCGTGG 26820
Db 26761 CCGCAGTGTACCGGCTGCGCATACGTTTAACTGCAACTGCGGCTCCGCGCGTGG 26820
Qy 26821 TACCTTAAGTTACGTGTAGCAATATAGCGGCTGTTCAGGCGCTCCGCCCTGA 26880
Db 26821 TACCTTAAGTTACGTGTAGCAATATAGCGGCTGTTCAGGCGCTCCGCCCTGA 26880
Qy 26881 GGAAGAAATGAATTTCTTTGCCAGTTATAGCTTTATAGAGGCGATCTTTCTTAA 26940
Db 26881 GGAAGAAATGAATTTCTTTGCCAGTTATAGCTTTATAGAGGCGATCTTTCTTAA 26940
Qy 26941 CTGTGGGCTCCGGGAGGCGGAGTACTGACATCCCGCTTTAGCCCTATTAAGAAAT 27000
Db 26941 CTGTGGGCTCCGGGAGGCGGAGTACTGACATCCCGCTTTAGCCCTATTAAGAAAT 27000
Qy 27001 TATCAGCGCTTCTCAAGAGAGCGCTCCCTGTACAGAGAGCTTTGCGCCACACGA 27060
Db 27001 TATCAGCGCTTCTCAAGAGAGCGCTCCCTGTACAGAGAGCTTTGCGCCACACGA 27060
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Db 27061 TTACGCTCTCTGCGGGGACTAAAGCCATAGGCCAAGGATGCTGCAATTAACACGA 27120
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Db 27121 CCGAGCCCAACTGGGCTGCGGCTTTGGCGCTTTGGGCTTTGGTGCATATGTGTGA 27180
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Db 27181 TAAAGTTAAAGACGAGAGCGCTTTTAACTGTCGCATAGCCGTTTACCCGTGTACGC 27240
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Db 27241 GTACAGGCGCTGAGTCTCATGTTTCTGTTTCAACAGGCGCAATGGAGGACTACGAA 27300
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Db 27301 TTACTGCGAGCAATACTAGGATAGCGCATGCGCAACCGAGAGAACATGTGTACGAGT 27360
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Db 27361 TCGGCGTGTCTTGTGGCGTATAGTGCGCTGTTGCCATACAGGCGATAGTGTGCTTAA 27420
Qy 27421 ACCGCGTATCCCGCACCTGACCTTAAGTAGCGGATTTGTATAGAACCAATAAACA 27480
Db 27421 ACCGCGTATCCCGCACCTGACCTTAAGTAGCGGATTTGTATAGAACCAATAAACA 27480
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Db 27481 AAACAAGCTAACGTGTATTCGTTGGAACATTTTATTTAGACAGTTCTCGCAGAAC 27540
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Db 27541 TTTTGTATCTGTACACAGGCGCGCTGTGCGCTGCGCTCCACCGGCGCCCGCGG 27600
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Db 27601 ACTGTCGATTCGTGATCGAGGCGGAGCAAGCGCCAGCGGCGGAGGAGAGGCTGAAG 27660
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Db 27721 CGAGACCGGCTGTGTGCGCTCCCGGCTCCGGGCGGAGTGTGCTTGTGCTGAGTCCCT 27780
Qy 27781 GCGGCGCTCGGTAGAGGCTGTGGGCGGTGAGATGAGTCCGGAATACCACTGCG 27840
Db 27781 GCGGCGCTCGGTAGAGGCTGTGGGCGGTGAGATGAGTCCGGAATACCACTGCG 27840
Qy 27841 GCTGTAGCTAGTGTAGGCGCAGAGCGTGTGCTGTGCGCAGAGAACTGAACGGCG 27900
Db 27841 GCTGTAGCTAGTGTAGGCGCAGAGCGTGTGCTGTGCGCAGAGAACTGAACGGCG 27900
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QY	27901	GTGGTTCGGGTCGTTGGTCGGGCTCCTGTGCGCGCGGAGGTCCTGCGACGCGGCTCGTTTAA	27960
Db	27901	GTGGTTCCGGGTCGTGGTCCGGGCTCCTGTGCGCGCGGAGGTCCTGCGACGCGGCTCGTTTAA	27960
QY	27961	GGTCCCGCAGATCCGCGCGGTAATGCCAATATGTTTTTGGACAGCGCCATGACGTCCTGT	28020
Db	27961	GGTCCCGCAGATCCGCGCGGTAATGCCAATATGTTTTTGGACAGCGCCATGACGTCCTGT	28020
QY	28021	GTATGCCGACCTCCTCCCTCGGAACACAGGGGCTCGTCGGAAAGCTCCACGTCGCCGTTTGC	28080
Db	28021	GTATGCCGACCTCCTCCCTCGGAACACAGGGGCTCGTCGGAAAGCTCCACGTCGCCGTTTGC	28080
QY	28081	GCTTCCTGTGGGCGCAGACGGTTCGGAGACGTACGCCCTGACGTCCGAGAAATAGTACGTGCGC	28140
Db	28081	GCTTCCTGTGGGCGCAGACGGTTCGGAGACGTACGCCCTGACGTCCGAGAAATAGTACGTGCGC	28140
QY	28141	CATACGGAGAGGGTTGGGGGGCAAAAGCCGACATGGAAGGAAAGCGTGGAGCGAGCGGCG	28200
Db	28141	CATACGGAGAGGGTTGGGGGGCAAAAGCCGACATGGAAGGAAAGCGTGGAGCGAGCGGCG	28200
QY	28201	GTGCGTACGATGGGACGGTACGTCAGGCGCGCGTATCCACGATGGATACGCCGCGTTGG	28260
Db	28201	GTGCGTACGATGGGACGGTACGTCAGGCGCGCGTATCCACGATGGATACGCCGCGTTGG	28260
QY	28261	CCGGCATTCGAGGGTGGCGCAGAAACGATGGGGGTGGGCCGTCGTCGACATGGTATGCA	28320
Db	28261	CCGGCATTCGAGGGTGGCGCAGAAACGATGGGGGTGGGCCGTCGTCGACATGGTATGCA	28320
QY	28321	GACTGCTCTGCACCATGGTCAGAAAGGTGCTTTGGGAAATGTGATGTTGTCTCCCGGGA	28380
Db	28321	GACTGCTCTGCACCATGGTCAGAAAGGTGCTTTGGGAAATGTGATGTTGTCTCCCGGGA	28380
QY	28381	GGGGGCTCATGGTTCGGGGTGTCCCGGTTACCCGATGTCGAGCGCAGCGGAAACTGGCTTG	28440
Db	28381	GGGGGCTCATGGTTCGGGGTGTCCCGGTTACCCGATGTCGAGCGCAGCGGAAACTGGCTTG	28440
QY	28441	CGTTTAAATACGTACTTCTCGGCACTGTGGCCACAGGCTTTATCTGTTTTGAGCAGGTCG	28500
Db	28441	CGTTTAAATACGTACTTCTCGGCACTGTGGCCACAGGCTTTATCTGTTTTGAGCAGGTCG	28500
QY	28501	TGCGATCTCGGATTAATCCGGGCTCGATCGCCTTTGGCCATCACTGTCTCAAGAGGGCGC	28560
Db	28501	TGCGATCTCGGATTAATCCGGGCTCGATCGCCTTTGGCCATCACTGTCTCAAGAGGGCGC	28560
QY	28561	-CGAATTCCTGGGGGTGTCACCTGACGTTCGCAAAAGATCTAAACAATAGACCGTATTATTC	28620
Db	28561	CGAATTCCTGGGGGTGTCACCTGACGTTCGCAAAAGATCTAAACAATAGACCGTATTATTC	28620
QY	28621	CGGCTTCCTCTCGCGTAAGAGAAATCAAATTTGGAGACGACCCATGTAGGCTGTGTCGT	28680
Db	28621	CGGCTTCCTCTCGCGTAAGAGAAATCAAATTTGGAGACGACCCATGTAGGCTGTGTCGT	28680
QY	28681	AAAGGGGATTTGACCCGCTACGCTCCCGACGTCCGACAGAGAGAGCTCTGAAGCGCG	28740
Db	28681	AAAGGGGATTTGACCCGCTACGCTCCCGACGTCCGACAGAGAGAGCTCTGAAGCGCG	28740
QY	28741	GTGGGTATTGGGGTCTTTGACGCTCTTCTGGGTGAGAGGACGAGAGAGGAGCTCCGGGA	28800
Db	28741	GTGGGTATTGGGGTCTTTGACGCTCTTCTGGGTGAGAGGACGAGAGAGGAGAGCTCCGGGA	28800
QY	28801	GCCATGTGTGTACATCTCCACAGGGGGTCCCGAGGCAATGGGGTTTAACTGGATCTGGG	28860
Db	28801	GCCATGTGTGTACATCTCCACAGGGGGTCCCGAGGCAATGGGGTTTAACTGGATCTGGG	28860
QY	28861	CCGCTCCAGATCCCGCGAGCGGTACGCCACGAGGCGCAAGAATGCTGCGTCGTACGT	28920
Db	28861	CCGCTCCAGATCCCGCGAGCGGTACGCCACGAGGCGCAAGAATGCTGCGTCGTACGT	28920
QY	28921	TGCCCAGGCAAAATATCCGCTGTGTACTTGGGAAGACCGATGTTGTGACCTACGTGGG	28980
Db	28921	TGCCCAGGCAAAATATCCGCTGTGTACTTGGGAAGACCGATGTTGTGACCTACGTGGG	28980

QY	28981	CTTTCGGGAGACGTCTATGTTTATATCGGTAGAGGCTCGCTATACGGAGACAGGGCTCGCA	29040
Db	28981	CTTTCGGGAGACGTCTATGTTTATATCGGTAGAGGCTCGCTATACGGAGACAGGGCTCGCA	29040
QY	29041	CGATTGAGGGCTCTAAATACAGTCCCTTTTCTATCTTTGTGTAGGGTGACACGTCCACGT	29100
Db	29041	CGATTGAGGGCTCTAAATACAGTCCCTTTTCTATCTTTGTGTAGGGTGACACGTCCACGT	29100
QY	29101	ATCCCCCAACGTAACAGGGAGTCATGTGGGTGCGGTGCTGCGTGAAGCCGAAGAGATGA	29160
Db	29101	ATCCCCCAACGTAACAGGGAGTCATGTGGGTGCGGTGCTGCGTGAAGCCGAAGAGATGA	29160
QY	29161	GCGCCGCTCTTCGGGGGCTGATGTGCGCGCTTATCCGTTGTGAAATTTAAATACGTTTC	29220
Db	29161	GCGCCGCTCTTCGGGGGCTGATGTGCGCGCTTATCCGTTGTGAAATTTAAATACGTTTC	29220
QY	29221	TTCCCTGGCGAGTCAGGTTTCTTACCTGGTGTGTGGAAATGTATCAACTACGGTCTTA	29280
Db	29221	TTCCCTGGCGAGTCAGGTTTCTTACCTGGTGTGTGGAAATGTATCAACTACGGTCTTA	29280
QY	29281	ACGTTGTACCTTCTGAAAGGAGCAATTTGCCAATACCGGAACGAGAGCATATTTGTCCTCG	29340
Db	29281	ACGTTGTACCTTCTGAAAGGAGCAATTTGCCAATACCGGAACGAGAGCATATTTGTCCTCG	29340
QY	29341	GGCGTAAGGTTCCGGTGGAGTCTTGAAAAATCGTTTACGATGGGTTAAAGAGATGGGG	29400
Db	29341	GGCGTAAGGTTCCGGTGGAGTCTTGAAAAATCGTTTACGATGGGTTAAAGAGATGGGG	29400
QY	29401	TTTCTGACGCAAGCTTCTCCTCAGAAACCAAAAGGGGGGCTCTGTGGCTTACTTCAACG	29460
Db	29401	TTTCTGACGCAAGCTTCTCCTCAGAAACCAAAAGGGGGGCTCTGTGGCTTACTTCAACG	29460
QY	29461	GGCGTCCGTCCTGTTTAAAGGTCATAGGCACATCACTTTTTCGCCAATCGGGGTTAAGC	29520
Db	29461	GGCGTCCGTCCTGTTTAAAGGTCATAGGCACATCACTTTTTCGCCAATCGGGGTTAAGC	29520
QY	29521	ACAGCGTACGCGTGTTCCGGAAAAACCTAACGGAGTGGAAATATCTTATTAACCTAAGCA	29580
Db	29521	ACAGCGTACGCGTGTTCCGGAAAAACCTAACGGAGTGGAAATATCTTATTAACCTAAGCA	29580
QY	29581	GGCTCATACCATGTCGCGCTGCTGTGGCACTGAGCTACGTTTGGCGTTTGGGGGCACG	29640
Db	29581	GGCTCATACCATGTCGCGCTGCTGTGGCACTGAGCTACGTTTGGCGTTTGGGGGCACG	29640
QY	29641	CTGACCAAGAGCCCTGGGTGAGGTTGTGCGCCGGAAGATTTTATACTGTACTTAATTA	29700
Db	29641	CTGACCAAGAGCCCTGGGTGAGGTTGTGCGCCGGAAGATTTTATACTGTACTTAATTA	29700
QY	29701	TTTTCGGGCACTTATGCCAGGAAGTCACTTTAGAACAGGTGGGACGTCGCGGTACG	29760
Db	29701	TTTTCGGGCACTTATGCCAGGAAGTCACTTTAGAACAGGTGGGACGTCGCGGTACG	29760
QY	29761	GTGGCTTCGTGAGAGCAGTGTGTGCGGATGTCGCCGGTACACGGGATTCGGCGTGG	29820
Db	29761	GTGGCTTCGTGAGAGCAGTGTGTGCGGATGTCGCCGGTACACGGGATTCGGCGTGG	29820
QY	29821	ATTTTGGGTCCGCGGCTCCGGCCCTTAACGTCCTAACAGAGACGACTCTGTTTGGCTTCA	29880
Db	29821	ATTTTGGGTCCGCGGCTCCGGCCCTTAACGTCCTAACAGAGAGCTCTGTTTGGCTTCA	29880
QY	29881	ATTAACACGCTAGTGTAGAGTGCAGCTCAACACTTACCGAGAGTGGCAGCCGAGGTATCCAG	29940
Db	29881	ATTAACACGCTAGTGTAGAGTGCAGCTCAACACTTACCGAGAGTGGCAGCCGAGGTATCCAG	29940
QY	29941	GACCAAAAAATTAACCTGTGTGAGTGTGCTGTAACCTCCGAATTTGGCTTTATATATC	30000
Db	29941	GACCAAAAAATTAACCTGTGTGAGTGTGCTGTAACCTCCGAATTTGGCTTTATATATC	30000
QY	30001	GTGTGCGCAAGACGGGGGGCGATGGGTGCGAAAGAGATGGCGGCAAGGCTTTCCTCGGCGT	30060
Db	30001	GTGTGCGCAAGACGGGGGGCGATGGGTGCGAAAGAGATGGCGGCAAGGCTTTCCTCGGCGT	30060
QY	30061	TAAACGTAGGACGCTTTGACCTGAAATACAGGCTGCGCAGCGTCCCTTAACGTACGCTTTTG	30120

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Db 30061 TAAAGCTAGCGAGCTTTGAGCTGAAATCAGGCTGCCAGCGTCCCTGAAAGTAAAGCTTTTG 30120
Qy 30121 GTTCAGAGATCAAAAGATTTCGTTAAATCTGGAAACCGGTCAGCTTGACAGCAAGCAAGAT 30180
Db 30121 GTTCAGAGATCAAAAGATTTCGTTAAATCTGGAAACCGGTCAGCTTGACAGCAAGCAAGAT 30180
Qy 30181 GTGTTTATAGATGGGATATGCGCTTTGCTCCAGCGCCGCTAGATACGACCCGGGAAACA 30240
Db 30181 GTGTTTATAGATGGGATATGCGCTTTGCTCCAGCGCCGCTAGATACGACCCGGGAAACA 30240
Qy 30241 AAACGAGTGGGGGGGCTGGGGCGGCGAAAGATTTGGGGAGTAAATTTTCTGTGAG 30300
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Qy 31981 GGTGTTGTTTAACCGTGGGTATCTGCTAAGTGGGCGGAGTTCCACGCGGTTGGCGTG 32040
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Db 32101 AAGGAGGCTGTGGCTTTGGCGACGAGCTTTCGCTCAATGATGCGGAGTGGGAAGCCTTAACT 32160
Qy 32161 GGGACGATCTTCCGACGATCTGATGACGTTGACACGGAAGCAACGATCTTGATGATG 32220
Db 32161 GGGACGATCTTCCGACGATCTGATGACGTTGACACGGAAGCAACGATCTTGATGATG 32220
Qy 32221 ATGATGTTTCCCGCTGTGATAGCAGCGGCTTAATAGCCTTGAAGTCAAAAACCTATG 32280
Db 32221 ATGATGTTTCCCGCTGTGATAGCAGCGGCTTAATAGCCTTGAAGTCAAAAACCTATG 32280
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QY	32281	ACGTACCCACGTCCTCGGTCCGGAAGCCCGTGGGAATTACTGCACCCCGACGCCCTGTATG	323400
Db	32281	ACGTACCCACGTCCTCGGTCCGGAAGCCCGTGGGAATTACTGCACCCCGACGCCCTGTATG	323400
QY	32341	CACATCCGAGGTGCCCCCTAAAAAGGCGGTGTGCCGGGCGGTGGCGGCGCTCCCAAG	324000
Db	32341	CACATCCGAGGTGCCCCCTAAAAAGGCGGTGTGCCGGGCGGTGGCGGCGCTCCCAAG	324000
QY	32401	TGTCGCGGTCCTCGGCTACGACTTCATATATTGTGGACAGACAGATTGTGGGATAGAGAGA	324600
Db	32401	TGTCGCGGTCCTCGGCTACGACTTCATATATTGTGGACAGACAGATTGTGGGATAGAGAGA	324600
QY	32461	CGCGGACGCTTACCGGGGCTCAGTTTCTTCCGAGAGCGAGCCGAAATATCGGAAATAC	325200
Db	32461	CGCGGACGCTTACCGGGGCTCAGTTTCTTCCGAGAGCGAGCCGAAATATCGGAAATAC	325200
QY	32521	CGAGGCTTACTACTACACGCGCGGTGAAAGCGGTGACAAAGAAATTTTCACTCTCCGGC	325800
Db	32521	CGAGGCTTACTACTACACGCGCGGTGAAAGCGGTGACAAAGAAATTTTCACTCTCCGGC	325800
QY	32581	GTAAGGCTGCAATCTCGGAGCCCTCGTGCACAAACCTGATCGATCGGTGGGGTTAAAC	326400
Db	32581	GTAAGGCTGCAATCTCGGAGCCCTCGTGCACAAACCTGATCGATCGGTGGGGTTAAAC	326400
QY	32641	GTAAGACTAAACGTCGCTGAGTGTATAGTCTTAAAACTTGCTCGCGATTAAGAGAGATG	327000
Db	32641	GTAAGACTAAACGTCGCTGAGTGTATAGTCTTAAAACTTGCTCGCGATTAAGAGAGATG	327000
QY	32701	ATGCTAAGGTTGATGTACCCAGGCGGGTTACGCGGCGGGTCAATGACAGCCGATC	327600
Db	32701	ATGCTAAGGTTGATGTACCCAGGCGGGTTACGCGGCGGGTCAATGACAGCCGATC	327600
QY	32761	CTATGAGCGAATATAGAAATGCGTTTAACTATCTATGAGGGGCTCATGGGTGTGGAA	328200
Db	32761	CTATGAGCGAATATAGAAATGCGTTTAACTATCTATGAGGGGCTCATGGGTGTGGAA	328200
QY	32821	AAACACGCGTATTTGAATTCATATGATGCTGTGCCGACAGAAAACTTTAAGCTGTC	328800
Db	32821	AAACACGCGTATTTGAATTCATATGATGCTGTGCCGACAGAAAACTTTAAGCTGTC	328800
QY	32881	CCGAGGCCATGAATTTTGGACGCGTGTAAATTCATTAATGCCCTTAAAGAAACAGCGAGCA	329400
Db	32881	CCGAGGCCATGAATTTTGGACGCGTGTAAATTCATTAATGCCCTTAAAGAAACAGCGAGCA	329400
QY	32941	TAGTTAAGCAAGGACCCAGGGGAAATTGATCACTTGTGCTGCGATACGCGTGTACAGA	330000
Db	32941	TAGTTAAGCAAGGACCCAGGGGAAATTGATCACTTGTGCTGCGATACGCGTGTACAGA	330000
QY	33001	GCAAGTTTGGCGTACCGTTTGTGTGTCGACACGCCCGGCAATCGGTGCGCAACCTGCAACCGT	330600
Db	33001	GCAAGTTTGGCGTACCGTTTGTGTGTCGACACGCCCGGCAATCGGTGCGCAACCTGCAACCGT	330600
QY	33061	GGCTGTGTGGGAAAGCGTAGCAAAAGCCAGCATTTGATTTTGTGACAGACCTTAC	331200
Db	33061	GGCTGTGTGGGAAAGCGTAGCAAAAGCCAGCATTTGATTTTGTGACAGACCTTAC	331200
QY	33121	TGTCCGCAAGCGTGTGTTTCCGCTGTGTACGTAAGTAAGTACACAGGCTAACCGCGGATC	331800
Db	33121	TGTCCGCAAGCGTGTGTTTCCGCTGTGTACGTAAGTAAGTACACAGGCTAACCGCGGATC	331800
QY	33181	ATCTGTTTCAAAATCTTATCTTCTTCTCGGACACACAGCGGCAATGTGTGCTTTTCTTAA	332400
Db	33181	ATCTGTTTCAAAATCTTATCTTCTTCTCGGACACACAGCGGCAATGTGTGCTTTTCTTAA	332400
QY	33241	CGCTCAACAGTTCGGAGGCGCACAGGCGCATTCAAATGCAAGGCCGTAAAGAAAGAAAG	333000
Db	33241	CGCTCAACAGTTCGGAGGCGCACAGGCGCATTCAAATGCAAGGCCGTAAAGAAAGAAAG	333000
QY	33301	GAATCACGCAAAACTTACTGCGACAGGTACGTTGGCGTACATGCGCTGTCTGTACGT	333600
Db	33301	GAATCACGCAAAACTTACTGCGACAGGTACGTTGGCGTACATGCGCTGTCTGTACGT	333600

QY	33361	GGGATGATGATGCAATATCTCACACGGGACCAATGGTTACGCTGGTGTACAAACTGTGT	33420
Db	33361	GGGGATGAAGATGCAATATCTCACACGGGACCAATGGTTACGCTGGTGTACAAACTGTGT	33420
QY	33421	CCATAGAGGACATATGCAATATATAATTCAGATTGACTCATGCGTTTCTAACCCCTAACAA	33480
Db	33421	CCATAGAGGACATATGCAATATATAATTCAGATTGACTCATGCGTTTCTAACCCCTAACAA	33480
QY	33481	AACATCATGAAACAGAGTATGATACCCATGGTGGCAGAAATGTTAGTATCGTTTAAAGAAC	33540
Db	33481	AACATCATGAAACAGAGTATGATACCCATGGTGGCAGAAATGTTAGTATCGTTTAAAGAAC	33540
QY	33541	ACGTGACCTTAATAGGAGCGTCTGTTGGGACTCTTTAAGACGTAAGCAAGCTTCAAAATTT	33600
Db	33541	ACGTGACCTTAATAGGAGCGTCTGTTGGGACTCTTTAAGACGTAAGCAAGCTTCAAAATTT	33600
QY	33601	TAATTGTTGACGACGAGAACATCTAGATGATCGGTGGCGCTGGGGCAAAATATTTATG	33660
Db	33601	TAATTGTTGACGACGAGAACATCTAGATGATCGGTGGCGCTGGGGCAAAATATTTATG	33660
QY	33661	GGCAGGATGATGTCAAATAGAGGCTATTTAAACACAGACAGTGAACGTGGCAGCTCTTGAAA	33720
Db	33661	GGCAGGATGATGTCAAATAGAGGCTATTTAAACACAGACAGTGAACGTGGCAGCTCTTGAAA	33720
QY	33721	GCTACATTTCAAAGCGCTAACCAATTTGGAGGCAATGGCGCGTATTAAGTTTATATTTT	33780
Db	33721	GCTACATTTCAAAGCGCTAACCAATTTGGAGGCAATGGCGCGTATTAAGTTTATATTTT	33780
QY	33781	TTTACTATTAATAGGCTGTCTGTACAGGCAAAATAGCTGTATGATGATAAAATCAAAATGTA	33840
Db	33781	TTTACTATTAATAGGCTGTCTGTACAGGCAAAATAGCTGTATGATGATAAAATCAAAATGTA	33840
QY	33841	GAGTTGGAAATTTAATGAGAACATTTTACCAATTAATTTGAGAAACGTAAAGCAAGATTA	33900
Db	33841	GAGTTGGAAATTTAATGAGAACATTTTACCAATTAATTTGAGAAACGTAAAGCAAGATTA	33900
QY	33901	ACATCTATTTGATATGAGAATGCGTGGTACGATTTCTTACTGCTGGAACCATTTGCTGTG	33960
Db	33901	ACATCTATTTGATATGAGAATGCGTGGTACGATTTCTTACTGCTGGAACCATTTGCTGTG	33960
QY	33961	ACCTTGGAAAAACAAAAGATTTGCTGCTGCAAGATATAGTTAATGCTAATATATATGAC	34020
Db	33961	ACCTTGGAAAAACAAAAGATTTGCTGCTGCAAGATATAGTTAATGCTAATATATATGAC	34020
QY	34021	TATACATTTTGTATATCTTCAAGTACACATGATTAATTAACCTTACGCTGATTTTATATTC	34080
Db	34021	TATACATTTTGTATATCTTCAAGTACACATGATTAATTAACCTTACGCTGATTTTATATTC	34080
QY	34081	AGTTCCTTGGCAGGTTTTACTGGGAATTTTAATGTAATGACACATGCTTTTAAACACAGGC	34140
Db	34081	AGTTCCTTGGCAGGTTTTACTGGGAATTTTAATGTAATGACACATGCTTTTAAACACAGGC	34140
QY	34141	GTTTATTTAAGCAAGCTGGAATTAATTACCAACTCAACAAACCTTATGAGATCTTTTATTC	34200
Db	34141	GTTTATTTAAGCAAGCTGGAATTAATTACCAACTCAACAAACCTTATGAGATCTTTTATTC	34200
QY	34201	GCGGAAAAAAATTAATGACGAAATGTTCAAGATTAATTTGATTTATTCATGTAAATAT	34260
Db	34201	GCGGAAAAAAATTAATGACGAAATGTTCAAGATTAATTTGATTTATTCATGTAAATAT	34260
QY	34261	TCCGGCATTTATACGAAAAATTTGGATATTAAGTATCAAGTTTCAAAATTTCAAGTGAATCA	34320
Db	34261	TCCGGCATTTATACGAAAAATTTGGATATTAAGTATCAAGTTTCAAAATTTCAAGTGAATCA	34320
QY	34321	AATATGCAATGTGTGACGTGTTTGGTTCCTGACGCAATTTCCACGCTTAAAGGC	34380
Db	34321	AATATGCAATGTGTGACGTGTTTGGTTCCTGACGCAATTTCCACGCTTAAAGGC	34380
QY	34381	TATATATCTTAATCGTGAATTTATTTGCTGTTTAAATTTCAAAACATATGCTCTGGGTGAAT	34440
Db	34381	TATATATCTTAATCGTGAATTTATTTGCTGTTTAAATTTCAAAACATATGCTCTGGGTGAAT	34440
QY	34441	GCGCGGAATTCATTAATTAATCTTGTGATTTGACATTTTAAACAAAAATTTTACAGAAATG	34500

FT CDS complement (35865..37073)
 FT /tag- t
 FT /label- RRV_ORF23
 FT /note- "has similarity to KSHV ORF23"
 FT complement (37123..39321)
 FT /tag- u
 FT /label- RRV_ORF24
 FT /note- "has similarity to KSHV ORF24"
 FT 39323..43459
 FT /tag- v
 FT /product- "major capsid protein"
 FT /label- RRV_ORF25
 FT /note- "has similarity to KSHV ORF25"
 FT 43491..44408
 FT /tag- w
 FT /product- "capsid protein"
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 FT /note- "has similarity to KSHV ORF26"
 FT 44433..45242
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 FT /label- RRV_ORF27
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 FT 45408..45683
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 FT 52278..53585
 FT /tag- ah
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 FT 53566..55008
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 FT CDS

FT FT /tag- ak
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 FT /product- "helicase/prinase"
 FT FT /label- RRV_ORF40
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 FT CDS 57917..58528
 FT /tag- am
 FT /product- "helicase/prinase"
 FT FT /label- RRV_ORF41
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 FT CDS complement (58525..59343)
 FT /tag- an
 FT /label- RRV_ORF42
 FT /note- "has similarity to KSHV ORF42"
 FT complement (59297..61027)
 FT /tag- ao
 FT /product- "capsid protein"
 FT FT /label- RRV_ORF43
 FT FT /note- "has similarity to KSHV ORF43"
 FT FT

Query Match 84.1%; Score 29420; DB 24; Length 128139;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 29420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5581 CTGCTGCCCTTTATGTTGTTTCTAAATTAAGTGTGTTTCTTACAGAGTTGCC 5640
 DB 1 CTGCTGCCCTTTATGTTGTTTCTAAATTAAGTGTGTTTCTTACAGAGTTGCC 60
 QY 5641 AGGCAACTGCAGCATTAACCAATCGCAACCGCGTGTGATTCGGAAATTAAGTTA 5700
 DB 61 AGGCAACTGCAGCATTAACCAATCGCAACCGCGTGTGATTCGGAAATTAAGTTA 120
 QY 5701 CATTAATCAAGTGGCCAAATAAAGTGTTTAAATATTCATATGTTGTTTCATGTTT 5760
 DB 121 CATTAATCAAGTGGCCAAATAAAGTGTTTAAATATTCATATGTTGTTTCATGTTT 180
 QY 5761 ATGTTGACCCGTTTATGTTATTCGCGCCACCTGTGGCTAATTAATAGACATGCT 5820
 DB 181 ATGTTGACCCGTTTATGTTATTCGCGCCACCTGTGGCTAATTAATAGACATGCT 240
 QY 5821 TTCACGTTATCTTACGTTACGTTACGTTACGTTACGTTACGTTACGTTACGTT 5880
 DB 241 TTCACGTTATCTTACGTTACGTTACGTTACGTTACGTTACGTTACGTTACGTT 300
 QY 5881 TGTGGCCGGGCTGAAAAATACACAAAGGGGTATCATATCATCCAGGGGACACATTAG 5940
 DB 301 TGTGGCCGGGCTGAAAAATACACAAAGGGGTATCATATCATCCAGGGGACACATTAG 360
 QY 5941 ACACGTTTAAACTATATCGGATGGCCCAACATACGTGCTAGCGCACTGATA 6000
 DB 361 ACACGTTTAAACTATATCGGATGGCCCAACATACGTGCTAGCGCACTGATA 420
 QY 6001 GAAAAACATTTTAAAGTTGTTTACGCACTTGAATTAACATATATGCTTCCAAAGCA 6060
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 QY 6061 ACGCCGCAACCCCTGGAAGATATCAAGGGGTCTGTCGCCCGATAGGCTGCGGAT 6120
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 QY 6181 GACCATGTGATCTGGGCTTTCGCTACCAATCCCTTACGAGCTTACAGTTGAACACG 6240
 DB 601 GACCATGTGATCTGGGCTTTCGCTACCAATCCCTTACGAGCTTACAGTTGAACACG 660
 QY 6241 AATTCCCTCTCACCGTAAGCCGCAATACAAAAAGTTGACACGACGAGCTCCCGTTA 6300

Db 661 AATTCCCTCACCGRAAAAGCGCATACAAAAAGTTGACACACGACGCTGCGGTTA 720
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QY	8521	ACGAGGTTCCGGATTTCATCTGCTGCTAGCGGAGGATCAAACTGAAAGGGGCCATTCTAA	8580
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QY	8581	GGGCAATGCGCAGATTTCAGTTCTTACGCGACGAGCTGCACTGGCTTCACGCGGCTGTAC	8640
Db	3001	GGGCAATGCGCAGATTTCAGTTCTTACGCGACGAGCTGCACTGGCTTCACGCGGCTGTAC	3060
QY	8641	AGACGATTCGATTCGCGAGGAATACCCCAACGCTGCTGGGCTCGCGGCAATGCGCACACGG	8700
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Db	3121	TGGCTTACCTGGCAAGAAATATACGGCGCGCAACGCGCTCACGCTGCAACGACGCGCGCTC	3180
QY	8761	AGCCGCTGCGCGCACAGGCGCGCTGCGCTGATTAACGCTTCCATGGTAGTCAACA	8820
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QY	8821	AATACAGCGGGGCTCAACGGGAAACAACAACGTTTCCACTGCGGAAACCTGGGGTACTTCG	8880
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Db	3301	CGGGGCGGGGCTGGAGCCCAACCTGTGCGCGGAAACCTCCCTTTAAGAAACGCGGCG	3360
QY	8941	TCAGCGCCATGCTAAGAAAGACACGTATGATGACCCCATTAATGACCGCCTAATAA	9000
Db	3361	TCAGCGCCATGCTAAGAAAGACACGTATGATGACCCCATTAATGACCGCCTAATAA	3420
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QY	9061	AGGCGCTGTTTAGAGGATTAAGGACAACCTTAACCTATTGAAGTCCGTAACTTTGAGCTTA	9120
Db	3481	AGGCGCTGTTTAGAGGATTAAGGACAACCTTAACCTATTGAAGTCCGTAACTTTGAGCTTA	3540
QY	9121	TACGACACCTTGGGGAAGGGCTGCCAGACCTTAAGCTCCGAGAGCTGCATATTACTCG	9180
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QY	9301	ATCTTCAGTTCTGTAAGACAGGACGATATCGCCACCGCTTCTGTTCAGCCCCCGAGAAC	9360
Db	3721	ATCTTCAGTTCTGTAAGACAGGACGATATCGCCACCGCTTCTGTTCAGCCCCCGAGAAC	3780
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Db	3781	AGCTACGACCCCTAGCGCGCGGCGCTACTAGCGCGGGAAGAAACGAAATTAACCGCG	3840
QY	9421	TGCTGAGCGATCTAGACCTTTAGGAAACCGTGGCAGGCGGCAACATGCGCAGGGAAC	9480
Db	3841	TGCTGAGCGATCTAGACCTTTAGGAAACCGTGGCAGGCGGCAACATGCGCAGGGAAC	3900
QY	9481	TCGACAGCATTAATACGCGACGCTGTGCGGCTCGCGCTGCAGCTTGAGTCTGGTTATCTTTG	9540
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D 18061 GCGAGCAGGCGCAAAACAGGGCGCGGAGCGCGCAAGTGTGCGGCTTTTCCCG 18120
Qy 23701 CACGCGCGATTTGGCAAAATGCGGACCGCGCGGTGTGAGCGCGGAGCGCTCA 23760
D 18121 CACGCGCGATTTGGCAAAATGCGGACCGCGCGGTGTGAGCGCGGAGCGCTCA 18180
Qy 23761 TCACGACGAGAGAAAGCGCAAGTTGTGCTCCGTCAATCAACGAGGGCGCGCGG 23820

Db	18181	TCACGACGAGAGAACGCCAGTTGGTCAGTTGTCCCGTCATTCACCCAGGGCCGCCGCG	18240
Qy	23821	TTGGCGGATTAATGAAAACGGCGCGGCATTTGGACGCTGGCGGACGCCAATGGGCGCT	23880
Db	18241	TTGGCGGATTAATGAAAACGGCGCGGCATTTGGACGCTGGCGGACGCCAATGGGCGGT	18300
Qy	23881	TGCGTTTGTTTACAGAGTTCCCTATATATATATATATATATATATATATATATATAT	23940
Db	18301	TGGGTTTTGTTTACAGAGTTCCCTATATATATATATATATATATATATATATATATAT	18360
Qy	23941	CCATTTCTTAATCTAATCAGCTGGGTTATATATATATATATATATATATATATATATAT	24000
Db	18361	CCATTTCTTAATCTAATCAGCTGGGTTATATATATATATATATATATATATATATATAT	18420
Qy	24001	TACGTAT	24060
Db	18421	TACGTAT	18480
Qy	24061	TATTTATGTAATCAGATACTGGGAAATCTACTCCACGTTTAAATAAATAATATATAT	24120
Db	18481	TATTTATGTAATCAGATACTGGGAAATCTACTCCACGTTTAAATAAATAATATATAT	18540
Qy	24121	CTATTATGTTGGGGTTCTAATATATTTGACAAAACAAATTTTTTAAATATATATAC	24180
Db	18541	CTATTATGTTGGGGTTCTAATATATTTGACAAAACAAATTTTTTAAATATATATAC	18600
Qy	24181	TAAAAATGCTCCCATTTTACTTGTGACGTACATGTTAGAAATGTGGAGTGGTTTGAAC	24240
Db	18601	TAAAAATGCTCCCATTTTACTTGTGACGTACATGTTAGAAATGTGGAGTGGTTTGAAC	18660
Qy	24241	TATGTTTCAACAACACACCTTTTGGGCGCTGTAAACCTATATAGCGGAGGCTCGC	24300
Db	18661	TATGTTTCAACAACACACCTTTTGGGCGCTGTAAACCTATATAGCGGAGGCTCGC	18720
Qy	24301	GTTAATGCCACTGGCGCTACACAGTCCACCTGSCAGTTGGAGTTTATTTGCTGCTA	24360
Db	18721	GTTAATGCCACTGGCGCTACACAGTCCACCTGSCAGTTGGAGTTTATTTGCTGCTA	18780
Qy	24361	TGGCTTTACCTCGCATTCGCGGACAAAGCTGATTACGTAGACGACATTGGGGGTTTAAAC	24420
Db	18781	TGGCTTTACCTCGCATTCGCGGACAAAGCTGATTACGTAGACGACATTGGGGGTTTAAAC	18840
Qy	24421	CCGGTTGAATTAAGTGGTTTGCACGCTGTAACAAAACCCACCGAGGCTTGGGTTTAAAGCT	24480
Db	18841	CCGGTTGAATTAAGTGGTTTGCACGCTGTAACAAAACCCACCGAGGCTTGGGTTTAAAGCT	18900
Qy	24481	TTAAAGGCTTGGCTTTTATACATGAGATTTATATGCTATGGGAGCTAGCTTGTATTC	24540
Db	18901	TTAAAGGCTTGGCTTTTATACATGAGATTTATATGCTATGGGAGCTAGCTTGTATTC	18960
Qy	24541	CGCATGCTTTCGTTTATAGTATTTGTACAAAACAGAAATGTAGCCCCGAAATTTGACTGC	24600
Db	18961	CGCATGCTTTCGTTTATAGTATTTGTACAAAACAGAAATGTAGCCCCGAAATTTGACTGC	19020
Qy	24601	TACCCAAAAGGCGACCCCGCTTACACAGCCCCGCGCTGCGGCTTTGTTCTAGACCCGC	24660
Db	19021	TACCCAAAAGGCGACCCCGCTTACACAGCCCCGCGCTGCGGCTTTGTTCTAGACCCGC	19080
Qy	24661	TCGCAATTCATTCAGATTTTAAATTTAAATTTGGGCAATGGCGTATGCGAAATTTAAGCG	24720
Db	19081	TCGCAATTCATTCAGATTTTAAATTTAAATTTGGGCAATGGCGTATGCGAAATTTAAGCG	19140
Qy	24721	CGTCAAAAATTTAAATTTGAGCTAACGTAACGGGCTTATAGTATGAGCTATAGGGGAATTT	24780
Db	19141	CGTCAAAAATTTAAATTTGAGCTAACGTAACGGGCTTATAGTATGAGCTATAGGGGAATTT	19200
Qy	24781	AAAAATTTAAAGCCGTGGGTTTAAACACAGAGCTGCCAGCTTGAATACGTTGCATATACA	24840
Db	19201	AAAAATTTAAAGCCGTGGGTTTAAACACAGAGCTGCCAGCTTGAATACGTTGCATATACA	19260
Qy	24841	GTGCGCTTGTGATTTATGTTAAGTGAATTTTAACTGAATTTTGTAAATGTTGATAC	24900
Db	19261	GTGCGCTTGTGATTTATGTTAAGTGAATTTTAACTGAATTTTGTAAATGTTGATAC	19320
Qy	24901	GTGGAATTTTAAATTTGAATTTTAAATTTGAATTTACGTGGCGTGATATTTTAAATTTGAT	24960
Db	19321	GTGGAATTTTAAATTTGAATTTTAAATTTGAATTTACGTGGCGTGATATTTTAAATTTGAT	19380
Qy	24961	TTATGTACACTTGTATTAATTTTAACTGCGTATAGGTTGTATTTTGGTTAATTTATGTAT	25020
Db	19381	TTATGTACACTTGTATTAATTTTAACTGCGTATAGGTTGTATTTTGGTTAATTTATGTAT	19440
Qy	25021	TTTGCTTTTATGATTTTGTGGGTTGTAATTTCCGAGAGGTAAAGAGCTAGCTCTAATGT	25080
Db	19441	TTTGCTTTTATGATTTTGTGGGTTGTAATTTCCGAGAGGTAAAGAGCTAGCTCTAATGT	19500
Qy	25081	TTGCGCTTCCGAGCTACCTCTAATGTTTGCCTTCCGAGCTACCTCTAATGTTTGCCTTG	25140
Db	19501	TTGCGCTTCCGAGCTACCTCTAATGTTTGCCTTCCGAGCTACCTCTAATGTTTGCCTTG	19560
Qy	25141	CCGCGTACGCTCTAATGTTTGCCTTCCGAGCTACCTCTAATGTTTGCCTTCCGAGCT	25200
Db	19561	CCGCGTACGCTCTAATGTTTGCCTTCCGAGCTACCTCTAATGTTTGCCTTCCGAGCT	19620
Qy	25201	CTCCTAATGTTTGTGCTTCCGAGCTACCTCTAATGTTTGCCTTCCGAGCTACCTCTAAT	25260
Db	19621	CTCCTAATGTTTGTGCTTCCGAGCTACCTCTAATGTTTGCCTTCCGAGCTACCTCTAAT	19680
Qy	25261	GTTTGCCTTCCGAGCTACCTCTAATGTTTGCCTTCCGAGCTACCTCTAATGTTTGCCT	25320
Db	19681	GTTTGCCTTCCGAGCTACCTCTAATGTTTGCCTTCCGAGCTACCTCTAATGTTTGCCT	19740
Qy	25321	TGCGCGCTACCTCTAATGTTTGCCTTCCGAGCTACCTCTAATGTTTACAACTAAT	25380
Db	19741	TGCGCGCTACCTCTAATGTTTGCCTTCCGAGCTACCTCTAATGTTTACAACTAAT	19800
Qy	25381	GTTTAAAGCACTAATTAATTAAGAGCTTGTGTTTATATGACCAAGCTGGTACAA	25440
Db	19801	GTTTAAAGCACTAATTAATTAAGAGCTTGTGTTTATATGACCAAGCTGGTACAA	19860
Qy	25441	AACCTGCTGTGATTTTATACCAACAAATAATTAATTAATTAATTAATTAATTTG	25500
Db	19861	AACCTGCTGTGATTTTATACCAACAAATAATTAATTAATTAATTAATTTG	19920
Qy	25501	TTGTCTGTGTGATTTTGGGTTCCCGAGGCTCCCGGCTCCCGTTCCCGAGGCTCCCG	25560
Db	19921	TTGTCTGTGTGATTTTGGGTTCCCGAGGCTCCCGGCTCCCGTTCCCGAGGCTCCCG	19980
Qy	25561	GCTCCCGTTCCCGAGGCTCCCGGCTCCCGGCTCCCGGCTCCCGAGGCTCCCGGCT	25620
Db	19981	GCTCCCGTTCCCGAGGCTCCCGGCTCCCGGCTCCCGGCTCCCGAGGCTCCCGGCT	20040
Qy	25621	CCCGAGGCTCCCGGCTCCCGGCTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGT	25680
Db	20041	CCCGAGGCTCCCGGCTCCCGGCTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGT	20100
Qy	25681	CCCGGCTCCCGGCTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCCGGCTCC	25740
Db	20101	CCCGGCTCCCGGCTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCCGGCTCC	20160
Qy	25741	CCGTTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCCGGCTCCCGGCTCCCG	25800
Db	20161	CCGTTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCCGGCTCCCGGCTCCCG	20220
Qy	25801	AGGGTCCGGGGTCCCGGTTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCGG	25860
Db	20221	AGGGTCCGGGGTCCCGGTTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCGG	20280
Qy	25861	GCTCCCGTTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCCGGCTCCCGGCT	25920
Db	20281	GCTCCCGTTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCCGGCTCCCGGCT	20340
Qy	25921	CCCGAGGCTCCCGGCTCCCGTTCCCGAGAGGTCCCGGCTCCCGGCTCCCGAGGCT	25980
Db	20341	CCCGAGGCTCCCGGCTCCCGTTCCCGAGAGGTCCCGGCTCCCGGCTCCCGAGGCT	20400

OY	23581	CCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCC	26040
Db	20401	CCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCC	20460
OY	26041	CCGTTCCCGAGGGTCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCC	26100
Db	20461	CCGTTCCCGAGGGTCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCC	20520
OY	26101	AGGGTCCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCC	26160
Db	20521	AGGGTCCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCCCGTTC	CCCGAGGGTCCGGGCTCC	20580
OY	26161	GCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCC	26220
Db	20581	GCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCC	20640
OY	26221	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	26280
Db	20641	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	20700
OY	26281	CCCGGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	26340
Db	20701	CCCGGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	20760
OY	26341	CCGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	26400
Db	20761	CCGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	20820
OY	26401	AGGGTCCCGGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	26460
Db	20821	AGGGTCCCGGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	20880
OY	26461	GCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	26520
Db	20881	GCTCCCGGTTCCCGGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	CCCGAGGGTCCCGGCTCCCGTTC	20940
OY	26521	CCCGGATTCAACGTTAAAGGTTTATTAGCAAAACACAGTTTTCGCGGGTTGGG	CCCGGATTCAACGTTAAAGGTTTATTAGCAAAACACAGTTTTCGCGGGTTGGG	CCCGGATTCAACGTTAAAGGTTTATTAGCAAAACACAGTTTTCGCGGGTTGGG	26580
Db	20941	CCCGGATTCAACGTTAAAGGTTTATTAGCAAAACACAGTTTTCGCGGGTTGGG	CCCGGATTCAACGTTAAAGGTTTATTAGCAAAACACAGTTTTCGCGGGTTGGG	CCCGGATTCAACGTTAAAGGTTTATTAGCAAAACACAGTTTTCGCGGGTTGGG	21000
OY	26581	TTGTACATACACCGGGGTGGCATTTGGCCCGCATGCAAAAAAATAACGTTGGGTTTC	TTGTACATACACCGGGGTGGCATTTGGCCCGCATGCAAAAAAATAACGTTGGGTTTC	TTGTACATACACCGGGGTGGCATTTGGCCCGCATGCAAAAAAATAACGTTGGGTTTC	26640
Db	21001	TTGTACATACACCGGGGTGGCATTTGGCCCGCATGCAAAAAAATAACGTTGGGTTTC	TTGTACATACACCGGGGTGGCATTTGGCCCGCATGCAAAAAAATAACGTTGGGTTTC	TTGTACATACACCGGGGTGGCATTTGGCCCGCATGCAAAAAAATAACGTTGGGTTTC	21060
OY	26641	GAAACGCGTAGGTCCTTAGTGTTCATGGCACGTTTCGTACACGTTAGGAGTGTGTA	GAAACGCGTAGGTCCTTAGTGTTCATGGCACGTTTCGTACACGTTAGGAGTGTGTA	GAAACGCGTAGGTCCTTAGTGTTCATGGCACGTTTCGTACACGTTAGGAGTGTGTA	26700
Db	21061	GAAACGCGTAGGTCCTTAGTGTTCATGGCACGTTTCGTACACGTTAGGAGTGTGTA	GAAACGCGTAGGTCCTTAGTGTTCATGGCACGTTTCGTACACGTTAGGAGTGTGTA	GAAACGCGTAGGTCCTTAGTGTTCATGGCACGTTTCGTACACGTTAGGAGTGTGTA	21120
OY	26701	GTTTTTGGTAGGGAATGCAACACAGGTACGTGGCGGAGGAAAAAGGAACGTTTAAA	GTTTTTGGTAGGGAATGCAACACAGGTACGTGGCGGAGGAAAAAGGAACGTTTAAA	GTTTTTGGTAGGGAATGCAACACAGGTACGTGGCGGAGGAAAAAGGAACGTTTAAA	26760
Db	21121	GTTTTTGGTAGGGAATGCAACACAGGTACGTGGCGGAGGAAAAAGGAACGTTTAAA	GTTTTTGGTAGGGAATGCAACACAGGTACGTGGCGGAGGAAAAAGGAACGTTTAAA	GTTTTTGGTAGGGAATGCAACACAGGTACGTGGCGGAGGAAAAAGGAACGTTTAAA	21180
OY	26761	CCGCAAGTTACCGCGGTGGCGCATACGGTTTAACTGCACTGGCGGTCGCCGCCGAGG	CCGCAAGTTACCGCGGTGGCGCATACGGTTTAACTGCACTGGCGGTCGCCGCCGAGG	CCGCAAGTTACCGCGGTGGCGCATACGGTTTAACTGCACTGGCGGTCGCCGCCGAGG	26820
Db	21181	CCGCAAGTTACCGCGGTGGCGCATACGGTTTAACTGCACTGGCGGTCGCCGCCGAGG	CCGCAAGTTACCGCGGTGGCGCATACGGTTTAACTGCACTGGCGGTCGCCGCCGAGG	CCGCAAGTTACCGCGGTGGCGCATACGGTTTAACTGCACTGGCGGTCGCCGCCGAGG	21240
OY	26821	TACCTTAAGTTACGCTAGCAATTAATGGCGCTGTTACGGGCCCTCGCGGCCCTCGA	TACCTTAAGTTACGCTAGCAATTAATGGCGCTGTTACGGGCCCTCGCGGCCCTCGA	TACCTTAAGTTACGCTAGCAATTAATGGCGCTGTTACGGGCCCTCGCGGCCCTCGA	26880
Db	21241	TACCTTAAGTTACGCTAGCAATTAATGGCGCTGTTACGGGCCCTCGCGGCCCTCGA	TACCTTAAGTTACGCTAGCAATTAATGGCGCTGTTACGGGCCCTCGCGGCCCTCGA	TACCTTAAGTTACGCTAGCAATTAATGGCGCTGTTACGGGCCCTCGCGGCCCTCGA	21300
OY	26881	GGAAGAAATGAATCTTGTGGCACTTACGTTATGCTATATAGAGGATCTTCTTTA	GGAAGAAATGAATCTTGTGGCACTTACGTTATGCTATATAGAGGATCTTCTTTA	GGAAGAAATGAATCTTGTGGCACTTACGTTATGCTATATAGAGGATCTTCTTTA	26940
Db	21301	GGAAGAAATGAATCTTGTGGCACTTACGTTATGCTATATAGAGGATCTTCTTTA	GGAAGAAATGAATCTTGTGGCACTTACGTTATGCTATATAGAGGATCTTCTTTA	GGAAGAAATGAATCTTGTGGCACTTACGTTATGCTATATAGAGGATCTTCTTTA	21360
OY	26941	CTGAGGCTGGGCGAGGCGAGTCTGACCATCCCGTTTAGCCATTAAGAAAT	CTGAGGCTGGGCGAGGCGAGTCTGACCATCCCGTTTAGCCATTAAGAAAT	CTGAGGCTGGGCGAGGCGAGTCTGACCATCCCGTTTAGCCATTAAGAAAT	27000
Db	21361	CTGAGGCTGGGCGAGGCGAGTCTGACCATCCCGTTTAGCCATTAAGAAAT	CTGAGGCTGGGCGAGGCGAGTCTGACCATCCCGTTTAGCCATTAAGAAAT	CTGAGGCTGGGCGAGGCGAGTCTGACCATCCCGTTTAGCCATTAAGAAAT	21420
OY	27001	TATCAGCGCTTCTCAAGGACAGCGCTGCTGACGAGAGGCTTCGCGCACACGA	TATCAGCGCTTCTCAAGGACAGCGCTGCTGACGAGAGGCTTCGCGCACACGA	TATCAGCGCTTCTCAAGGACAGCGCTGCTGACGAGAGGCTTCGCGCACACGA	27060
Db	21421	TATCAGCGCTTCTCAAGGACAGCGCTGCTGACGAGAGGCTTCGCGCACACGA	TATCAGCGCTTCTCAAGGACAGCGCTGCTGACGAGAGGCTTCGCGCACACGA	TATCAGCGCTTCTCAAGGACAGCGCTGCTGACGAGAGGCTTCGCGCACACGA	21480

QY	27061	TTACCGCTCTCTCGGGGAGCTAAAGCCATAGGCCAAGGATGCTGCAATTAACACGGA	27120
Db	21481	TTACCGCTCTCTCGGGGAGCTAAAGCCATAGGCCAAGGATGCTGCAATTAACACGGA	21540
QY	27121	CGGACGCCAACACCTGGGGGTCGGCTTTGGCCGTTGGGGTCTTTGGGGCTAATGNGTGA	27180
Db	21541	CGGACGCCAACACCTGGGGGTCGGCTTTGGCCGTTGGGGTCTTTGGGGCTAATGNGTGA	21600
QY	27181	TAAAGTTAAAGACGAGAGCGTCTTTAAAGTTCCGCAATAGCCGTTCTACCCGTTACGC	27240
Db	21601	TAAAGTTAAAGACGAGAGCGTCTTTAAAGTTCCGCAATAGCCGTTCTACCCGTTACGC	21660
QY	27241	GTAAGAGCGCCCTGAGTCTCAGTGTTCCTACACGGCCGAATGGAGGACTCAGAA	27300
Db	21661	GTAAGAGCGCCCTGAGTCTCAGTGTTCCTACACGGCCGAATGGAGGACTCAGAA	21720
QY	27301	TTACTGGGACGAAATCTAGGAGATCGCCGCAAGCGGAGAGAACATGTGCTACGGAGT	27360
Db	21721	TTACTGGGACGAAATCTAGGAGATCGCCGCAAGCGGAGAGAACATGTGCTACGGAGT	21780
QY	27361	TGCGGCGGTCTTCTGGCGCTAGTGGCGCTGTTTGGCATCAGGCGATAGTGTGCGTTTA	27420
Db	21781	TGCGGCGGTCTTCTGGCGCTAGTGGCGCTGTTTGGCATCAGGCGATAGTGTGCGTTTA	21840
QY	27421	ACCGCGTATTTCCCCACCCCTGACCTTAAGTAGCGCATGTTATATAGACCAATAAACA	27480
Db	21841	ACCGCGTATTTCCCCACCCCTGACCTTAAGTAGCGCATGTTATATAGACCAATAAACA	21900
QY	27481	AAACACACTAAGCGGGATTCGTTGGAACATTTTATTTAGACAGTTCCCTGCGAACA	27540
Db	21901	AAACACACTAAGCGGGATTCGTTGGAACATTTTATTTAGACAGTTCCCTGCGAACA	21960
QY	27541	TTTTTTGTATCTGTGACACGGGGGCGCGCTGTGCGCTGCGCTCCACACGGGGCCCGCGG	27600
Db	21961	TTTTTTGTATCTGTGACACGGGGGCGCGCTGTGCGCTGCGCTCCACACGGGGCCCGCGG	22020
QY	27601	ACTGTCCGCATTTCTGCATCGAGGGGGGCGCACGCCGCGGGGGGCGAGAGCTGAAG	27660
Db	22021	ACTGTCCGCATTTCTGCATCGAGGGGGGCGCACGCCGCGGGGGGCGAGAGCTGAAG	22080
QY	27661	GAATGGCGTTTGACATTAACAGATTTCTTGGGCGGGGCGCTGAGTGTCCGACTCGTGG	27720
Db	22081	GAATGGCGTTTGACATTAACAGATTTCTTGGGCGGGGCGCTGAGTGTCCGACTCGTGG	22140
QY	27721	CGAAGCCGCGCTGTGCTCGCCGCGTGCGGGGGCGGTGGTTCGTTTCTCGATGCCCT	27780
Db	22141	CGAAGCCGCGCTGTGCTCGCCGCGTGCGGGGGCGGTGGTTCGTTTCTCGATGCCCT	22200
QY	27781	GCGCGCTCTGATACGGCTGTGGGGCGTGAAGATGGTGTTCCTCCGGAATACCACTGCG	27840
Db	22201	GCGCGCTCTGATACGGCTGTGGGGCGTGAAGATGGTGTTCCTCCGGAATACCACTGCG	22260
QY	27841	GCCTGTACGCTAGGTACGGCGCACAGACGCTAGTCTGTGGCCACGGAATCAAGGGGCG	27900
Db	22261	GCCTGTACGCTAGGTACGGCGCACAGACGCTAGTCTGTGGCCACGGAATCAAGGGGCG	22320
QY	27901	GTTGGTTACGGTCTGTGGTCCGCTCCTGTGTCGCGCGGAGGTCGTGCACCGCGCTCTTTTA	27960
Db	22321	GTTGGTTACGGTCTGTGGTCCGCTCCTGTGTCGCGCGGAGGTCGTGCACCGCGCTCTTTTA	22380
QY	27961	GGTCCCTCAGATCCGCTGAATGTCCCAATATGTTTTTGGACAGCGCCATGAGCTCTTGT	28020
Db	22381	GGTCCCTCAGATCCGCTGAATGTCCCAATATGTTTTTGGACAGCGCCATGAGCTCTTGT	22440
QY	28021	GTAAGCCGACCTCTCGCTCTGGAACAACGGGCTCTGTGCGAAGAGTCCACGTCCTTTGC	28080
Db	22441	GTAAGCCGACCTCTCGCTCTGGAACAACGGGCTCTGTGCGAAGAGTCCACGTCCTTTGC	22500
QY	28081	GCTTCTGTGGCGAGAGGTCGCGGAGCGAGCGCTAGTCGAGAGATAGTACGTGCGGCG	28140
Db	22501	GCTTCTGTGGCGAGAGGTCGCGGAGCGAGCGCTAGTCGAGAGATAGTACGTGCGGCG	22560
QY	28141	CATTCGAGAGAGGTTGGGGGGCAACACGCCGACTGTGAAGGGAACGGTTGGCGCGACGGCG	28200

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Db 22561 CATACGAGAGGGTTGGGGGCAACGCCACTGGAAGGGAACGGGGCGACAGCGCG 22620
QY 28201 GTGCTACGATGGAGCGCTCAGCTCAGGCGGGTATCCAGATGATACGCCGCTTG 28260
Db 22621 GTGCTACGATGGAGCGCTCAGCTCAGGCGGGTATCCAGATGATACGCCGCTTG 22680
QY 28261 CCGGCATCGAGGCTGGCGCAGAAACGTACGCTGCGTGGCCCTGGTCCGATTTATCGA 28320
Db 22681 CCGGCATCGAGGCTGGCGCAGAAACGTACGCTGCGTGGCCCTGGTCCGATTTATCGA 22740
QY 28321 GACTGCTGACCATGATGATGAGAAAGTGTCTGGGAAAGTATGTTCTCTCCGGGA 28380
Db 22741 GACTGCTGACCATGATGATGAGAAAGTGTCTGGGAAAGTATGTTCTCTCCGGGA 22800
QY 28381 GGGCGCTCATGTTCTGGGTGTCCGGGTACCGCAGTGTAGGCGCAGGAAATGGCTTG 28440
Db 22801 GGGCGCTCATGTTCTGGGTGTCCGGGTACCGCAGTGTAGGCGCAGGAAATGGCTTG 22860
QY 28441 CCTTTAAATACGTACTTCTCGCGACGCTGGCCACGCCCTTATCTGTTTGGAGAGTCTG 28500
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QY 28501 TGGGATCTGGGATAAATCCGGGCTGATGCGCTTGGCCATGATGTTCTCAAGAGGGCGG 28560
Db 22921 TGGGATCTGGGATAAATCCGGGCTGATGCGCTTGGCCATGATGTTCTCAAGAGGGCGG 22980
QY 28561 CGAATTCGCGGCTGTACCTGTACCTGTCCGAAAGATCTAAACAAATGACCGTTATTTTAC 28620
Db 22981 CGAATTCGCGGCTGTACCTGTGTACCTGTCCGAAAGATCTAAACAAATGACCGTTATTTTAC 23040
QY 28621 CGGCTTCCTCTCGCGTAAAGAGATCAAACTTGGAGACGACCCATGTAAGGCTGTGCTCGT 28680
Db 23041 CGGCTTCCTCTCGCGTAAAGAGATCAAACTTGGAGACGACCCATGTAAGGCTGTGCTCGT 23100
QY 28681 AAACGCGATTGACCCCTACGCGCTCCGACAGTGTGCGACAGAGAGAGTGTGTAAGCGCG 28740
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QY 28741 GTGGGTGATTGGGGTCTTCAAGCTCTTGGGTGAGGAGCAGAGAGGAGAGTCCGGGA 28800
Db 23161 GTGGGTGATTGGGGTCTTCAAGCTCTTGGGTGAGGAGCAGAGAGGAGAGTCCGGGA 23220
QY 28801 GGCATCTGTCTAAACATCTCCACACAGGGGCTCCGAGAGCATGGGCTTACGTGATCTGGG 28860
Db 23221 GGCATCTGTCTAAACATCTCCACACAGGGGCTCCGAGAGCATGGGCTTACGTGATCTGGG 23280
QY 28861 CCGCTGCGAGTCCCGCGAGGCGGTGACGCCAGGSCAAAGAAATGCTGGCTGTAGCT 28920
Db 23281 CCGCTGCGAGTCCCGCGAGGCGGTGACGCCAGGSCAAAGAAATGCTGGCTGTAGCT 23340
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Db 23341 TGGCCAGGCAAAATATCCGCTGTACTTGGGAAGAGACCGATTTGTGACCTACGTTGG 23400
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Db 23401 CTTCGGGAGCGTCTATGTTTATGAGAGGCTCCATATCCGAGAGAGGCTGCCA 23460
QY 29041 CGATTAGAGGCTTAATACAGCTCTTTTCTATCTTTGGTAGCTGACACGCTCCACGT 29100
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QY 29101 ATTCGCCAACGTACACAGGAGTCAATGTTGGTGGTGTGCTGCGTGAAGCGAAGAGATGA 29160
Db 23521 ATTCGCCAACGTACACAGGAGTCAATGTTGGTGGTGTGCTGCGTGAAGCGAAGAGATGA 23580
QY 29161 GGGCGGCTCTGGGGGCTGATGTGCGGCTTATCCGTTGTGAGATTTAATACGTTTC 29220
Db 23581 GGGCGGCTCTGGGGGCTGATGTGCGGCTTATCCGTTGTGAGATTTAATACGTTTC 23640
QY 29221 TCCCTGGAGGCTCAGGTTCTTCACTGTGTGCGAAATGTCAACTACGCTTA 29280
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Db 23641 TCCCTGGAGCTCAGGTTTCTTCACTGTGTGCGAAATGTCAACTACGCTTA 23700
QY 29281 ACGTGTACCTTCTGAAGAGCAATTCCTAATACCGGAACGAGAGCATATTTCTCTG 29340
Db 23701 ACGTGTACCTTCTGAAGAGCAATTCCTAATACCGGAACGAGAGCATATTTCTCTG 23760
QY 29341 GGGGTAAAGTTCGGGTGAGTCTTGGAAATCGTTTACATGGGTTTAAAGACATGGGG 29400
Db 23761 GGGGTAAAGTTCGGGTGAGTCTTGGAAATCGTTTACATGGGTTTAAAGACATGGGG 23820
QY 29401 TTTCTGACGACGTTGCTCTCAAGAAACCAAGAGGGGCTGTGGCTTACTTCAACG 29460
Db 23821 TTTCTGACGACGTTGCTCTCAAGAAACCAAGAGGGGCTGTGGCTTACTTCAACG 23880
QY 29461 GGGCTCGTCCCTGTTAAAGGTCTAGGCGACTACGTTTTTCCCACTGGGTTAAGCC 29520
Db 23881 GGGCTCGTCCCTGTTAAAGGTCTAGGCGACTACGTTTTTCCCACTGGGTTAAGCC 23940
QY 29521 ACAGCGTACCGCTGTTCGGGAAACCTTAACGATGGGAATTTCTATACCTTAGCA 29580
Db 23941 ACAGCGTACCGCTGTTCGGGAAACCTTAACGATGGGAATTTCTATACCTTAGCA 24000
QY 29581 GCGTCAATACATGTCGCTGCTGTGGACACTAGCTACGTTTGGGGTGGGGGACG 29640
Db 24001 GCGTCAATACATGTCGCTGCTGTGGACACTAGCTACGTTTGGGGTGGGGGACG 24060
QY 29641 CTGACACGAGCCCTGGGTCAGGTTGTCCCGCAGAAATTTTATACCTTAATAA 29700
Db 24061 CTGACACGAGCCCTGGGTCAGGTTGTCCCGCAGAAATTTTATACCTTAATAA 24120
QY 29701 TTTCCGGCCCATTTATGCCAGGAATGCAATCTTAACACAGTGGGAGCTCCGGGTACG 29760
Db 24121 TTTCCGGCCCATTTATGCCAGGAATGCAATCTTAACACAGTGGGAGCTCCGGGTACG 24180
QY 29761 GTGCTTCGTCGAGGAGTGTGCGGATTTGCCGAGTACACGGGATTCGCGCTGGG 29820
Db 24181 GTGCTTCGTCGAGGAGTGTGCGGATTTGCCGAGTACACGGGATTCGCGCTGGG 24240
QY 29821 ATTTGCGTCCGCGCTCGGCGTTAAGCTCTCACAGACGACTACTTGTTCGCTCA 29880
Db 24241 ATTTGCGTCCGCGCTCGGCGTTAAGCTCTCACAGACGACTACTTGTTCGCTCA 24300
QY 29881 ATACACGCGTAGTGTAGGCTGCGCTACACTACGACGTGGGACCGGACGATATCCGAG 29940
Db 24301 ATACACGCGTAGTGTAGGCTGCGCTACACTACGACGTGGGACCGGACGATATCCGAG 24360
QY 29941 GACCAAAAATAAATCTGTCTGATGCTGTGTAATCTCGAATTTGGCTTTCTATATCTC 30000
Db 24361 GACCAAAAATAAATCTGTCTGATGCTGTGTAATCTCGAATTTGGCTTTCTATATCTC 24420
QY 30001 GTGTGCCAGACCGGGGGCGAGTGGTGCAGAAAGATGGCGGACGCTTCTCGGCGCT 30060
Db 24421 GTGTGCCAGACCGGGGGCGAGTGGTGCAGAAAGATGGCGGACGCTTCTCGGCGCT 24480
QY 30061 TAAACGTAGGAGCTTTGAGCCTGAATCAAGGCTGCCAGGCTCCCTAAGCTGAGCTTTG 30120
Db 24481 TAAACGTAGGAGCTTTGAGCCTGAATCAAGGCTGCCAGGCTCCCTAAGCTGAGCTTTG 24540
QY 30121 GTTCAGAGTGTCAAAATTTGTTAATCTGGAACCGGTACGTTGACGAACGAGAGT 30180
Db 24541 GTTCAGAGTGTCAAAATTTGTTAATCTGGAACCGGTACGTTGACGAACGAGAGT 24600
QY 30181 GTGTTTTAGATGGGATATGGCTTTCCTCCACGCGGCTAGTATACGACCGGGAAACA 30240
Db 24601 GTGTTTTAGATGGGATATGGCTTTCCTCCACGCGGCTAGTATACGACCGGGAAACA 24660
QY 30241 AAACGAGTGGGGGCTGTGGCGGCGGCAAAATTTGGGAGATATATTTCTGTGAG 30300
Db 24661 AAACGAGTGGGGGCTGTGGCGGCGGCAAAATTTGGGAGATATATTTCTGTGAG 24720
QY 30301 GAAATCAAAAAGTTCCTTTTAAAGTATTTTGAACCGGAGGGTCTTCACTCT 30360
Db 24721 GAAATCAAAAAGTTCCTTTTAAAGTATTTTGAACCGGAGGGTCTTCACTCT 24780
|||||

OY	30361	GGAAATCTCCAC	CCAGAGGAGGCGCAGGTTGAGCGCCGGTGGGCGATCTGGTGT	30420
Db	24781	GGAAAACTCTCCAC	CCAGAGGAGGCGCAGGTTGAGCGCCGGTGGGCGATCTGGTGT	24840
OY	30421	GATTTGGGCGCAGGTC	CAATAGCAGTAAACCAAACTAAACAGCCATAGTGGCAGAGGCG	30480
Db	24841	GATTTGGGCGCAGGTC	CAATAGCAGTAAACCAAACTAAACAGCCATAGTGGCAGAGGCG	24900
OY	30481	GGCTCGGAGGTTCCAT	TGTGGTACGTTGAAAGGGAGGACAGTCTTTCCTTAACAAAGTGT	30540
Db	24901	GGCTCGGAGGTTCCAT	TGTGGTACGTTGAAAGGGAGGACAGTCTTTCCTTAACAAAGTGT	24960
OY	30541	CGCAGAGATATATAC	AGATCTCTGTCAGGTGGCTACCGGTTACCGGGGTTCTTGGAC	30600
Db	24961	CGCAGAGATATATAC	AGATCTCTGTCAGGTGGCTACCGGTTACCGGGGTTCTTGGAC	25020
OY	30601	GGGATGAGACGTCCG	CTGTGTCCAAAGTCGGGTATACATGAGTTGTAAAGAGTCGCG	30660
Db	25021	GGGATGAGACGTCCG	CTGTGTCCAAAGTCGGGTATACATGAGTTGTAAAGAGTCGCG	25080
OY	30661	GTTGTACTTTGTTTCT	TGTTTAGGGGCGCTAGAGAGCGCGTTGCTTGGATTGGAAT	30720
Db	25081	GTTGTACTTTGTTTCT	TGTTTAGGGGCGCTAGAGAGCGCGTTGCTTGGATTGGAAT	25140
OY	30721	TGTAAACTCGAAACCC	AGGCGCTCGTGTTTGTAAAGTGAGACAAAGGTCGCCAG	30780
Db	25141	TGTAAACTCGAAACCC	AGGCGCTCGTGTTTGTAAAGTGAGACAAAGGTCGCCAG	25200
OY	30781	CTTTGTGCGCAGGTT	ATCCAGAGCGCTTCGAGTTGGCGCAACGGGGTACTGTCCG	30840
Db	25201	CTTTGTGCGCAGGTT	ATCCAGAGCGCTTCGAGTTGGCGCAACGGGGTACTGTCCG	25260
OY	30841	GTCGACATATACCCG	TGTAGAGGACACAGCGGCGCTCGTCCGATACGTTGGGAC	30900
Db	25261	GTCGACATATACCCG	TGTAGAGGACACAGCGGCGCTCGTCCGATACGTTGGGAC	25320
OY	30901	ATCCGCGCTAAAGCT	CTGTGTGATCGAGGCGCTGTGTGAGATTACGGCAGACATTAGCTT	30960
Db	25321	ATCCGCGCTAAAGCT	CTGTGTGATCGAGGCGCTGTGTGAGATTACGGCAGACATTAGCTT	25380
OY	30961	TAGAGACGTGAGATT	TGTTGTTGTGTCTCCGAATCTCTGGGACACCTCTGCG	31020
Db	25381	TAGAGACGTGAGATT	TGTTGTTGTGTCTCCGAATCTCTGGGACACCTCTGCG	25440
OY	31021	TTCGATGCGCTTAT	CTGTGTAGGCGTACTGTACACAGCGCGGTATTTGGGAGCATTTGTT	31080
Db	25441	TTCGATGCGCTTAT	CTGTGTAGGCGTACTGTACACAGCGCGGTATTTGGGAGCATTTGTT	25500
OY	31081	TTCGTTATGTATAC	AGGCTTGGCAGAGCTCCAAACGAGATCCTGTGTTTACGTTAGTATC	31140
Db	25501	TTCGTTATGTATAC	AGGCTTGGCAGAGCTCCAAACGAGATCCTGTGTTTACGTTAGTATC	25560
OY	31141	CGGGTCTCCGGGGGCT	TATGTGACAAAGAAAGCGGTCCATATGTGTGGGGGCGATTTT	31200
Db	25561	CGGGTCTCTCGGGGCT	ATGTGACAAAGAAAGCGGTCTCCATATGTGTGGGGGCGATTTT	25620
OY	31201	GGGTTGGCGGTTT	AGTATGTTGGGATTTGGCGATTTGCCCTCCGGGGAGCGCAGATC	31260
Db	25621	GGGTTGGCGGTTT	AGTATGTTGGGATTTGGCGATTTGCCCTCCGGGGAGCGCAGATC	25680
OY	31261	CCCGACCATGTTT	GAAATTTGTTCTTAGGTGGCGCATGACACATCTTGTTCCCGTTGGTG	31320
Db	25681	CCCGACCATGTTT	GAAATTTGTTCTTAGGTGGCGCATGACACATCTTGTTCCCGTTGGTG	25740
OY	31321	CGTTTGACAGACGTT	GTCTAGCTTCTAGCCGAGACAGTTTTCGACGCGTGGAAACCTT	31380
Db	25741	CGTTTGACAGACGTT	GTCTAGCTTCTAGCTAGTCTAGCCGAGACAGATTTTCGACGCGTGGAAACCTT	25800
OY	31381	TAGCGCCAGCTGTT	GATTTGCGATCACAAAGCGGTTTCTTCTTTATCAGAGATGG	31440
Db	25801	TAGCGCCAGCTGTT	GATTTGCGATCACAAAGCGGTTTCTTCTTTATCAGAGATGG	25860

QY	31441	TTTGTGAATAAACAGACGTTGTTGGATGGGGGCCCAAAAGTTGGCGTATTTGGCG	31500
Db	25861	TTTGTGAATAAACAGACGTTGTTGGATGGGGGCCCAAAAGTTGGCGTATTTGGCG	25920
QY	31501	CGCGGTTTTGCGGGGATCTCATACAGATTTTCTGACGGGCGATCTTCCCAATTGGC	31560
Db	25921	CGCGGTTTTGCGGGGATCTCATACAGATTTTCTGACGGGCGATCTTCCCAATTGGC	25980
QY	31561	TAAAAAACCCGTTAAGCGCGCGGAGGTGGTGTGTAATATGAGCGGAACGCTGATG	31620
Db	25981	TAAAAAACCCGTTAAGCGCGCGGAGGTGGTGTGTAATATGAGCGGAACGCTGATG	26040
QY	31621	ACTCAGTATGAATTTGTTTAAGTGTCTTCTGTTCTTAATATAGACCGACGGGCTTACCG	31680
Db	26041	ACTCAGTATGAATTTGTTTAAGTGTCTTCTGTTCTTAATATAGACCGACGGGCTTACCG	26100
QY	31681	ACCGATTGTCGTCCTTGGGGGCGCTGGCTATATATGCGACGGAATCTGTCAGTT	31740
Db	26101	ACCGATTGTCGTCCTTGGGGGCGCTGGCTATATATGCGACGGAATCTGTCAGTT	26160
QY	31741	GGTTAAGCCCTGCATCGCTGATATTTTATTCGTTGGCGGAAATACAGCGCGCG	31800
Db	26161	GGTTAAGCCCTGCATCGCTGATATTTTATTCGTTGGCGGAAATACAGCGCGCG	26220
QY	31801	TTAGGCACGTCCTGAGTTCAATTACGTAGCAGTCTTTTGTATGTTGCTATTACGGTAA	31860
Db	26221	TTAGGCACGTCCTGAGTTCAATTACGTAGCAGCCTTTTGTATGTTGCTATTACGGTAA	26280
QY	31861	GCACACATCTGCTATTGCGCTACCTAAGGAAACCTCGAAGAAATCCTAAATTTAACCT	31920
Db	26281	GCACACATCTGCTATTGCGCTACCTAAGGAAACCTCGAAGAAATCCTAAATTTAACCT	26340
QY	31921	TTTTGGTTGGCCTAGTGTGGCGAATTAAGAAACCTTAATATATCATAAGGAGAC	31980
Db	26341	TTTTGGTTGGCCTAGTGTGGCGAATTAAGAAACCTTAATATATCATAAGGAGAC	26400
QY	31981	GGTGTATTGAATTAACCGTGGTATACGTAAAGTGGGCGGAGTTCAGGCCGTTTGGCGTG	32040
Db	26401	GGTGTATTGAATTAACCGTGGTATACGTAAAGTGGGCGGAGTTCAGGCCGTTTGGCGTG	26460
QY	32041	AGGCCGGAAGGCTTCAGAGGTGGCGACGTCCTTACATTGATTTGGAAACGCGATGGCGG	32100
Db	26461	AGGCCGGAAGGCTTCAGAGGTGGCGACGTCCTTACATTGATTTGGAAACGCGATGGCGG	26520
QY	32101	AAGAGGGGTGGGTTTGGGAGAGAGTTTCCGTACAGATGGCGGATCGGAAGCCTAAGT	32160
Db	26521	AAGAGGGGTGGGTTTGGGAGAGAGTTTCCGTACAGATGGCGGATCGGAAGCCTAAGT	26580
QY	32161	GGGACGAGTCTCCGACGATACTGATAGCTTGACACCGAAGACCGATCTTGAGTATG	32220
Db	26581	GGGACGAGTCTCCGACGATACTGATAGCTTGACACCGAAGACCGATCTTGAGTATG	26640
QY	32221	ATGATGTGTTCCCGTGGTAGATACGACGCGCTTAATGAGCCTCGGAAGTCAAAACTATG	32280
Db	26641	ATGATGTGTTCCCGTGGTAGATACGACGCGCTTAATGAGCCTCGGAAGTCAAAACTATG	26700
QY	32281	ACGATACCCAGTCTCCGTCGCGGAACGCGCGGAATTACTGACCCGGAAGCCCTGTATG	32340
Db	26701	ACGATACCCAGTCTCCGTCGCGGAACGCGCGGAATTACTGACCCGGAAGCCCTGTATG	26760
QY	32341	CACATCCGAGTGGCCGCTAAAGAGGGCGGTGGTGGCGGGCGGTGGCGGCTGCCAAGG	32400
Db	26761	CACATCCGAGTGGCCGCTAAAGAGGGCGGTGGTGGCGGGCGGTGGCGGCTGCCAAGG	26820
QY	32401	TGTCCGCGTCTCGGCTAGACCTTCATATGTGAGACACAGAGTTTGGGATAGAGAGA	32460
Db	26821	TGTCCGCGTCTCGGCTAGACCTTCATATGTGAGACACAGAGTTTGGGATAGAGAGA	26880
QY	32461	CGGGGACGCTTACCGGGGCTCAGTTTCTTCGAGAGCGGACGGAATTTGGGGAATATC	32520
Db	26881	CGGGGACGCTTACCGGGGCTCAGTTTCTTCGAGAGCGGACGGAATTTGGGGAATATC	26940
QY	32521	CGGAGCGTACTACTACAGCGCGGTTGAAAGCGGTACAGAGAAATTTTCACCTCGGCGC	32580

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Db 26941 CGGACGCTACTACTACAGCCCGGTTGAAAGCGGTGACAGAAATTTCCACTCCGGC 27000
Oy 32581 GTAGGGGTGCAATCTCGGGACCTCTGTCACAAAAGTACAGGTGGGGTTAACAC 32640
Db 27001 GTAGGGGTGCAATCTCGGGACCTCTGTCACAAAAGTACAGGTGGGGTTAACAC 27060
Oy 32641 GTAAAGCTAAAAAGCGGTGAGTGTAGCTTTAAAGCTGCTGGGGTAAAGGACGATG 32700
Db 27061 GTAAAGCTAAAAAGCGGTGAGTGTAGCTTTAAAGCTGCTGGGGTAAAGGACGATG 27120
Oy 32701 ATGTAGAGTGTATGATACCAAGCGGTACCGTCCGGTTCATCTCATGACGCGCATC 32760
Db 27121 ATGTAGAGTGTATGATACCAAGCGGTACCGTCCGGTTCATCTCATGACGCGCATC 27180
Oy 32761 CTATACGGAATATGAAATGCTTTTATCTATCTAGAGGGGTCAATGGTGTGAA 32820
Db 27181 CTATACGGAATATGAAATGCTTTTATCTATCTAGAGGGGTCAATGGTGTGAA 27240
Oy 32821 AAACAGCGCTATTTGAATTCATGACTGGCATGTCGCGAGGAAAAGCTTAAGCTGTC 32880
Db 27241 AAACAGCGCTATTTGAATTCATGACTGGCATGTCGCGAGGAAAAGCTTAAGCTGTC 27300
Oy 32881 CCGAGCCCATGAATTTTGGAGCTGTATTATTCAAATTTGCTTAAGACAGCGCAGCA 32940
Db 27301 CCGAGCCCATGAATTTTGGAGCTGTATTATTCAAATTTGCTTAAGACAGCGCAGCA 27360
Oy 32941 TAGTTAAGCAAGGCAACCCAGGGAAATGATCATCTTCTGCTGATACCGGTGCTAGA 33000
Db 27361 TAGTTAAGCAAGGCAACCCAGGGAAATGATCATCTTCTGCTGATACCGGTGCTAGA 27420
Oy 33001 GCAAGTTTGGCTTACGCTTGTGTCGACAGCGCGCGGATGSGTGGCAACCTGAACGCT 33060
Db 27421 GCAAGTTTGGCTTACGCTTGTGTCGACAGCGCGCGGATGSGTGGCAACCTGAACGCT 27480
Oy 33061 GCGTGTGGGAAACGGTAGACAAAGCAGCGAATTTGATTTTGAACAGACACCTAC 33120
Db 27481 GCGTGTGGGAAACGGTAGACAAAGCAGCGAATTTGATTTTGAACAGACACCTAC 27540
Oy 33121 TGTCGGCAACGGTGTGTTTTCCGTGCTTACGTTAAATGATCAACAGGCTTAAGCGCGATC 33180
Db 27541 TGTCGGCAACGGTGTGTTTTCCGTGCTTACGTTAAATGATCAACAGGCTTAAGCGCGATC 27600
Oy 33181 ATCTGTTTCAATCTATCTCTTTTCTCGGACAGACGCGCATGCTGTTTGTCTAA 33240
Db 27601 ATCTGTTTCAATCTATCTCTTTTCTCGGACAGACGCGCATGCTGTTTGTCTAA 27660
Oy 33241 CGCTCACAGTTCGGAGCGCACAGCGCATTTCAAAGTTCGAGGCGGTAAAGAAAG 33300
Db 27661 CGCTCACAGTTCGGAGCGCACAGCGCATTTCAAAGTTCGAGGCGGTAAAGAAAG 27720
Oy 33301 GAATCAGCAAAACACTTCTGGACAGGTAGCGTGGGCTTACCATGCCGTGTTCTAGCT 33360
Db 27721 GAATCAGCAAAACACTTCTGGACAGGTAGCGTGGGCTTACCATGCCGTGTTCTAGCT 27780
Oy 33361 GGGGTGATGATCAATATCTCACACCGAGCAAAATGCTCAGCTGTGTACAAACTGCT 33420
Db 27781 GGGGTGATGATCAATATCTCACACCGAGCAAAATGCTCAGCTGTGTGTACAAACTGCT 27840
Oy 33421 CCATAGAGCATATGCAATATGCAATTTCCAGATTGACATCGGTTCTAACCCCTAACAA 33480
Db 27841 CCATAGAGCATATGCAATATGCAATTTCCAGATTGACATCGGTTCTAACCCCTAACAA 27900
Oy 33481 AACTACATGAACAGATGATGATACCATGTGGCAGAAATGTTAGTATCGGTTAAAGAAC 33540
Db 27901 AACTACATGAACAGATGATGATACCATGTGGCAGAAATGTTAGTATCGGTTAAAGAAC 27960
Oy 33541 ACGTACCTTAATGGAGGTGTTGGGACTCTTTAAAGAGCTACGAAGAAGCTTCAATTT 33600
Db 27961 ACGTACCTTAATGGAGGTGTTGGGACTCTTTAAAGAGCTACGAAGAAGCTTCAATTT 28020
Oy 33601 TAATTTGTCAGCAGAGACATCATAGATGATGCGTGTGGCTCTGGGAAATATTTATG 33660
Db 28021 TAATTTGTCAGCAGAGACATCATAGATGATGCGTGTGGCTCTGGGAAATATTTATG 28080
Oy 33661 GCGAGGTATGTCAAATGAGCTATTAAACGACGAGTGAAGTACCTGCGCATTTGAAA 33720
Db 28081 GCGAGGTATGTCAAATGAGCTATTAAACGACGAGTGAAGTGAAGTGAAGTGAAGTGA 28140
Oy 33721 GCTACATTCAAACGCTTAACCAATTTGGAAGGCAATGGCGCGATATGTTTATTTT 33780
Db 28141 GCTACATTCAAACGCTTAACCAATTTGGAAGGCAATGGCGCGATATGTTTATTTT 28200
Oy 33781 TTTACTATTAATGAGTGTCTGTACGCAAGCAAAATGCTATGATGAAAATCAATGTA 33840
Db 28201 TTTACTATTAATGAGTGTCTGTACGCAAGCAAAATGCTATGATGAAAATCAATGTA 28260
Oy 33841 GAGTTGCAATTTAATGGAACAATTTACCAATTTATTTGAGAGAACGTAAGCAAAATTA 33900
Db 28261 GAGTTGCAATTTAATGGAACAATTTACCAATTTATTTGAGAGAACGTAAGCAAAATTA 28320
Oy 33901 ACATCTATTGTAAATGGAAGATCGGTGACGATTTCTTACTGCTGGAACATGCTGCTG 33960
Db 28321 ACATCTATTGTAAATGGAAGATCGGTGACGATTTCTTACTGCTGGAACATGCTGCTG 28380
Oy 33961 ACTTTGAAAAAGAAAAAGTTTCTGCGATCAAGTATAGTTATGTCATATATATGAC 34020
Db 28381 ACTTTGAAAAAGAAAAAGTTTCTGCGATCAAGTATAGTTATGTCATATATATGAC 28440
Oy 34021 TATACATTTTGTAAATCTTCAAGTACCATGTAATTAACCTTACGCTGATTTTATATAC 34080
Db 28441 TATACATTTTGTAAATCTTCAAGTACCATGTAATTAACCTTACGCTGATTTTATATAC 28500
Oy 34081 AGTCTTTTCCAGGTTTTTACTGGAATTTATGTAAGACACATGCTTTAACACAGGC 34140
Db 28501 AGTCTTTTCCAGGTTTTTACTGGAATTTATGTAAGACACATGCTTTAACACAGGC 28560
Oy 34141 GTTTTATTAACGAACGTAATTTATTAACCACTAACCAACATTTATGATCTTTTAC 34200
Db 28561 GTTTTATTAACGAACGTAATTTATTAACCACTAACCAACATTTATGATCTTTTAC 28620
Oy 34201 GCGGAAAAATTAATGCAAGAAATGTTCAAGATTTACTTTGATTTCCAAATGTAATTT 34260
Db 28621 GCGGAAAAATTAATGCAAGAAATGTTCAAGATTTACTTTGATTTCCAAATGTAATTT 28680
Oy 34261 TCCGCAATTAATTAACGAATAATTTGATTTAGTATGATAGTTAACAAATTAAGTAAATCA 34320
Db 28681 TCCGCAATTAATTAACGAATAATTTGATTTAGTATGATAGTTAACAAATTAAGTAAATCA 28740
Oy 34321 AATATGCAATGTGTGCACTGTTGTTGTTGTTCTTACCAATTTCCAGCGTTAAAGGC 34380
Db 28741 AATATGCAATGTGTGCACTGTTGTTGTTGTTCTTACCAATTTCCAGCGTTAAAGGC 28800
Oy 34381 TATGATCTTTATCGATTTATTTGCTGTTAAATTTCAACTATGCTGCGGTATTT 34440
Db 28801 TATGATCTTTATCGATTTATTTGCTGTTAAATTTCAACTATGCTGCGGTATTT 28860
Oy 34441 GCGCGGAATCTTATATATCTCTGATTTTGGCATTTTACCAAAAAATTTTACAGAAATG 34500
Db 28861 GCGCGGAATCTTATATATCTCTGATTTTGGCATTTTACCAAAAAATTTTACAGAAATG 28920
Oy 34501 TTTGTTTCAATTAATGATAGTCCGTTAATGCAATGTTATCTCAAAAGAAACTTTTG 34560
Db 28921 TTTGTTTCAATTAATGATAGTCCGTTAATGCAATGTTATCTCAAAAGAAACTTTTG 28980
Oy 34561 GCTATTAAGCAAGAGGCTGCTGCAAAATCCTTCAATGGAAGATGATCTTATCTTTC 34620
Db 28981 GCTATTAAGCAAGAGGCTGCTGCAAAATCCTTCAATGGAAGATGATCTTATCTTTC 29040
Oy 34621 TTTTGTGAAGTTTACGCAATTAATTTTATTTATTAATAATCTTCAAAAGCAAGTAA 34680
Db 29041 TTTTGTGAAGTTTACGCAATTAATTTTATTTATTAATAATCTTCAAAAGCAAGTAA 29100
Oy 34681 GTTAAAGTTGGGTGTGTGTACAGGATGTCAGCGTTAAGAAAGTTTATGCAATTTATTA 34740
Db 29101 GTTAAAGTTGGGTGTGTGTGTACAGGATGTCAGCGTTAAGAAAGTTTATGCAATTTATTA 29160
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DE RRV macrophage inflammatory protein (MIP) DNA sequence SEQ ID NO:22.
 XX
 XX Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
 KW genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;
 KW IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
 KW cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
 KW lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
 KW splenomegaly; hypergammaglobulinemia; autoimmune haemolytic anaemia;
 KW ds.
 XX
 OS Macaca mulatta rhadinovirus 17577.
 XX
 PN WO200028040-A2.
 XX
 PD 18-MAY-2000.
 XX
 PF 05-NOV-1999; 99WO-US26260.
 XX
 PR 06-NOV-1998; 98US-0107507.
 XX
 PR 20-NOV-1998; 98US-0109409.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PI Wong SW, Axthelm MK, Searles RP;
 XX
 XX MPI: 2000-376552/32.
 DR P-PSDB: AAB53213.
 XX
 XX New rhesus rhadino virus for producing non-human primate model useful
 PT for testing potential treatments and efficacy of the candidate vaccine
 PT for conditions associated with RRV infection -
 XX
 PS Claim 9; Fig 11; 141pp; English.
 XX
 CC The present invention describes a novel rhesus macaque rhadinovirus
 CC called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
 CC RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
 CC encoded by the genome sequence. The present invention also specifically
 CC claims the individual open reading frame (ORF) nucleotide sequences from
 CC the genome which encode the individual proteins, but these sequences are
 CC not given. A non-human animal infected with RRV can be used for testing
 CC the efficacy of drug in the treatment of condition associated with
 CC infection with RRV such as Kaposi's sarcoma, lymphoproliferative
 CC disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
 CC hypergammaglobulinemia or autoimmune haemolytic anaemia, by
 CC administering the drug to an immuno-compromised non-human primate
 CC preferably Rhesus macaque monkey obtained by as a result of infection
 CC by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
 CC non-human primate model for testing potential treatments for conditions
 CC associated with RRV infection. It is also useful for testing the
 CC efficacy of the candidate vaccine against RRV infection or conditions
 CC associated with its infection by administering the vaccine to the
 CC subject capable of infection with RRV. Inoculating the subject with RRV
 CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
 CC to AAB53213 represent sequence used in the exemplification of the
 CC present invention.
 CC
 XX Sequence 348 BP; 67 A; 91 C; 105 G; 85 T; 0 other;
 SQ

Query Match 1.0%; Score 348; DB 21; Length 348;
 Best Local Similarity 100.0%; Pred. No. 5,8e-134;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22245 CTAATTCGCGCTGCCAAGGCCCTCTTGGAAATCGTAATCAGGCTGCCGCGGTTCTTCT 22304
 DB 348 CTAATTCGCGCTGCCAAGGCCCTCTTGGAAATCGTAATCAGGCTGCCGCGGTTCTTCT 289
 QY 22305 GCCCTTTTGGAGCGCTGTGCACCGCCTGAAGAGCTTTCTTCACTGCGTCTCCCGGG 22364
 DB 288 GCCCTTTTGGAGCGCTGTGCACCGCCTGAAGAGCTTTCTTCACTGCGTCTCCCGGG 229
 QY 22365 ATTGGCACACAGCTTTTACCGCGCGAGTGTATTATATACAGGGGTCCACGACACATG 22424
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 228 ATTGGCACACAGCTTTTACCGCGCGAGTGTATTATATACAGGGGTCCACGACACATG 169
 QY 22425 CGACGAGTGTGGAGTAAGACACCTAACC GGGTGGCGGACAGATGATTACATACC 22484
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 168 CGACGAGTGTGGAGTAAGACACCTAACC GGGTGGCGGACAGATGATTACATACC 109
 QY 22485 CAACACGACGAGTTGGGCGGGTCCGTCTATGAGCCCATAGGAAAGGCTAATCAAC 22544
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 108 CAACACGACGAGTTGGGCGGGTCCGTCTATGAGCCCATAGGAAAGGCTAATCAAC 49
 QY 22545 TACACACGCGAACCACCGCAAAAAAAGCGACAGAAAGGCCCTCAT 22592
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 48 TACACACGCGAACCACCGCAAAAAAAGCGACAGAAAGGCCCTCAT 1

RESULT 5
 AAI64294
 ID AAI64294 standard; DNA; 630 BP.
 XX
 AC AAI64294;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE JMHV nucleotide sequence from cosmid 3 fragment 5 T7.
 XX
 KW RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KW JMHV; cytostatic; antiallergic; antiallergic; dermatological;
 KW vulnary; gene therapy; leucopenia; thrombocytopenia;
 KW inflammatory disease; asthma; allergy; dermatitis; ds.
 OS
 XX Japanese macaque herpesvirus.
 XX
 PN WO200186203-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US16274.
 XX
 PR 18-MAY-2000; 2000US-205652P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PI Wong SW, Axthelm MK;
 XX
 XX MPI: 2002-075323/10.
 DR
 XX
 XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis -
 XX
 PS Claim 9; Page 67; 175pp; English.
 XX
 CC The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug used for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the
 CC efficacy of candidate vaccine against JMHV infection, or conditions
 CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
 CC invention are useful for diagnosing the presence of JMHV or a related
 CC virus in a biological specimen. JMHV genome possesses an interleukin
 CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 CC to induce stimulation of haematopoietic stem cells to enhance
 CC proliferation, differentiation and terminal maturation of erythroid
 CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 CC ex vivo to treat diseases involving leukaemia or thrombocytopenia.
 CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 CC and platelets, and for the inhibition of tumour growth and for treating

DE JMHV cosmid 3 EcoRI fragment 1 Kpn 1 fragment 2 Sp6.
 XX
 XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KM JMHV; cytostatic; antiasthmatic; anti-allergic; dermatological;
 KM vulnery; gene therapy; leucopenia; thrombocytopenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX
 OS Japanese macaque herpesvirus.
 XX
 FH Key Location/Qualifiers
 FT 2..496
 FT CDS /*tag= a
 FT /partial
 FT /product= "DNA polymerase"
 FT /transl_except= (pos:440..442, aa:Xaa)
 FT /note= "no start or stop codon present; Xaa is unknown"
 XX
 PN W0200188203-A1.
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US16274.
 XX
 PR 18-MAY-2000; 2000US-205652P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCT.
 XX
 PI Wong SW, Axthelm MK;
 XX
 DR WPI: 2002-075323/10.
 DR P-PSDB: AAG78586.
 XX
 PT New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis
 XX
 PS Claim 9; Page 70; 175pp; English.
 CC The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the
 CC efficacy of candidate vaccine against JMHV infection, or conditions
 CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
 CC invention are useful for diagnosing the presence of JMHV or a related
 CC virus in a biological specimen. JMHV genome possesses an interleukin
 CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 CC to induce stimulation of haematopoietic stem cells to enhance
 CC proliferation, differentiation and terminal maturation of erythroid
 CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
 CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 CC and platelets, and for the inhibition of tumour growth and for treating
 CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
 CC purposes, to produce antibodies for diagnostic purposes to diagnose
 CC diseases characterized by increased or decreased production of IL-6,
 CC and as a targeting molecule for identifying cells with receptors for
 CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
 CC useful for treating wounds and other inflammatory diseases including
 CC asthma, allergies and dermatitis. They are also useful for producing
 CC antibodies for diagnostic purposes, and as a targeting molecule for
 CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
 CC the JMHV proteins are useful in gene therapy techniques for treating
 CC the above mentioned conditions. The current sequence represents the
 CC JMHV Orf1 nucleotide sequence from cosmid 3 EcoRI fragment Kpn 1
 CC fragment 2 Sp6. Orf 10 encodes a DNA polymerase.
 CC Note: In example 22 of the specification there is a protein sequence

CC (see AAG78599) that has been allocated the same sequence identification
 CC number as this sequence. This sequence is also from Orf 10.
 XX
 SQ Sequence 497 BP; 98 A; 162 C; 146 G; 90 T; 1 other;
 Query Match 0.3%; Score 107; DB 24; Length 497;
 Best Local Similarity 100.0%; Pred. No. 7.8e-34;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14746 GAATCAGCGTATCGTCCGGTTCATGCTTCGACCCCTGACGACCGCTGCGCGTGC 14805
 DB 269 GAAATCAGCGTATCGTCCGGTTCATGCTTCGACCCCTGACGACCGCTGCGCGTGC 328
 QY 14806 GGGTCGAGGCTGTTGAGTCAAGCTGACGCGCTTCCCGGTTGCT 14852
 DB 329 GGGTCGAGGCTGTTGAGTCAAGCTGACGCGCGCTTCCCGGTTGCT 375
 RESULT 8
 AAI64298
 ID AAI64298 standard; DNA; 398 BP.
 XX
 AC AAI64298;
 XX
 DT 22-APR-2002 (first entry)
 XX
 XX JMHV Orf7 nucleotide sequence from cosmid 3 fragment 1 T7.
 DE
 XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KM JMHV; cytostatic; antiasthmatic; anti-allergic; dermatological;
 KM vulnery; gene therapy; leucopenia; thrombocytopenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX
 OS Japanese macaque herpesvirus.
 XX
 FH Key Location/Qualifiers
 FT 1..396
 FT CDS /*tag= a
 FT /product= "transport protein"
 FT /partial
 FT /note= "no start or stop codon present"
 XX
 PN W0200188203-A1.
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US16274.
 XX
 PR 18-MAY-2000; 2000US-205652P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCT.
 XX
 PI Wong SW, Axthelm MK;
 XX
 DR WPI: 2002-075323/10.
 DR P-PSDB: AAG78586.
 XX
 PT New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis
 XX
 PS Claim 9; Page 69; 175pp; English.
 CC The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the

CC efficacy of candidate vaccine against JMHV infection, or conditions
CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
CC invention are useful for diagnosing the presence of JMHV or a related
CC virus in a biological specimen. JMHV genome possesses an interleukin
CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
CC to induce stimulation of haematopoietic stem cells to enhance
CC proliferation, differentiation and terminal maturation of erythroid
CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
CC and platelets, and for the inhibition of tumour growth and for treating
CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHV Orf7 nucleotide sequence from cosmid 3 fragment 1 T7. Orf 7
CC encodes a transport protein.
XX
SQ Sequence 398 BP; 111 A; 107 C; 108 G; 72 T; 0 other;
Query Match 0.2%; Score 74; DB 24; Length 398;
Best Local Similarity 100.0%; Pred. No. 4,1e-20;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10731 TATCGCAAGAACAGTACATGAAAGGTGGCGGCGGCTTTAAAAAATAACAGAG 10790
Db 265 TATCGCAAGAACAGTACATGAAAGGTGGCGGCGGCTTTAAAAAATAACAGAG 324
OY 10791 TGTCTGCAGACGCA 10804
Db 325 TGTCTGCAGACGCA 338
RESULT 9
AA164292/C
ID AA164292 standard; DNA; 426 BP.
XX
AC AA164292;
XX
DT 22-APR-2002 (first entry)
XX
DE JMHV Orf21 nucleotide sequence from cosmid 3 fragment 7 T7.
XX
XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
KM JMHV; cytostatic; antiallergic; antiallergic; dermatological;
KM inflammatory; gene therapy; leucopenia; thrombocytopenia;
KM inflammatory disease; asthma; allergy; dermatitis; ds.
OS Japanese macaque herpesvirus.
XX
XX WO200182203-A1.
XX
XX 22-NOV-2001.
XX
XX 17-MAY-2001; 2001WO-US16274.
XX
XX 18-MAY-2000; 2000US-205652P.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Mong SM, Axthelm MK;
XX
XX WPI; 2002-075323/10.
XX
XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
PT reading frames in virus, useful for producing animal models for

PT assessing efficacy of drugs for treatment or prevention of multiple
PT sclerosis
XX
XX Claim 9; Page 66; 175pp; English.
XX
XX The invention relates to an isolated virus (Japanese macaque virus (JMHV)
CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
CC primate models infected with the new virus are useful for testing the
CC efficacy of a drug for treating a condition associated with JMHV,
CC preferably a drug used to treat multiple sclerosis. This involves
CC administering the drug to a non-human primate infected with JMHV and
CC observing the non-human primate to determine if the drug prevents or
CC reduces the presentation of one or more symptoms associated with JMHV
CC infection. Methods of the invention are also useful for testing the
CC efficacy of candidate vaccine against JMHV infection, or conditions
CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
CC invention are useful for diagnosing the presence of JMHV or a related
CC virus in a biological specimen. JMHV genome possesses an interleukin
CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
CC to induce stimulation of haematopoietic stem cells to enhance
CC proliferation, differentiation and terminal maturation of erythroid
CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
CC and platelets, and for the inhibition of tumour growth and for treating
CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHV Orf21 nucleotide sequence from cosmid 3 fragment 7 T7. Orf 21
CC encodes a thymidine kinase.
CC Note: In the specification the deduced amino acid sequence of this
CC fragment is also given (see AMG78581). However, the sequence here does
CC not decode to the amino acid sequence in that record.
XX
SQ Sequence 426 BP; 101 A; 111 C; 104 G; 110 T; 0 other;
Query Match 0.2%; Score 71; DB 24; Length 426;
Best Local Similarity 99.2%; Pred. No. 7.2e-19;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 33222 GATGTGTCGTTTGTCTAACGCTCAACAGTTCGGAGCGGCGGATTCAAAGTGA 33281
Db 227 GATGTGTCGTTTGTCTAACGCTCAACAGTTCGGAGCGGCGGATTCAAAGTGA 168
OY 33282 GCCCGTAAGGAAGAAAGAAATCAGCGAAACATCTTGGCAGAGTGGCGGCTAC 33341
Db 167 GCCCGCAAGGAAGAAAGAAATCAGCGAAACATCTTGGCAGAGTGGCGGCTAC 108
OY 33342 CA 33343
Db 107 CA 106
RESULT 10
AA164293
ID AA164293 standard; DNA; 524 BP.
XX
AC AA164293;
XX
DT 22-APR-2002 (first entry)
XX
XX JMHV Orf21 nucleotide sequence from cosmid 3 fragment 7 SP6.
XX
XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
KM JMHV; cytostatic; antiallergic; antiallergic; dermatological;

KM vulnery; gene therapy; leucopenia; thrombocytopaenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX Japanese macaque herpesvirus.
 FH Key Location/Qualifiers
 FT CDS 2..523
 FT /tag= a
 FT /product= "thymidine kinase"
 FT /partial
 FT /note= "no start or stop codon present"
 PN MO200188203-A1.
 XX 22-NOV-2001.
 PD 17-MAY-2001; 2001WO-US16274.
 PF 18-MAY-2000; 2000US-205652P.
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA Wong SW, Axthelm MK;
 PI MPI: 2002-075323/10.
 DR P-PSDB; AAG78582.
 XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis
 XX
 PS Claim 9; Page 66-67; 175pp; English.
 XX
 CC The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug used for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the
 CC efficacy of candidate vaccine against JMHV infection, or conditions
 CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
 CC invention are useful for diagnosing the presence of JMHV or a related
 CC virus in a biological specimen. JMHV genome possesses an interleukin
 CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 CC to induce stimulation of haematopoietic stem cells to enhance
 CC proliferation, differentiation and terminal maturation of erythroid
 CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 CC ex vivo to treat diseases involving leukopenia or thrombocytopaenia.
 CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 CC and platelets, and for the inhibition of tumour growth and for treating
 CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
 CC purposes, to produce antibodies for diagnostic purposes to diagnose
 CC diseases characterized by increased or decreased production of IL-6,
 CC and as a targeting molecule for identifying cells with receptors for
 CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
 CC useful for treating wounds and other inflammatory diseases including
 CC asthma, allergies and dermatitis. They are also useful for producing
 CC antibodies for diagnostic purposes, and as a targeting molecule for
 CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
 CC the JMHV proteins are useful in gene therapy techniques for treating
 CC the above mentioned conditions. The current sequence represents the
 CC JMHV Orf21 nucleotide sequence from cosmid 3 fragment 7 Sp6. Orf 21
 CC encodes a thymidine kinase.
 XX
 SQ Sequence 524 BP; 131 A; 132 C; 136 G; 125 T; 0 other;
 Query Match 0.2%; Score 71; DB 24; Length 524;
 Best Local Similarity 99.2%; Pred. No. 7.le-19;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33222 GATGTGCTGCTTTTGCTAAAGCTCAACAGTTCGAGCGCACAGCGCATTTCAAGTCGA 33281
 |||||||
 Db 389 GATGTGCTGCTTTTGCTAAAGCTCAACAGTTCGAGCGCACAGCGCATTTCAAGTCGA 448
 QY 33282 GGCCGTAAGAGAAAGAAAGATTCACGCAAACTCTTCCGACAGTACCCTGGCGCTAC 33341
 |||||
 Db 449 GGCCGCAAGAGAAAGAAAGATTCACGCAAACTCTTCCGACAGTACCCTGGCGCTAC 508
 QY 33342 CA 33343
 ||
 Db 509 CA 510
 RESULT 11
 ABA97191/C
 ID ABA97191 standard; DNA; 314 BP.
 XX
 AC ABA97191;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE JMHV cosmid 3 EcoRI fragment 1 kpn 1 fragment 2 T7.
 XX
 KW RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KW JMHV; cytosstatic; antiaesthetic; antiallergic; dermatological;
 KW vulnery; gene therapy; leucopenia; thrombocytopaenia;
 KW inflammatory disease; asthma; allergy; dermatitis; ds.
 XX
 OS Japanese macaque herpesvirus.
 XX
 PN WO200188203-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US16274.
 XX
 PR 18-MAY-2000; 2000US-205652P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PI Wong SW, Axthelm MK;
 XX MPI: 2002-075323/10.
 DR
 XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis
 XX
 PS Claim 9; Page 71; 175pp; English.
 XX
 CC The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug used for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the
 CC efficacy of candidate vaccine against JMHV infection, or conditions
 CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
 CC invention are useful for diagnosing the presence of JMHV or a related
 CC virus in a biological specimen. JMHV genome possesses an interleukin
 CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 CC to induce stimulation of haematopoietic stem cells to enhance
 CC proliferation, differentiation and terminal maturation of erythroid
 CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 CC ex vivo to treat diseases involving leukopenia or thrombocytopaenia.
 CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 CC and platelets, and for the inhibition of tumour growth and for treating
 CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic

FT /note- "no start or stop codon present"
 XX
 PN WO200188203-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US16274.
 XX
 PR 18-MAY-2000; 2000US-205652P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Mong SW, Axtheim MK;
 XX
 DR WPI; 2002-075323/10.
 DR P-PSDB; AAG785590.
 XX
 PT New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis -
 XX
 PS Claim 9; Page 71; 175pp; English.
 XX
 CC The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the
 CC efficacy of candidate vaccine against JMHV infection, or conditions
 CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
 CC invention are useful for diagnosing the presence of JMHV or a related
 CC virus in a biological specimen. JMHV genome possesses an interleukin
 CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 CC to induce stimulation of haematopoietic stem cells to enhance
 CC proliferation, differentiation and terminal maturation of erythroid
 CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
 CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 CC and platelets, and for the inhibition of tumour growth and for treating
 CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
 CC purposes, to produce antibodies for diagnostic purposes to diagnose
 CC diseases characterized by increased or decreased production of IL-6,
 CC and as a targeting molecule for identifying cells with receptors for
 CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
 CC useful for treating wounds and other inflammatory diseases including
 CC asthma, allergies and dermatitis. They are also useful for producing
 CC antibodies for diagnostic purposes, and as a targeting molecule for
 CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
 CC the JMHV proteins are useful in gene therapy techniques for treating
 CC the above mentioned conditions. The current sequence represents the
 CC JMHV Orf8 nucleotide sequence from cosmid 3 EcoRI fragment Kpn 1
 CC fragment 3 SP6. Orf 8 encodes glycoprotein B.
 XX
 CC Sequence 681 BP; 163 A; 203 C; 186 G; 129 T; 0 other;
 XX
 SQ
 Query Match 0.2%; Score 58; DB 24; Length 681;
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12152 GAACGACGGTCAACTGCGAGATGATGTCGGGCTTGGCGAAGCTACTC 12209
 DB 310 GAACGACGGTCAACTGCGAGATGATGTCGGGCTTGGCGAAGCTACTC 367
 RESULT 14
 AA164300
 ID AA164300 standard; DNA; 438 BP.
 XX

AC AA164300;
 XX
 XX 22-APR-2002 (first entry)
 DT
 XX
 DE JMHV cosmid 3 EcoRI fragment 1 Kpn 1 fragment 1 T7.
 XX
 XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KW JMHV; cytostatic; antiallergic; dermatological;
 KW vulnery; gene therapy; leucopenia; thrombocytopenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX
 OS Japanese macaque herpesvirus.
 XX
 FH Key Location/Qualifiers
 FT 1..231
 FT CDS /*tag= a
 FT /partial
 FT /note- "no start codon present"
 FT
 XX WO200188203-A1.
 XX
 XX 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US16274.
 XX
 PR 18-MAY-2000; 2000US-205652P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Mong SW, Axtheim MK;
 XX
 DR WPI; 2002-075323/10.
 DR P-PSDB; AAG785590.
 XX
 PT New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis -
 XX
 XX Claim 9; Page 70; 175pp; English.
 PS
 CC The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the
 CC efficacy of candidate vaccine against JMHV infection, or conditions
 CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
 CC invention are useful for diagnosing the presence of JMHV or a related
 CC virus in a biological specimen. JMHV genome possesses an interleukin
 CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 CC to induce stimulation of haematopoietic stem cells to enhance
 CC proliferation, differentiation and terminal maturation of erythroid
 CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
 CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 CC and platelets, and for the inhibition of tumour growth and for treating
 CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
 CC purposes, to produce antibodies for diagnostic purposes to diagnose
 CC diseases characterized by increased or decreased production of IL-6,
 CC and as a targeting molecule for identifying cells with receptors for
 CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
 CC useful for treating wounds and other inflammatory diseases including
 CC asthma, allergies and dermatitis. They are also useful for producing
 CC antibodies for diagnostic purposes, and as a targeting molecule for
 CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
 CC the JMHV proteins are useful in gene therapy techniques for treating
 CC the above mentioned conditions. The current sequence represents the
 CC JMHV Orf10 nucleotide sequence from cosmid 3 EcoRI fragment Kpn 1

CC fragment 1 T7. Orf 10 encodes an unknown protein.
 XX Sequence 438 BP; 76 A; 146 C; 142 G; 74 T; 0 other;
 SO Query Match 0.1%; Score 50; DB 24; Length 438;
 Best Local Similarity 100.0%; Pred. No. 3.8e-10;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 18571 GTGGACAGCGGACGCGGATCCGCTGCTGGGGCGCCACTAT 18620
 DB 291 GTGGACAGCGGACGCGGATCCGCTGCTGGGGCGCCACTAT 340
 RESULT 15
 ID ABA97193 standard; DNA; 389 BP.
 AC ABA97193;
 DT 22-APR-2002 (first entry)
 XX JMHV cosmid 3 EcorI fragment 1 kpn 1 fragment 3 T7.
 DE JMHV cosmid 3 EcorI fragment 1 kpn 1 fragment 3 T7.
 XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KM JMHV; cytostatic; antileukemic; antiallergic; dermatological;
 KM vulnery; gene therapy; leucopenia; thrombocytopenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX Japanese macaque herpesvirus.
 OS WO20018203-A1.
 PN 22-NOV-2001.
 PD 17-MAY-2001; 2001WO-US16274.
 PF 18-MAY-2000; 2000US-205652P.
 PR (UYOR-) UNIV OREGON HEALTH SCI.
 PA Wong SM, Axthelm MK;
 PI WPI: 2002-075323/10.
 DR New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 XX reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis -
 XX Claim 9; Page 72; 175pp; English.
 PS The invention relates to an isolated virus (Japanese macaque virus (JMHV))
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the
 CC efficacy of candidate vaccine against JMHV infection, or conditions
 CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
 CC invention are useful for diagnosing the presence of JMHV or a related
 CC virus in a biological specimen. JMHV genome possesses an interleukin
 CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 CC to induce stimulation of hematopoietic stem cells to enhance
 CC proliferation, differentiation and terminal maturation of erythroid
 CC cells from hematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
 CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 CC and platelets, and for the inhibition of tumour growth and for treating
 CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
 CC purposes, to produce antibodies for diagnostic purposes to diagnose

CC diseases characterized by increased or decreased production of IL-6,
 CC and as a targeting molecule for identifying cells with receptors for
 CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
 CC useful for treating wounds and other inflammatory diseases including
 CC asthma, allergies and dermatitis. They are also useful for producing
 CC antibodies for diagnostic purposes, and as a targeting molecule for
 CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
 CC the JMHV proteins are useful in gene therapy techniques for treating
 CC the above mentioned conditions. The current sequence represents the
 CC JMHV Orf9 nucleotide sequence from cosmid 3 fragment 1 kpn 1 fragment 3
 CC T7. Orf 9 encodes a DNA polymerase.
 CC Note: In the specification the deduced amino acid sequence of this
 CC fragment is also given (see AAG78591). However, the sequence here does
 CC not decode to the amino acid sequence in that record. There is also an
 CC amino acid sequence (see AAG78596) given in example 22 of the
 CC specification that has the same sequence identification number as the
 CC current sequence, but is said to be from Orf 8.
 XX Sequence 389 BP; 61 A; 114 C; 147 G; 67 T; 0 other;
 SO Query Match 0.1%; Score 41; DB 24; Length 389;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 14269 GGGGACGCGGATGATCCGCGTCACGATCCCGTTCCCGCC 14309
 DB 215 GGGGACGCGGATGATCCGCGTCACGATCCCGTTCCCGCC 175
 RESULT 16
 ID AAI64296 standard; DNA; 630 BP.
 AC AAI64296;
 DT 22-APR-2002 (first entry)
 XX JMHV Orf21 nucleotide sequence from cosmid 3 fragment 3 T7.
 DE RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KM JMHV; cytostatic; antileukemic; antiallergic; dermatological;
 KM vulnery; gene therapy; leucopenia; thrombocytopenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX Japanese macaque herpesvirus.
 OS Key Location/Qualifiers
 FH CDS 153..527
 FT /*tag= a
 FT /product= "thymidine kinase"
 FT /partial
 FT /note= "no start codon present"
 XX WO20018203-A1.
 PN 22-NOV-2001.
 PD 17-MAY-2001; 2001WO-US16274.
 PF 18-MAY-2000; 2000US-205652P.
 PR (UYOR-) UNIV OREGON HEALTH SCI.
 PA Wong SM, Axthelm MK;
 PI WPI: 2002-075323/10.
 DR P-PSDB; AAG78584.
 DR New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 XX reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis -
 XX

PA (UYOR-) UNIV OREGON HEALTH SCI.

kw inflammatory disease: asthma: allergy: dermatitis: virus: ds.
kw vulnerary; gene therapy; leucopenia; chromocytopenia;

KW inflammatory disease; asthma; allergy; dermatitis; virus; ds.

```

OS Macaca mulatta rhadinovirus 17577.
XX Key Location/Qualifiers
FT CDS 1353..2674
FT /*tag- a
FT /product- "RV R1"
FT /note- "complement (2692..3258)"
FT CDS /*tag- b
FT /product- "dihydrofolate reductase"
FT /label- RV_ORF2
FT /note- "has similarity to Kaposi's sarcoma-associated
FT virus (KSHV) open reading frame (ORF) 2"
FT CDS 3676..5613
FT /*tag- c
FT /product- "complement binding protein"
FT /label- RV_ORF4
FT /note- "has similarity to KSHV ORF4"
FT CDS 6045..9443
FT /*tag- d
FT /product- "sADNA binding protein"
FT /label- RV_ORF6
FT /note- "has similarity to KSHV ORF6"
FT CDS 9468..11528
FT /*tag- e
FT /product- "transport protein"
FT /label- RV_ORF7
FT /note- "has similarity to KSHV ORF7"
FT CDS 11515..14004
FT /*tag- f
FT /product- "glycoprotein B"
FT /label- RV_ORF8
FT /note- "has similarity to KSHV ORF8"
FT CDS 14122..17166
FT /*tag- g
FT /product- "DNA polymerase protein"
FT /label- RV_ORF9
FT /note- "has similarity to KSHV ORF9"
FT CDS 17261..18511
FT /*tag- h
FT /label- RV_ORF10
FT /note- "has similarity to KSHV ORF10"
FT CDS 18520..19749
FT /*tag- i
FT /label- RV_ORF11
FT /note- "has similarity to KSHV ORF11"
FT CDS complement (19921..20544)
FT /*tag- j
FT /product- "RV R2"
FT /label- RV_ORF
FT /note- "has similarity to KSHV Interleukin (IL)-6 gene"
FT CDS complement (20777..21778)
FT /*tag- k
FT /product- "thymidylate synthase"
FT /label- RV_ORF70
FT /note- "has similarity to KSHV ORF70"
FT CDS complement (22245..22592)
FT /*tag- l
FT /product- "RV R3"
FT /note- "has similarity to KSHV K4 viral MIP gene"
FT CDS 26846..27409
FT /*tag- m
FT /product- "Bcl2-homologue"
FT /label- RV_ORF16
FT /note- "has similarity to KSHV ORF16"
FT CDS complement (27515..29125)
FT /*tag- n
FT /label- RV_ORF17
FT /note- "has similarity to KSHV ORF17"
FT CDS 28998..29897
FT /*tag- o
FT /label- RV_ORF18
FT /note- "has similarity to KSHV ORF18"
FT CDS complement (29905..31548)
FT /*tag- p
FT /product- "tegument protein"
FT /label- RV_ORF19
FT /note- "has similarity to KSHV ORF19"
FT CDS complement (31043..32095)
FT /*tag- q
FT /label- RV_ORF20
FT /note- "has similarity to KSHV ORF20"
FT CDS 32094..33767
FT /*tag- r
FT /product- "thymidine kinase"
FT /label- RV_ORF21
FT /note- "has similarity to KSHV ORF21"
FT CDS 33754..35868
FT /*tag- s
FT /product- "glycoprotein H"
FT /label- RV_ORF22
FT /note- "has similarity to KSHV ORF22"
FT CDS complement (35865..37073)
FT /*tag- t
FT /label- RV_ORF23
FT /note- "has similarity to KSHV ORF23"
FT CDS complement (37123..39321)
FT /*tag- u
FT /label- RV_ORF24
FT /note- "has similarity to KSHV ORF24"
FT CDS 39323..43459
FT /*tag- v
FT /product- "major capsid protein"
FT /label- RV_ORF25
FT /note- "has similarity to KSHV ORF25"
FT CDS 43491..44408
FT /*tag- w
FT /product- "capsid protein"
FT /label- RV_ORF26
FT /note- "has similarity to KSHV ORF26"
FT CDS 44433..45242
FT /*tag- x
FT /label- RV_ORF27
FT /note- "has similarity to KSHV ORF27"
FT CDS 45408..45683
FT /*tag- y
FT /label- RV_ORF28
FT /note- "has similarity to KSHV ORF28"
FT CDS complement (45733..46779)
FT /*tag- z
FT /label- RV_ORF29b
FT /note- "has similarity to KSHV ORF29b"
FT CDS 46905..47135
FT /*tag- aa
FT /label- RV_ORF30
FT /note- "has similarity to KSHV ORF30"
FT CDS 47093..47746
FT /*tag- ab
FT /label- RV_ORF31
FT /note- "has similarity to KSHV ORF31"
FT CDS 47683..49077
FT /*tag- ac
FT /label- RV_ORF32
FT /note- "has similarity to KSHV ORF32"
FT CDS 49049..50059
FT /*tag- ad
FT /label- RV_ORF33
FT /note- "has similarity to KSHV ORF33"
FT CDS complement (49977..50960)
FT /*tag- ae
FT /label- RV_ORF29a
FT /note- "has similarity to KSHV ORF29a"
FT CDS 50959..51942
FT /*tag- af
FT /label- RV_ORF34
FT /note- "has similarity to KSHV ORF34"
FT CDS 51923..52372

```

```
FT      /*tag= ag
FT      /label= RVV_ORF35
FT      /note= "has similarity to KSHV ORF35"
FT      CDS
FT      52278..53585
FT      /tag= ah
FT      /product= "kinase"
FT      /label= RVV_ORF36
FT      /note= "has similarity to KSHV ORF36"
FT      CDS
FT      53566..55008
FT      /tag= ai
FT      /product= "alkaline exonuclease"
FT      /label= RVV_ORF37
FT      /note= "has similarity to KSHV ORF37"
FT      CDS
FT      54963..55172
FT      /tag= aj
FT      /label= RVV_ORF38
FT      /note= "has similarity to KSHV ORF38"
FT      CDS
FT      complement (55255..55391)
FT      /tag= ak
FT      /product= "glycoprotein M"
FT      /label= RVV_ORF39
FT      /note= "has similarity to KSHV ORF39"
FT      CDS
FT      56526..57932
FT      /tag= al
FT      /product= "helicase/primase"
FT      /label= RVV_ORF40
FT      /note= "has similarity to KSHV ORF40"
FT      CDS
FT      57917..58528
FT      /tag= am
FT      /product= "helicase/primase"
FT      /label= RVV_ORF41
FT      /note= "has similarity to KSHV ORF41"
FT      CDS
FT      complement (58525..59343)
FT      /tag= an
FT      /label= RVV_ORF42
FT      /note= "has similarity to KSHV ORF42"
FT      CDS
FT      complement (59297..61027)
FT      /tag= ao
FT      /product= "capsid protein"
FT      /label= RVV_ORF43
FT      /note= "has similarity to KSHV ORF43"

Query Match      0.1%; Score 33; DB 24; Length 128139;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23879 GTTGGTTTGTTCACAGTCCCTATATAT 23911
      |||
      111995 GTTGGTTTGTTCACAGTCCCTATATAT 11963

DB      111995 GTTGGTTTGTTCACAGTCCCTATATAT 11963

RESULT 19
AAC64754/C
ID      AAC64754 standard: DNA; 133719 BP.
XX
AC      AAC64754;
XX
DT      28-FEB-2001 (first entry)
XX
DE      Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1.
XX
KW      Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
KW      genome; Kaposi's sarcoma-associated herpesvirus; KSHV; Interleukin 6;
KW      IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
KW      cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
KW      lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
KW      splenomegaly; hypergammaglobulinaemia; autoimmune haemolytic anaemia;
KW      ds.
XX
XX      Macaca mulatta rhadinovirus 17577.
OS
XX
XX      WO200028040-A2.
PN
XX
```

```
PD      18-MAY-2000.
XX
XX      05-NOV-1999; 99WO-US26260.
XX
XX      06-NOV-1998; 98US-0107507.
XX      20-NOV-1998; 98US-0109409.
XX      (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX      Wong SW, Axthelm MK, Searles RP;
XX      MPI; 2000-376552/32.
XX
XX      New rhesus rhadino virus for producing non-human primate model useful
XX      for testing potential treatments and efficacy of the candidate vaccine
XX      for conditions associated with RRV infection
XX
XX      Claim 2; Page 83-122; 141pp; English.
XX
XX      The present invention describes a novel rhesus macaque rhadinovirus
XX      called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
XX      RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
XX      encoded by the genome sequence. The present invention also specifically
XX      claims the individual open reading frame (ORF) nucleotide sequences from
XX      the genome which encode the individual proteins, but these sequences are
XX      not given. A non-human animal infected with RRV can be used for testing
XX      the efficacy of drug in the treatment of condition associated with
XX      infection with RRV such as Kaposi's sarcoma, lymphoproliferative
XX      disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
XX      hypergammaglobulinaemia or autoimmune haemolytic anaemia, by
XX      administering the drug to a immuno-compromised non-human primate
XX      preferably Rhesus macaque monkey obtained by as a result of infection
XX      by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
XX      non-human primate model for testing potential treatments for conditions
XX      associated with RRV infection. It is also useful for testing the
XX      efficacy of the candidate vaccine against RRV infection or conditions
XX      associated with its infection by administering the vaccine to the
XX      subject capable of infection with RRV, inoculating the subject with RRV
XX      and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
XX      to AAB53213 represent sequence used in the exemplification of the
XX      present invention.
XX
XX      Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;

Query Match      0.1%; Score 33; DB 21; Length 133719;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23879 GTTGGTTTGTTCACAGTCCCTATATAT 23911
      |||
      117575 GTTGGTTTGTTCACAGTCCCTATATAT 117543

DB      117575 GTTGGTTTGTTCACAGTCCCTATATAT 117543

RESULT 20
AAT51553
ID      AAT51553 standard: DNA; 2511 BP.
XX
AC      AAT51553;
XX
DT      06-NOV-1997 (first entry)
XX
DE      Herpes virus DNA polymerase segment KSHV encoding DNA.
XX
XX      Retroperitoneal fibromatosis herpes virus; detection; infection;
XX      Kaposi's sarcoma herpes virus; viral DNA; viral RNA; vaccine;
XX      antigen; antibody; ss.
XX
XX      Kaposi's sarcoma herpes virus.
OS
XX
XX      Key Location/Qualifiers
XX      CDS 1..2511
XX      FT /*tag= a
XX      /product= DNA_polymerase
FT
```

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FT      /note- "No stop codon given"
XX
XX      MO9704105-A1.
XX
XX      06-FEB-1997.
XX
XX      12-JUL-1996; 96WO-US11688.
XX
XX      11-JUL-1996; 96US-0001148.
XX      14-JUL-1995; 95US-0001148.
XX
XX      (UNIW ) UNIV WASHINGTON.
XX
XX      Bosch ML, Rose TM, Strand K, Todaro GJ:
XX
XX      WPI: 1997-132644/12.
XX      P-P-SDB; AAM11995.
XX
XX      Herpes virus DNA polymerase and corresponding nucleotide sequence -
XX      used in the detection and treatment of herpes virus infection
XX
XX      Claim 9; Page 88-90; 132pp; English.
XX
XX      The present sequence represents a novel isolated polynucleotide
XX      with a region encoding a DNA polymerase designated KSHV of a
XX      herpes virus. This DNA polymerase was isolated from Kaposi's
XX      sarcoma herpes virus (KSHV) found in tissue samples taken from
XX      humans. Primers used in the amplification of polynucleotides
XX      encoding DNA polymerases may be used for detecting viral DNA or
XX      RNA in a sample of primate origin, especially in the diagnosis of
XX      herpes viral infection. Herpes virus DNA polymerases of this
XX      infection, may be used in vaccines for the protection against
XX      infection by a herpes virus of the RFHV/KSHV family. They may also
XX      be used in the design and screening of anti-viral drugs. Antibodies
XX      raised against the polymerase or fragments of it, may be used in the
XX      detection of herpes virus infection and for drug targeting for the
XX      therapy of herpes virus infection.
XX
XX      Sequence 2511 BP; 624 A; 708 C; 662 G; 513 T; 4 other;
XX
XX      Query Match      0.1%; Score 29; DB 18; Length 2511;
XX      Best Local Similarity 100.0%; Pred. No. 0.18;
XX      Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      14938 CTGGAGTTTGACTGACCTGGAGGACCT 14966
XX      |||||||
XX      391 CTGGAGTTTGACTGACCTGGAGGACCT 419
XX
XX      RESULT 21
XX      AAV73802
XX      ID AAV73802 standard; DNA: 35100 BP.
XX
XX      AAV73802:
XX
XX      25-FEB-1999 (first entry)
XX
XX      KSHV LUR DNA (nucleotides 1-35,100).
XX
XX      Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;
XX      dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis;
XX      diagnosis; treatment; HHV8; complement binding protein; v-CBP; SSBP;
XX      ssDNA binding protein; transport protein; glycoprotein B; pol; vIL-6;
XX      DNA polymerase; viral interleukin-6; BHV4-IE1 I; thymidylate synthase;
XX      vMIP-II; BHV4-IE1 II; vMIP-I; capsid protein I; tegument protein I; ds.
XX
XX      Kaposi's sarcoma-associated herpesvirus.
XX
XX      US5849564-A.
XX
XX      15-DEC-1998.
XX
XX      29-NOV-1996; 96US-0770379.

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XX      29-NOV-1996; 96US-0770379.
XX
XX      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX      Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JU;
XX      WPI: 1999-069741/06.
XX
XX      Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
XX      dihydrofolate reductase and is useful for treatment, prophylaxis
XX      or diagnosis of Kaposi's sarcoma
XX
XX      Disclosure; Column 67-96; 109pp; English.
XX
XX      This sequence is a fragment of the Kaposi's sarcoma-associated
XX      herpesvirus (KSHV) LUR (long unique region). This fragment contains
XX      coding regions for K1, ORF4 which encodes the complement binding protein
XX      v-CBP, ORF6 which encodes a ssDNA binding protein (SSBP), ORF7 which
XX      encodes a transport protein, ORF8 which encodes glycoprotein B, ORF9
XX      which encodes DNA polymerase (pol), ORF10, ORF11, K2 which encodes viral
XX      interleukin-6 (vIL-6), ORF02 which encodes dihydrofolate reductase
XX      (DHFR), K3 which encodes BHV4-IE1 I, ORF70 which encodes thymidylate
XX      synthase, K4 which encodes vMIP-II, K5 which encodes BHV4-IE1 II, K6
XX      which encodes vMIP-I, K7, ORF16 which encodes Bcl-2, ORF17 which encodes
XX      capsid protein I, ORF18 and ORF19 which encodes tegument protein I.
XX      KSHV is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma
XX      (KS) which is the most common form of neoplasm occurring in persons with
XX      acquired immune deficiency syndrome (AIDS). The DHFR protein is useful
XX      for vaccination, prophylaxis, diagnosis and treatment of a subject with
XX      Kaposi's sarcoma and for detecting expression of a DNA virus associated
XX      with Kaposi's sarcoma in a cell.
XX
XX      Sequence 35100 BP; 8703 A; 9395 C; 8921 G; 8081 T; 0 other;
XX
XX      Query Match      0.1%; Score 29; DB 20; Length 35100;
XX      Best Local Similarity 100.0%; Pred. No. 0.15;
XX      Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      14938 CTGGAGTTTGACTGACCTGGAGGACCT 14966
XX      |||||||
XX      12167 CTGGAGTTTGACTGACCTGGAGGACCT 12195
XX
XX      RESULT 22
XX      AAV19941
XX      ID AAV19941 standard; DNA: 137507 BP.
XX
XX      AAV19941:
XX
XX      03-AUG-1998 (first entry)
XX
XX      KSHV long unique coding region and terminal repeat.
XX
XX      KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II;
XX      interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis;
XX      complement-binding protein; glycoprotein; capsid protein IV; infection;
XX      immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
XX      lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides;
XX      HIV immune status; anti-inflammatory agent; therapy; ds.
XX
XX      Kaposi's sarcoma-associated herpes virus.
XX
XX      Location/Qualifiers
XX      key 1142..2794
XX      CDS 8699..11236
XX      /product= complement-binding protein
XX      /tag= a
XX      /tag= b
XX      /product= glycoprotein B
XX      /complement (11761..117875)
XX      /tag= c
XX      /product= interleukin 6
XX
XX      CDS
XX
XX      FT
XX
XX      FT
XX
XX      FT

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FT      CDS      complement (21548..21832)
FT      /tag= d
FT      /product= macrophage inflammatory protein II
FT      CDS      complement (27137..27424)
FT      /tag= e
FT      /product= interferon regulatory factor 1
FT      CDS      28661..29741
FT      /tag= f
FT      /product= protein TI.1
FT      CDS      complement (58976..60175)
FT      /tag= g
FT      /product= glycoprotein M
FT      CDS      complement (69412..69915)
FT      /tag= h
FT      /product= glycoprotein L
FT      CDS      complement (88410..88910)
FT      /tag= i
FT      /product= interferon regulatory factor 2
FT      CDS      89600..90541
FT      /tag= j
FT      /product= interferon regulatory factor 3
FT      CDS      90173..90643
FT      /tag= k
FT      /product= glycoprotein X
FT      CDS      complement (93636..94127)
FT      /tag= l
FT      /product= interferon regulatory factor 4
FT      CDS      complement (111931..112443)
FT      /tag= m
FT      /product= capsid protein IV
FT      CDS      complement (123808..127296)
FT      /tag= n
FT      /product= immediate early protein

XX      WO9804576-A1.
XX
XX      05-FEB-1998.
XX
XX      22-JUL-1997; 97WO-US13346.
XX
XX      29-NOV-1996; 96US-0757669.
XX      PR      25-JUL-1996; 96US-0686243.
XX      PR      25-JUL-1996; 96US-0686349.
XX      PR      25-JUL-1996; 96US-0686350.
XX      PR      25-JUL-1996; 96US-0687253.
XX      PR      25-JUL-1996; 96US-0688814.
XX      PR      05-SEP-1996; 96US-0708678.
XX      PR      10-OCT-1996; 96US-0728323.
XX      PR      13-NOV-1996; 96US-0747887.
XX      PR      13-NOV-1996; 96US-0748640.
XX
XX      (UNIV ) UNIV COLUMBIA NEW YORK.
XX
XX      Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
XX      WPI; 1998-130615/12.
XX
XX      New nucleic acid encoding Kaposi's sarcoma associated herpes virus
XX      proteins - useful for, e.g. detecting levels of HHV8 in, and
XX      preparation of vaccines for treatment of, HIV patients
XX
XX      Example 2; Page 135-203; 230pp; English.
XX
XX      This sequence represents the long unique region and terminal repeat of
XX      the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known
XX      as human herpes virus 8 (HHV8). This sequence contains the DNAs of the
XX      invention which encode KSHV polypeptides selected from: (a) viral
XX      macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6);
XX      (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;
XX      (d) capsid protein IV encoded by ORF5; and (e) immediate early protein
XX      encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded
XX      by it, and antibodies (Ab) specific for the proteins are useful for
XX      detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body

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CC      fluids or tissue samples. HHV8 infections can be treated with antisense
CC      or triplex forming molecules or agents that bind specifically to the
CC      protein. Ab may be used for prophylaxis or treatment of HHV8 infection,
CC      while the protein can be used in protective vaccines. Ab may also be used
CC      to differentiate between lymphomas, and HHV8 may be implicated in many
CC      other lymphoproliferative diseases such as lymphomas, leukemia,
CC      splenomegaly and mycosis fungoides. Cells and animals containing the
CC      nucleic acid are useful for drug screening. HHV8-derived peptides can be
CC      used as targets for antiviral drugs, e.g. dihydrofolate reductase gene
CC      can be inhibited with methotrexate. These can also be used to determine
CC      the immune status of a patient infected with HIV. HHV8 derived protein
CC      viral MIP III may be used as an anti-inflammatory agent for,
CC      e.g. treating rheumatoid arthritis. This sequence is stated as containing
CC      81 open reading frames.
CC
XX      SQ      Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
XX
XX      Query Match      0.1%; Score 29; DB 19; Length 137507;
XX      Best Local Similarity 100.0%; Pred. No. 0.14;
XX      Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy      14938 CTGAGTTTGACTGCAGCTGGAGGACCT 14966
XX      |||||||
XX      Db      12167 CTGAGTTTGACTGCAGCTGGAGGACCT 12195
XX
XX      RESULT 23
XX      AAT51545
XX      ID      AAT51545 standard; DNA; 536 BP.
XX      AC      AAT51545;
XX      XX
XX      Dt      06-NOV-1997 (first entry)
XX
XX      Herpes virus DNA polymerase PCR segment RFHV encoding DNA.
XX
XX      DE      Retroperitoneal fibromatosis herpes virus; detection;
XX      KW      Kaposi's sarcoma herpes virus; viral DNA; viral RNA; vaccine;
XX      KW      antigen; antibody; polymerase chain reaction; ss.
XX      XX
XX      OS      Retroperitoneal fibromatosis herpes virus.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      1..536
XX      CDS      /tag= a
XX      FT      /product= DNA_polymerase
XX      FT      /note= "No stop codon given"
XX
XX      WO9704105-A1.
XX
XX      PD      06-FEB-1997.
XX
XX      PF      12-JUL-1996; 96WO-US11688.
XX      PR      11-JUL-1996; 96US-0001148.
XX      PR      14-JUL-1995; 95US-0001148.
XX
XX      (UNIV ) UNIV WASHINGTON.
XX
XX      Bosch ML, Rose TM, Strand K, Todaro GJ;
XX      WPI; 1997-132644/12.
XX      DR      P-PSDB; AAM11993.
XX
XX      Herpes virus DNA polymerase and corresponding nucleotide sequence -
XX      used in the detection and treatment of herpes virus infection
XX
XX      PS      Claim 1; Page 78; 132pp; English.
XX
XX      The present sequence represents a novel isolated polynucleotide with
XX      a region encoding a DNA polymerase designated RFHV of a herpes virus.
XX      This DNA polymerase was isolated from Retroperitoneal fibromatosis
XX      herpes virus (RFHV) found in tissue samples taken from Macaque

```

CC nemestrina monkeys. Primers used in the amplification of
CC polynucleotides encoding DNA polymerases may be used for detecting
CC viral DNA or RNA in a sample of primate origin, especially in the
CC diagnosis of herpes viral infection. Herpes virus DNA polymerases of
CC this invention, may be used in vaccines for the protection against
CC infection by a herpes virus of the RRV/KSHV family. They may also be
CC used in the design and screening of anti-viral drugs. Antibodies
CC raised against the polymerase or fragments of it, may be used in the
CC detection of herpes virus infection and for drug targeting for the
CC therapy of herpes virus infection.

XX
SQ Sequence 536 BP; 137 A; 165 C; 134 G; 100 T; 0 other:
Query Match 0.1%; Score 26; DB 18; Length 536;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16150 GATTAACACAGCTGCCATCAGCT 16175
Db 274 GATTAACACAGCTGCCATCAGCT 299
|||||

RESULT 24
ID AAS84956 standard; CDNA: 651 BP.
XX
AC AAS84956;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #20760.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB: ABG20769.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID NO 20760; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcr_sequences.
XX
SQ Sequence 651 BP; 152 A; 86 C; 241 G; 172 T; 0 other:
Query Match 0.1%; Score 26; DB 23; Length 651;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21075 CTCGTGACAGCTGCAGACAGCTC 21100
Db 425 CTCGTGACAGCTGCAGACAGCTC 400
|||||

RESULT 25
ID AB283296 standard; CDNA: 1024 BP.
XX
AC AB283296;
XX
DT 14-MAY-2003 (first entry)
XX
DE Toxicologically relevant human nucleotide sequence #455.
XX
KW Toxicologically relevant gene; toxicological response; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003016500-A2.
XX
PD 27-FEB-2003.
XX
PF 16-AUG-2002; 2002WO-US26514.
XX
PR 16-AUG-2001; 2001US-313080P.
XX
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI Neft RE, Dunn RT, Adkins K, Pickett GG, Klier LD, Schmeisler K;
PI Alen P;
XX
DR WPI: 2003-268322/26.
XX
PT Determining a toxicological response to an agent, useful for screening
PT of drugs, comprises comparing the expression profile of one or more
PT human toxic response genes to a reference gene expression profile
PT indicative of toxicity -
XX
PS Claim 1; Page 162; 455pp; English.

XX
CC The present invention describes a method (M1) for determining a
CC toxicological response to an agent, which comprises comparing the
CC expression profile of one or more human toxic response genes to a
CC reference gene expression profile indicative of toxicity, and so
CC determining the presence of a toxic response to the agent. Also
CC described: (1) an array comprising one or more polynucleotides selected
CC from the genes corresponding to the partial sequences given in AB282842
CC to AB284764, or their fragments of at least 20 nucleotides, or
CC homologues; and (2) determining if a gene putatively identified to be a
CC toxic response gene plays a role on toxic response pathways by
CC determining the expression profile of the gene after exposure of cells
CC or a human subject to a known toxic pharmaceutical or industrial agent,
CC comprising: (a) exposing cells to an agent or isolating cells from a
CC human subject who was exposed to an agent; (b) obtaining the test gene
CC expression profile for a putatively identified toxic response gene after
CC exposure to a known toxic pharmaceutical or industrial agent; and
CC (c) comparing the test profile to the expression profile of a gene with

CC a similar function or comparing the test profile to the expression
CC profile of that gene after exposure to other known toxic compounds. The
CC methods are useful for predicting and determining toxicological responses
CC on a cellular, organ or system level. The arrays comprising the human
CC genes are useful for toxicological screening of drugs, pharmaceutical
CC compounds and chemicals.

SQ Sequence 1024 BP; 232 A; 299 C; 284 G; 209 T; 0 other;

Query Match 0.1%; Score 26; DB 25; Length 1024;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21075 CTCTGTACAGCTGGCAGACAGCTC 21100
|||||
DB 749 CTCTGTACAGCTGGCAGACAGCTC 724

RESULT 26
AB082701/c
ID AB082701 standard; DNA; 1536 BP.

AC AB082701;
XX
XX
DT 02-JAN-2003 (first entry)
XX
DE Human thymidylate synthase encoding cDNA SEQ ID NO:13.
XX
XX Thymidylate synthase; enzyme; binding; neoplastic disorder;
KW chemotherapeutic; cytostatic; thymidylate synthase inhibitor;
KW cancer; gene; ss.
XX
XX Homo sapiens.
OS

FH Key Location/Qualifiers
FT CDS 106..1047
FT /tag= a
FT /product= "thymidylate synthase"
FT
XX
XX
PN WO200272753-A2.
XX
XX
PD 19-SEP-2002.
XX
XX
PF 05-MAR-2002; 2002MO-US06634.
XX
XX
PR 07-MAR-2001; 2001US-274107P.
XX
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Allegra CJ, Voeller DM;
PI
XX
XX
DR WPI: 2002-732823/79.
DR P-PSDB: ABP53744.
XX
XX
PT New isolated peptide binding to an mRNA encoding thymidylate synthase,
PT useful for treating and/or diagnosing disorders such as cancer of a
PT head and neck, breast, prostate, liver, lung, gastric, colon or
PT esophagus -
XX
XX
PS Claim 7; Fig 2A; 59pp; English.

CC The present invention describes a peptide (1) which binds to an mRNA
CC encoding a thymidylate synthase (TS) polypeptide. Also described:
CC (1) Inhibiting translation of a mRNA encoding TS comprising contacting
CC the mRNA, or a cell expressing the mRNA with a peptide comprising 10-25
CC consecutive amino acids of the peptide interface region of the TS, where
CC the peptide binds to the mRNA encoding TS, and inhibits the translation
CC of the mRNA encoding TS; and (2) treating a subject with a neoplastic
CC disorder comprising administering to the subject a chemotherapeutic agent
CC and a TS peptide or a therapeutic nucleic acid sequence encoding a
CC promoter operably linked to a nucleic acid sequence encoding TS peptide
CC that comprises 10-25 amino acids of the peptide interface region of the
CC TS, where the peptide binds to the mRNA encoding TS, and inhibits the

CC translation of the mRNA encoding TS, treating the neoplastic disorder.
CC (1) has cytostatic activity, and can be used as a TS inhibitor. The
CC methods and compositions of the present invention are useful for treating
CC and/or diagnosing disorders associated with the TS peptide, such as
CC cancer of a head and neck, breast, prostate, liver, lung, gastric, colon
CC or esophagus. They are also used to enhance the effect of other
CC chemotherapeutic agents. The present sequence encodes human thymidylate
CC synthase, which is used in an example from the present invention.
XX

SQ Sequence 1536 BP; 390 A; 369 C; 399 G; 378 T; 0 other;

Query Match 0.1%; Score 26; DB 24; Length 1536;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21075 CTCTGTACAGCTGGCAGACAGCTC 21100
|||||
DB 749 CTCTGTACAGCTGGCAGACAGCTC 724

RESULT 27
ABK90458/c
ID ABK90458 standard; DNA; 1536 BP.
XX
XX
AC ABK90458;
XX
XX
DT 21-OCT-2002 (first entry)
XX
XX
DE Human thymidylate synthase (TS) gene.
XX
XX
KW Human: excision repair cross-complementing gene; ERCC1; gene; ds; TS;
KW cytostatic; 5-Fluorouracil; oxaliplatin; thymidylate synthase; cancer;
KW chemotherapy; tumour; colorectal adenocarcinoma.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200257489-A2.
XX
XX
PD 25-JUL-2002.
XX
XX
PF 09-NOV-2001; 2001MO-US43039.
XX
XX
PR 01-DEC-2000; 2000US-250358P.
PR 04-DEC-2000; 2000US-250471P.
PR 11-JUN-2001; 2001US-0877178.
XX
XX
PA (RESP-) RESPONSE GENETICS INC.
XX
XX
XX Danenberg KD;
PI
XX
XX
DR WPI: 2002-590758/63.
XX
XX
PT Determining a chemotherapeutic regimen for treating a tumour, by
PT determining the amount of thymidylate synthase (TS) and/or excision
PT repair cross-complementing (ERCC1) mRNA and the threshold level for TS
PT and/or ERCC1 gene expression -
XX
XX
PS Disclosure: Page 67; 67pp; English.

CC The invention relates to methods of determining a chemotherapeutic
CC regimen with 5-Fluorouracil, oxaliplatin or their combination comprising
CC determining the amount of thymidylate synthase (TS) and/or excision
CC repair cross-complementing (ERCC1) mRNA in the amplified sample and the
CC threshold level for TS and/or ERCC1 gene expression. The method involves
CC obtaining a tissue sample of the tumour and fixing the sample to obtain a
CC fixed tumour sample, isolating mRNA from the fixed tumour sample,
CC subjecting the mRNA to amplification using a pair of oligonucleotide
CC primers that hybridise under stringent conditions to a region of the
CC ERCC1 gene and/or the TS gene to obtain an ERCC1 and/or TS amplified
CC sample, determining the amount of TS and/or ERCC1 mRNA in the amplified
CC sample, comparing the amount of mRNA to an amount of mRNA of an internal
CC control gene and determining a chemotherapeutic regimen comprising
CC 5-Fluorouracil, oxaliplatin or their combination based on the amount of

CC TS and/or ERCC1 mRNA in the amplified sample and the threshold level for
CC TS and/or ERCC1 gene expression. The method is useful in medicine,
CC particularly cancer chemotherapy, i.e. treating tumours, e.g. colorectal
CC adenocarcinoma and in assessing tumour cell gene expression in a patient
CC and may also be used in prognosticating the efficacy of 5-Fluorouracil
CC and oxaliplatin-based therapies. This sequence represents the human TS
CC gene.
XX
SQ Sequence 1536 BP; 390 A; 369 C; 399 G; 378 T; 0 other;
Query Match 0.1%; Score 26; DB 24; Length 1536;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21075 CTCGTACAGCTGCAGACAGCTC 21100
|||||
Db 749 CTCGTACAGCTGCAGACAGCTC 724
RESULT 28
ABK43335/C
ID ABK43335 standard; CDNA: 1536 BP.
XX
AC ABK43335;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human Thymidylate synthase cDNA sequence.
XX
KW HKNG1; ss: gene: chromosome 18p; bipolar affective disorder; BAD;
KW severe bipolar affective (mood) disorder; BP-I; schizophrenia; TS;
KW Hong Kong new gene 1; antimanic; antidepressant; neuroleptic;
KW Thymidylate synthase.
XX
OS Homo sapiens.
XX
PN WO200210366-A2.
XX
PD 07-FEB-2002.
XX
PE 02-AUG-2001; 2001WO-US24417.
XX
PR 02-AUG-2000; 2000US-0631275.
PR 28-NOV-2000; 2000US-0722544.
XX
XX
PA (MILL-) MILENNIUM PHARM INC.
PA (RGC) UNIV CALIFORNIA.
PI Chen H, Frelmer NB, Novak T;
PI
XX
DR WPI: 2002-195962/25.
DR P-PSDB; AAU87071.
XX
PT New nucleic acid molecule Hong Kong New Gene 1 (HKNG1), useful for
PT screening for molecules which modulate HKNG1 expression for the
PT treatment of bipolar disorder and schizophrenia -
XX
PS Disclosure: Fig 45; 367pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
CC nucleotide sequence that encodes a Hong Kong New Gene (HKNG) 1 gene
CC product. The human gene for HKNG1 is located on chromosome 18p in
CC an area associated with bipolar affective disorder, BAD. Also
CC included are an expression vector comprising the nucleic acid, a
CC host cell expressing the nucleic acid, an anti-HKNG1 antibody, a method
CC of identifying modulators of HKNG1, and identifying an individual (at
CC risk of) having HKNG1-mediated disorder comprising detecting the presence
CC or absence of a polymorphism that correlates with an HKNG1 allele
CC associated with the disorder, where the presence of the polymorphism
CC indicates that the individual (is at risk of) having HKNG1-mediated
CC disorder. A (small molecule) compound which modulates (inhibits or
CC potentiates) expression of a HKNG1 gene or gene product in a human
CC individual is useful for the treatment of a HKNG1-mediated disorder

CC such as bipolar affective disorder (BAD), severe bipolar affective (mood)
CC disorder (BP-I) and schizophrenia. The present sequence is the cDNA
CC encoding thymidylate synthase, TS. The gene for TS
CC overlaps that of HKNG1 and therefore TS may also be involved in the
CC diseases listed above.
XX
SQ Sequence 1536 BP; 390 A; 369 C; 399 G; 378 T; 0 other;
Query Match 0.1%; Score 26; DB 24; Length 1536;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21075 CTCGTACAGCTGCAGACAGCTC 21100
|||||
Db 749 CTCGTACAGCTGCAGACAGCTC 724
RESULT 29
AAT84648
ID AAT84648 standard; DNA: 3056 BP.
XX
AC AAT84648;
XX
DT 02-JAN-1998 (first entry)
XX
DE KSHV capsid maturation and glycoprotein B genes.
XX
KW KSHV; gamma herpes virus; glycoprotein B; vaccine; infection;
KW diagnosis; ss.
XX
OS Human Kaposi's sarcoma-associated herpesvirus.
XX
FH Key Location/Qualifiers
FH CDS 2..409
FT /*tag= a
FT /product= capsid/maturation/transport protein
FT 393..2930
FT /*tag= b
FT /product= glycoprotein B
XX
XX
PN WO9712042-A2.
XX
PD 03-APR-1997.
XX
PF 26-SEP-1996; 96WO-US15702.
XX
PR 26-SEP-1995; 95US-0004297.
XX
XX (UNIW) UNIV WASHINGTON.
PA
PI Bosch ML, Rose TM, Strand K;
PI
XX
DR WPI: 1997-212901/19.
DR P-PSDB; AAM26475; AAM26487.
XX
PT DNA encoding glycoprotein B of retroperitoneal fibromatosis and
PT Kaposi's sarcoma associated herpes viruses - useful in vaccines for
PT treatment of herpes infection or for detection of viral DNA
XX
PS Claim 7; Fig 19a-c; 138pp; English.
XX
XX This DNA sequence contains overlapping open reading frames coding
CC for the capsid maturation protein (AAM26487) and claimed glycoprotein
CC B (9B) (AAM26475) of human Kaposi's sarcoma-associated herpes virus
CC (KSHV). It is a consensus of sequences obtained by PCR
CC amplification of Kaposi's sarcoma tissue DNA using primers based on
CC consensus segments of gamma herpes viruses. Herpes viruses
CC glycoprotein B molecules are associated with fibroproliferative and
CC neoplastic conditions in primates, including humans. Glycoprotein
CC B polypeptides and polynucleotides (see also AAT84641-42; AAT84649) can
CC be used in vaccines, e.g. live virus or viral expression vectors,
CC for the treatment of herpes virus infection, or for the detection
CC of viral DNA or RNA in a sample. Polynucleotides can also be used

CC for recombinant production of glycoprotein B. Probes (see AAT84643-46, AAT84650-96) are claimed and can be used for the detection of gamma herpes viruses, of KSHV and retroperitoneal fibromatosis-associated herpes virus (RFHV), or for the specific detection of RFHV or KSHV. CC primers based on RFHV or KSHV sequences can be used in the PCR amplification of glycoprotein B polynucleotides.

CC
XX
SQ Sequence 3056 BP; 823 A; 847 C; 741 G; 641 T; 4 other;

Query Match 0.1%; Score 26; DB 18; Length 3056;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11454 GGCTGGATATTTAAAGACCTGTACGC 11479
|||||
DB 332 GGCTGGATATTTAAAGACCTGTACGC 357

RESULT 30
AAS94945/C
ID AAS94945 standard; DNA; 3298 BP.
XX
AC AAS94945;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human DNA sequence #200 expressed during foam cell differentiation.
XX
KW Human: foam cell differentiation; atherosclerosis; cerebral stroke;
KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200177389-A2.
XX
PD 18-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US11128.
XX
PR 05-APR-2000; 2000US-195106P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Shiffman D, Somogyi R, Lawn R, Sellhammer JJ, Porter CJ, Mikita T;
PI Tai J;
XX
DR WPI; 2002-010925/01.
XX
PT Composition useful for diagnosis of conditions, disorders or diseases
PT associated with atherosclerosis, comprises several polynucleotides that
PT are differentially expressed in foam cell development -
XX
PS Claim 1; Page 250-251; 315pp; English.
XX
CC The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell
CC differentiation. The polynucleotide sequences of the invention or a
CC composition comprising these polynucleotides are useful as a high
CC throughput method for detecting altered expression of one or more
CC polynucleotides in a sample. The polynucleotides can be used in the
CC diagnosis of disorders associated with foam cell development such as
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC coronary artery disease. The polynucleotide sequences can also be used
CC as PCR primers and probes. The polynucleotides of the invention are also
CC useful in gene therapy. AAS94746-AAS95021 represent the human
CC polynucleotide sequences of the invention which are differentially
CC expressed during foam cell differentiation.
XX
SQ Sequence 3298 BP; 898 A; 709 C; 744 G; 919 T; 28 other;

Query Match 0.1%; Score 26; DB 24; Length 3298;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21075 CTCTGTACAGCTGCAGACAGCTC 21100
|||||
DB 728 CTCTGTACAGCTGCAGACAGCTC 703

RESULT 31
AAT84697
ID AAT84697 standard; DNA; 3612 BP.
XX
AC AAT84697;
XX
DT 02-JAN-1998 (first entry)
XX
DE KSHV capsid maturation, glycoprotein B, DNA polymerase genes.
XX
KW KSHV; gamma herpes virus; glycoprotein B; vaccine; infection;
KW diagnosis; capsid maturation; DNA polymerase; ss.
XX
OS Human Kaposi's sarcoma-associated herpesvirus.
XX
FH Key Location/Qualifiers
FH CDS 2..409
FT /*tag= a
FT /product= capsid/maturation/transport protein
FT 393..2930
FT /*tag= b
FT /product= glycoprotein B
FT CDS 3057..3611
FT /*tag= c
FT /product= DNA polymerase
XX
PN WO9712042-A2.
XX
PD 03-APR-1997.
XX
PF 26-SEP-1996; 96WO-US15702.
XX
PR 26-SEP-1995; 95US-0004297.
XX
PA (UNITV) UNITV WASHINGTON.
XX
PI Bosch ML, Rose TM, Strand K;
XX
DR WPI; 1997-212901/19.
XX
PT P-PSDB; AAM26475, AAM26487, AAM26488.
XX
PT DNA encoding glycoprotein B of retroperitoneal fibromatosis and
PT Kaposi's sarcoma associated herpes viruses - useful in vaccines for
PT treatment of herpes infection or for detection of viral DNA
XX
PS Example 7; Fig 19a-c; 138pp; English.
XX
CC This DNA sequence contains open reading frames coding for the
CC capsid maturation protein (AAM26487), the claimed glycoprotein
CC B (9b) (AAM26475) and the DNA polymerase (AAM26488) of human Kaposi's
CC sarcoma-associated herpes virus (KSHV). It is a consensus of
CC sequences obtained by PCR amplification of Kaposi's sarcoma tissue
CC DNA using primers based on consensus segments of gamma herpes
CC viruses. Herpes viruses glycoprotein B molecules are associated
CC with fibroproliferative and neoplastic conditions in primates,
CC including humans. Glycoprotein B polypeptides and polynucleotides
CC (see also AAT84641-42, AAT84648-49) can be used in vaccines, e.g. live
CC virus or viral expression vectors, for the treatment of herpes
CC virus infection, or for the detection of viral DNA or RNA in a
CC sample. Polynucleotides can also be used for recombinant
CC production of glycoprotein B. Probes (see AAT84643-46, AAT84650-96)
CC are claimed and can be used for the detection of gamma herpes
CC viruses, of KSHV and retroperitoneal fibromatosis-associated
CC herpes virus (RFHV), or for the specific detection of RFHV or KSHV.
CC primers based on RFHV or KSHV sequences can be used in the PCR
CC amplification of glycoprotein B polynucleotides.

Sequence 3612 BP; 944 A; 1033 C; 883 G; 748 T; 4 other;
Query Match 0.1%; Score 26; DB 18; Length 3612;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11454 GGCTGATATTAAAGACCTGTACGC 11479
|||||
DB 332 GGCTGATATTAAAGACCTGTACGC 357

RESULT 32
AAF31109/c
ID AAF31109 standard; cDNA; 18596 BP.
XX
AC AAF31109;
XX
DT 27-APR-2001 (first entry)
XX
DE Thymidylate synthase coding sequence.
XX
KM Analyze-binding enzyme; analyze analysis; ss.
XX
OS Homo sapiens.
XX
PN WO200102600-A2.
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18057.
XX
PR 06-JUL-1999; 99US-0347878.
PR 06-DEC-1999; 99US-0457205.
XX
PA (GRAT) GEN ATOMICS.
XX
PI Yuan C;
DR WPI; 2001-071583/08.
XX
PT Assaying method, useful for prognosis and diagnosis of disease,
PT comprises contacting sample with a mutant analyze-binding enzyme and
PT detecting binding -
XX
PS Disclosure: Page -: 187pp; English.
XX
CC The present invention relates to a method for assaying an analyze in a
CC sample comprising: contacting the sample with a mutant analyze-binding
CC enzyme which has binding affinity for the analyze or an immediate
CC analog; and detecting resulting binding. The method is useful in
CC activity; and detecting resulting binding. The method is useful in
CC monitoring biological systems/processes, or prognosis/diagnosis of
CC disease caused by imbalances of the analyzes. The present sequence is
CC a coding sequence used in the present invention.
CC Note: the present sequence is not shown in the specification, but was
CC from Genbank, using information given in the specification.
XX
SQ Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;

Query Match 0.1%; Score 26; DB 22; Length 18596;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21075 CTCTGTACAGCTGCGACAGACGCTC 21100
|||||
DB 13536 CTCTGTACAGCTGCGACAGACGCTC 13511

RESULT 33
AAC91215/c
ID AAC91215 standard; DNA; 18596 BP.
XX
AC AAC91215;

XX 20-MAR-2001 (first entry)
DT
XX
DE Human thymidylate synthase gene SRQ ID NO: 11.
XX
KM Human; schizophrenia; developmental disorder; spina bifida cystica;
KM Tourette's syndrome; bipolar illness; conduct disorder;
KM attention deficit disorder; obsessive compulsive disorder;
KM chronic multiple tic syndrome; learning disorder; polymorphism; ds.
XX
OS Homo sapiens.
XX
PN WO200071754-A1.
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-US14354.
XX
PR 25-MAY-1999; 99US-0318448.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Johnson WG, Stenroos ES;
DR WPI; 2001-025174/03.
XX
PT Diagnosing a developmental disorder, e.g. schizophrenia, by forming
PT datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
PT and environmental variables affecting an individual and then comparing
PT these DS with reference DS -
XX
PS Disclosure: Page 125-131; 156pp; English.
XX
CC The present invention provides a novel method of estimating the
CC susceptibility of an individual to a developmental disorder using genetic
CC and environmental variables. The method can be used in the diagnosis,
CC prevention and treatment of disorders such as schizophrenia, spina bifida
CC cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
CC attention deficit disorder, obsessive compulsive disorder, chronic
CC multiple tic syndrome and learning disorders such as dyslexia.
XX
SQ Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;

Query Match 0.1%; Score 26; DB 22; Length 18596;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21075 CTCTGTACAGCTGCGACAGACGCTC 21100
|||||
DB 13536 CTCTGTACAGCTGCGACAGACGCTC 13511

RESULT 34
ABN95092/c
ID ABN95092 standard; DNA; 18596 BP.
XX
AC ABN95092;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #1590 used to diagnose liver cancer.
XX
KM Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KM metastatic liver tumour; cytostatic; expression profile; disease state;
KM disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30589.

PR		02-0CT-2000; 2000US-237054P.
PX		(GENE-) GENE LOGIC INC.
PA		Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
PI		WPI: 2002-426119/45.
PJ		
DR		
XX		
XX		Diagnosing and detecting the progression of liver cancer,
PT		hepatocellular carcinoma or metastatic liver tumor in a patient,
PT		involves detecting the level of expression of two or more genes in a
XX		liver tissue sample -
PS		Claim 1: SEQ ID NO 1590; 298pp; English.
XX		
CC		The invention relates to a novel method for diagnosing and detecting the
CC		progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC		tumour in a patient, and differentiating metastatic liver cancer from
CC		hepatocellular carcinoma in a patient, involving detecting the level of
CC		expression of two or more genes represented in ABN93503-ABN97455 in a
CC		tissue sample. The method of the invention has hepatotropic, and
CC		cytostatic activity. The method is useful for diagnosing and detecting
CC		the progression of liver cancer, hepatocellular carcinoma and metastatic
CC		liver carcinoma in a patient. The method is useful for identifying
CC		expression profiles which serve as useful diagnostic markers as well as
CC		markers that can be used to monitor disease states, disease progression,
CC		drug toxicity, drug efficacy and drug metabolism.
CC		Note: The sequence data for this patent did not form part of the printed
CC		specification, but was obtained in electronic format directly from WIPO
XX		at ftp.wipo.int/pub/published_pct_sequences.
SQ		Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
OY		
Dy		
Query Match	0.1%; Score 26; DB 24; Length 18596;	
Best Local Similarity	100.0%; Pred. No. 2.7;	
Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
21075	CTCTGGTACAGCTGGCAGACAGCTC	21100
13536	CTCTGTGCACAGCTGGCAGACAGCTC	13511
RESULT 35		
ABK43334/C		
ID	ABK43334 standard; DNA; 18596 BP.	
XX		
XX	ABK43334;	
XX		
DT	05-JUN-2002 (first entry)	
XX		
DE		
XX	Human Thymidylate synthase gene sequence.	
KW	HKNG1; ds; gene; chromosome 18p; bipolar affective disorder; BAD;	
XX	severe bipolar affective (mood) disorder; BP-I; schizophrenia; TS;	
KW	Hong Kong new gene I; antimanic; antidepressant; neuroleptic;	
XX	Thymidylate synthase.	
OS	Homo sapiens.	
XX		
PN	WO200210366-A2.	
XX		
PD	07-FEB-2002.	
XX		
PF	02-AUG-2001; 2001WO-US24417.	
XX		
PR	02-AUG-2000; 2000US-0631275.	
XX		
PR	28-NOV-2000; 2000US-0722544.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
PA	(REGC) UNIV CALIFORNIA.	
TI	Chen H, Freimer NB, Novak T;	

XX	WPI: 2002-195962/25.
DR	
PT	New nucleic acid molecule Hong Kong New Gene 1 (HKNG1), useful for
PT	screening for molecules which modulate HKNG1 expression for the
PT	treatment of bipolar disorder and schizophrenia -
XX	
PS	Disclosure: Fig 44; 367pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule comprising a
CC	nucleotide sequence that encodes a Hong Kong New Gene (HKNG) 1 gene
CC	product. The human gene for HKNG1 is located on chromosome 18p in
CC	an area associated with bipolar affective disorder, BAD. Also
CC	included are an expression vector comprising the nucleic acid, a
CC	host cell expressing the nucleic acid, an anti-HKNG1 antibody, a method
CC	of identifying modulators of HKNG1, and identifying an individual (at
CC	risk of) having HKNG1-mediated disorder comprising detecting the presence
CC	or absence of a polymorphism that correlates with an HKNG1 allele
CC	associated with the disorder, where the presence of the polymorphism
CC	indicates that the individual (is at risk of) having HKNG1-mediated
CC	disorder. A (small molecule) compound which modulates (inhibits or
CC	potentiates) expression of a HKNG1 gene or gene product in a human
CC	individual is useful for the treatment of a HKNG1-mediated disorder
CC	such as bipolar affective disorder (BAD), severe bipolar affective
CC	disorder (BP-I) and schizophrenia. The present sequence is a
CC	thymidylate synthase, TS, genomic DNA sequence. The gene for TS
CC	overlaps that of HKNG1 and therefore TS may also be involved in the
CC	diseases listed above.
XX	
SO	Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
	Query Match 0.1%; Score 26; DB 24; Length 18596;
	Best Local Similarity 100.0%; Pred. No. 2.7;
	Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	21075 CTCTGTACAGCTGCGACAGACGTC 21100
DB	13536 CTCTGTACAGCTGCGACAGACGTC 13511
RESULT 36	
ABL62854/C	
ID	ABL62854 standard; DNA; 18596 BP.
XX	
AC	ABL62854;
XX	
XX	
DT	15-MAY-2002 (first entry)
DE	Breast cancer related gene sequence SEQ ID NO:1191.
XX	
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW	gene; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200194629-A2.
XX	
PD	13-DEC-2001.
XX	
PF	30-MAY-2001; 2001WO-US10838.
XX	
PR	05-JUN-2000; 2000US-209473P.
PR	05-JUN-2000; 2000US-209531P.
PR	18-SEP-2000; 2000US-233133P.
PR	18-SEP-2000; 2000US-233617P.
PR	20-SEP-2000; 2000US-234009P.
PR	20-SEP-2000; 2000US-234034P.
PR	20-SEP-2000; 2000US-234052P.
PR	22-SEP-2000; 2000US-234509P.
PR	22-SEP-2000; 2000US-234567P.
PR	25-SEP-2000; 2000US-234923P.
PR	

PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
XX (AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Sopet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PI determining a change in expression of a gene of a signature gene set -
XX
XX Claim 1; SEQ ID 1191; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.
XX
XX Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;

Query Match 0.1%; Score 26; DB 24; Length 18596;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21075 CTCGTGACAGCTGCGACAGACGTC 21100
DB 13536 CTCGTGACAGCTGCGACAGACGTC 13511

RESULT 37
ABL63078/C
ID ABL63078 standard; DNA; 18596 BP.
XX
XX ABL63078;
XX
XX 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:1415.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
XX gene; ds.
XX
XX Homo sapiens.
XX
XX WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US10838.
XX
XX 05-JUN-2000; 2000US-209473P.
XX 05-JUN-2000; 2000US-209531P.
XX 18-SEP-2000; 2000US-233133P.
XX 18-SEP-2000; 2000US-233617P.
XX 20-SEP-2000; 2000US-234009P.
XX 20-SEP-2000; 2000US-234034P.
XX 20-SEP-2000; 2000US-234052P.
XX 22-SEP-2000; 2000US-234509P.
XX 22-SEP-2000; 2000US-234567P.
XX 25-SEP-2000; 2000US-234923P.
XX 25-SEP-2000; 2000US-234924P.
XX 25-SEP-2000; 2000US-235077P.
XX 25-SEP-2000; 2000US-235082P.
XX 25-SEP-2000; 2000US-235134P.
XX 25-SEP-2000; 2000US-235637P.
XX 26-SEP-2000; 2000US-235638P.
XX 27-SEP-2000; 2000US-235711P.
XX 27-SEP-2000; 2000US-235720P.
XX 27-SEP-2000; 2000US-235840P.
XX 27-SEP-2000; 2000US-235863P.
XX 28-SEP-2000; 2000US-236028P.
XX 28-SEP-2000; 2000US-236032P.
XX 28-SEP-2000; 2000US-236033P.
XX 28-SEP-2000; 2000US-236034P.
XX 28-SEP-2000; 2000US-236109P.
XX 28-SEP-2000; 2000US-236111P.
XX 29-SEP-2000; 2000US-236842P.
XX 29-SEP-2000; 2000US-236891P.
XX 02-OCT-2000; 2000US-237172P.
XX 02-OCT-2000; 2000US-237173P.
XX 02-OCT-2000; 2000US-237278P.
XX 02-OCT-2000; 2000US-237294P.
XX 02-OCT-2000; 2000US-237295P.
XX 02-OCT-2000; 2000US-237316P.
XX 03-OCT-2000; 2000US-237425P.
XX 03-OCT-2000; 2000US-237598P.
XX 03-OCT-2000; 2000US-237604P.
XX 03-OCT-2000; 2000US-237606P.
XX 03-OCT-2000; 2000US-237608P.
XX 01-NOV-2000; 2000US-244867P.
XX 01-NOV-2000; 2000US-245084P.
XX
XX (AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX Sopet DR, Weaver Z;
XX

DR WPI: 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
PS Claim 1: SEQ ID 1415; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 18596 BP: 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
Query Match 0.1%; Score 26; DB 24; Length 18596;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21075 CTCTGTACAGCTGGCAGACAGCTC 21100
DB 13536 CTCTGTACAGCTGGCAGACAGCTC 13511
|||||
RESULT 38
ABL67927/C
ID ABL67927 standard; DNA; 18596 BP.
XX
AC ABL67927;
XX
DT 15-MAY-2002 (first entry)
XX
DE Ovary cancer related gene sequence SEQ ID NO:6264.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; anti-neoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.

PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237178P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Sopset DR, Weaver Z;
PI XX
DR WPI: 2002-188264/24.
XX
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
PS Claim 1: SEQ ID 6264; 44pp; English.
XX
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 18596 BP: 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
Query Match 0.1%; Score 26; DB 24; Length 18596;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21075 CTCTGTACAGCTGGCAGACAGCTC 21100
DB 13536 CTCTGTACAGCTGGCAGACAGCTC 13511
|||||
RESULT 39

ABL38559/C	ID	ABL38559 standard; cDNA: 535 BP.
xx	AC	ABL38559;
xx	DT	08-APR-2002 (first entry)
xx	DE	Human colon tumour antigen polynucleotide SEQ ID NO:2148.
xx	KW	Human; colon cancer; colon tumour antigen; cytostatic; vaccine;
xx	KW	colon tumour metastatic antigen; diagnosis; gene; ss.
xx	OS	Homo sapiens.
xx	WO	WO200196388-A2.
xx	PD	20-DEC-2001.
xx	PF	08-JUN-2001; 2001WO-US18557.
xx	PR	09-JUN-2000; 2000US-210899P.
xx	PR	20-FEB-2001; 2001US-270216P.
xx	PA	(CORI-) CORIXA CORP.
xx	PI	Jiang Y, Harlocker SL, Secretist H;
xx	DR	WPI; 2002-114514/15.
xx	PT	Novel isolated colon tumor polynucleotide differentially expressed in
xx	PT	colon tumor or colon metastatic tumor and polypeptides encoded by them,
xx	PT	useful for inhibiting development of cancer in patient -
xx	PS	Claim 1; SEQ ID 2148; 105pp; English.
xx	AB	ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)
xx	CC	which were isolated from human colon tumour and colon metastatic tumour
xx	CC	cDNA libraries. (I) have cytostatic activity and can be used in vaccine
xx	CC	production. (I) can be used for stimulating and/or expanding T cells
xx	CC	specific for a tumour protein on contact with the T cells. They are also
xx	CC	useful for inhibiting the development of cancer in a patient. (I) can be
xx	CC	used as probes or primers for nucleic acid hybridisation, for preparing
xx	CC	mutant species primers, or primers for use in genetic constructions. (I)
xx	CC	can be used in the diagnosis of a colon tumour.
xx	SQ	Sequence 535 BP; 135 A; 129 C; 151 G; 118 T; 2 other;
xx	QM	Query Match 0.1%; Score 24; DB 24; Length 535;
xx	QM	Best Local Similarity 100.0%; Pred. No. 24;
xx	QM	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	21442	TGATTAACACAGACACTCTCTCA 21465
DB	180	TGATTAACACAGACACTCTCTCA 157
RESULT 40		
AA584960	ID	AA584960 standard; cDNA: 1539 BP.
xx	AC	AA584960;
xx	DT	13-FEB-2002 (first entry)
xx	DE	DNA encoding novel human diagnostic protein #20764.
xx	KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
xx	KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.
xx	OS	Homo sapiens.
xx	WO	WO200175067-A2.
xx	PN	
xx	XX	

PD 11-OCT-2001.
PE 30-MAR-2001; 2001WO-US08631.
PR 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
PA (HYSE-) HYSEQ INC.
PI Drmenac RT, Liu C, Tang YT;
DR WPI: 2001-639362/73.
P-PsDB: ABG20773.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
PS Claim 1: SEQ ID No 20764; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPRO
CC at ftp.wipro.int/pub/published_pct_sequences.
XX
SQ Sequence 1539 BP; 396 A; 379 C; 347 G; 417 T; 0 other:

Query Match 0.1%; Score 24; DB 23; Length 1539;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21442 TGATTAACCAAGCAACTCTCCA 21465
XXXXXXXXXXXXXXXXXXXXX
DB 1263 TGATTAAACCACAGCAACTCTCCA 1286

RESULT 41
ABA09660
ID ABA09660 standard; DNA; 1692 BP.
XX
XX ABA09660;
DE
DT 15-JAN-2002 (first entry)
XX
XX Human bone marrow expressed oligonucleotide SEQ ID NO: 169.
Human bone marrow expressed oligonucleotide; antirheumatic; antiarthritic; vulnary;
antiinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
antiParkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
antileper; fungicide; antidabetic; antilasthmatic; antiallergic;
immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
XX
OS Homo sapiens.
XX

PN WO200174836-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10472.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PR 23-AUG-2000; 2000US-0649267.
 PR 30-NOV-2000; 2000US-250583P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
 XX
 DR WPI; 2001-626375/72.
 XX
 PT New bone marrow-expressed nucleic acids and polypeptides, useful for
 PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
 PT and increasing hematopoiesis, stem cell survival and bone growth and
 PT remodeling
 XX
 PS Claim 1; Page 249; 380pp; English.
 XX
 CC The present invention relates to bone marrow expressed polynucleotides
 CC and proteins. These sequences can be used in the treatment of
 CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
 CC and peripheral nervous system diseases and neuropathies, such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
 CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
 CC cell disorders, platelet disorders, stem cell disorders, bone
 CC degenerative disorders, autoimmune disorders, for example multiple
 CC sclerosis, diabetes and arthritis, viral and bacterial infections,
 CC allergies and blood coagulation disorders. The present sequence is a DNA
 CC of the invention.
 XX
 SQ Sequence 1692 BP; 467 A; 400 C; 410 G; 415 T; 0 other;
 XX
 Query Match 0.1%; Score 24; DB 22; Length 1692;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 21442 TGATAACGACGACCACTCTCCA 21465
 Db 1007 TGATAACGACGACCACTCTCCA 1030
 XX
 RESULT 42
 AAS84959
 ID AAS84959 standard; cDNA; 3422 BP.
 XX
 AC AAS84959;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #20763.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200175067-A2.
 PN
 PD 11-OCT-2001.
 PD
 PF 30-MAR-2001; 2001WO-US08631.
 PF
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PR
 PA (HYSE-) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG20772.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 1; SEQ ID NO 20763; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. A564197-A594564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 3422 BP; 1012 A; 780 C; 770 G; 860 T; 0 other;
 XX
 Query Match 0.1%; Score 24; DB 23; Length 3422;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 21442 TGATAACGACGACCACTCTCCA 21465
 Db 1655 TGATAACGACGACCACTCTCCA 1678
 XX
 RESULT 43
 AAV52595
 ID AAV52595 standard; DNA; 24 BP.
 XX
 AC AAV52595;
 XX
 DT 19-NOV-1998 (first entry)
 XX
 DE Primer HTS-2B, used to amplify Thymidylate synthase cDNA.
 XX
 KW Primer; amplification; PCR; thymidylate synthase; TS; HT1080; log phase;
 KW reverse transcription PCR; RT-PCR; mobility shift; SSCP;
 KW Single-Stranded Conformation Polymorphism; gene therapy; cancer;
 KW myelotoxicity; ss.
 XX
 OS Synthetic.
 OS
 PN Homo sapiens.
 PN
 PD WO9833518-A1.
 PD
 PF 06-AUG-1998.
 PF
 PR 03-FEB-1998; 98WO-US02145.
 PR 04-FEB-1997; 97US-0037163.
 PR
 PA (SLOAN) SLOAN KETTERING INST CANCER RES.
 XX

CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert in a
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNPs); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.

XX
SQ Sequence 542 BP; 336 A; 136 C; 64 G; 6 T; 0 other;

Query Match

0.1%; Score 23; DB 24; Length 542;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22550 AC CGCAACACCGCAAAAAAAGC 22572

DB 363 AC CGCAACACCGCAAAAAAAGC 385

Search completed: September 29, 2003, 12:41:21
Job time : 7652 secs


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FT /note="has similarity to KSHV ORF7"
FT 11515..14004
FT /tag= f
FT /product= "glycoprotein B"
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FT /note="has similarity to KSHV ORF8"
FT 14122..17166
FT /tag= g
FT /product= "DNA polymerase protein"
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FT /note="has similarity to KSHV ORF9"
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FT /tag= h
FT /label= RRV_ORF10
FT /note="has similarity to KSHV ORF10"
FT 18520..19749
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FT /note="has similarity to KSHV ORF11"
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Query Match 100.0%; Score 35101; DB 24; Length 128139;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 35101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ACCAATACAGTGAATTTATCAGCTAACCAACATTTAGGCGAATGTATACATG 120
DB 29380 ACCAATACAGTGAATTTATCAGCTAACCAACATTTAGGCGAATGTATACATG 29439

QY 121 TATGAATTTTAAACAATTAATTAAGCTCAGATTCCTGTGTTTATCCGAT 180
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QY 181 ATATTTGTCACATCATGTGTAAATGTAGAGATTCATATATATGATTAATCAATGCA 240
DB 29500 ATATTTGTCACATCATGTGTAAATGTAGAGATTCATATATGATTAATCAATGCA 29559

QY 241 AAGCCGATGACATCACCATATTTCCGGTGTGTTTCCGCTGTTTAAAGCTTAAAGCTT 300
DB 29560 AAGCCGATGACATCACCATATTTCCGGTGTGTTTCCGCTGTTTAAAGCTTAAAGCTT 29619

QY 301 GATTAGATGAACAAGCTACGATCGAGCAGCCGAGAGAGCTCAAAAAGAACCGGCTCG 360
DB 29620 GATTAGATGAACAAGCTACGATCGAGCAGCCGAGAGAGCTCAAAAAGAACCGGCTCG 29679

QY 361 GAATGCGACAAAGAGCGCTGTTTGGCGGCTGTGTCACGCTTTTACGCCACGCT 420
DB 29680 GAATGCGACAAAGAGCGCTGTTTGGCGGCTGTGTCACGCTTTTACGCCACGCT 29739

QY 421 ATTAAGAGTTTTCAGTCATTAATGTACAGAGCTGTCATGGAAGCAAGTAAACCGGCTG 480
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QY 721 GGACTACAGACATGATGATGATCAAAACCCACAGTTCAGCAACCTGTTTCCCG 780
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QY 841 GGTACGCTTGTGAATTTCCGGGATTTACAGAGACAGCAGTCTGATTTGCAATTA 900
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DB 30880 GACTGTACATTTGAATGCTGCTGCTGCGGTTGCTTGAAGATGATCGAAGTTTAA 30939

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2101 CAGAGTACTCGCGTTGGATAGTGCACACCGCCCGCCCACTAAGACACCTTAAAT 2160
Db CAGAGTACTCGCGTTGGATAGTGCACACCGCCCGCCCACTAAGACACCTTAAAT 31479
2161 GAGATTTTATCATGATTTTCTTGGTGTGATTCAGAACCGCAGCGGCTTGGCTCG 2220
Db GAGATTTTATCATGATTTTCTTGGTGTGATTCAGAACCGCAGCGGCTTGGCTCG 31539
2221 CGGTATATTTTGTCTTATGCTCGAGTGAAGTCCCAACGCTATATAGTGTGCAAT 2280
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3541 TTTACCTGATGATTTAGTCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 3600
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32860 TTTACCTGATGATTTAGTCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 32919
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Db ATTCTGATTAACACGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 33219
33160 ATTCTGATTAACACGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 33219
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Qy 13141 TATATGTCATTAATTTGGGCTTACAGAAACGCAATGCGAGTTTAAAGATTAAGTTTCG 13200
Dh 42460 TATATGTCATTAATTTGGGCTTACAGAAACGCAATGCGAGTTTAAAGATTAAGTTTCG 42519
Qy 13201 CAATGTACCATGATCCGCGCTGTGACGGTGTGAGCTTCACTTAACCGCTTTAAAAAGAGCG 13260
Dh 42520 CAATGTACCATGATCCGCGCTGTGACGGTGTGAGCTTCACTTAACCGCTTTAAAAAGAGCG 42579
Qy 13261 TTGGTATCACCGGACACTGCTACGCGACCCGTCGCGCGTGAACCTCTACAGATTTTG 13320
Dh 42580 TTGGTATCACCGGACACTGCTACGCGACCCGTCGCGCGTGAACCTCTACAGATTTTG 42639
Qy 13321 ACCGAGCTTTACAGTCTAGGATACGGGACGACTACGTGACACACACCCGTCGCTTGAA 13380
Dh 42640 ACCGAGCTTTACAGTCTAGGATACGGGACGACTACGTGACACACACCCGTCGCTTGAA 42699
Qy 13381 CGCCCAAGTATGTGAGGGGACAAATATGCCCCGACGCGACCGAGATGCCAAACGGA 13440
Dh 42700 CGCCCAAGTATGTGAGGGGACAAATATGCCCCGACGCGACCGAGATGCCAAACGGA 42759
Qy 13441 TCGCCAAAGTGTGAAGGCTTGAATTCGGGCTCCGCAACAAGCAACTATCCAAAGAGC 13500
Dh 42760 TCGCCAAAGTGTGAAGGCTTGAATTCGGGCTCCGCAACAAGCAACTATCCAAAGAGC 42819
Qy 13501 TGGGCGCAGGCGGCTGACGTTTTCTGCTTCGCGCATATTAAGTGTGCTATATGATTAAC 13560
Dh 42820 TGGGCGCAGGCGGCTGACGTTTTCTGCTTCGCGCATATTAAGTGTGCTATATGATTAAC 42879
Qy 13561 GAAGAACTAGATACCAAGTGTGACGCGCAAGATCCGCGCTTGCCCGTATGATGCTTC 13620
Dh 42880 GAAGAACTAGATACCAAGTGTGACGCGCAAGATCCGCGCTTGCCCGTATGATGCTTC 42939
Qy 13621 GATCCGCTGCGTACCTGTTAGAGGGGATTTGTTTTAGAGGCAAGCAATGCTTT 13680
Dh 42940 GATCCGCTGCGTACCTGTTAGAGGGGATTTGTTTTAGAGGCAAGCAATGCTTT 42999
Qy 13681 GTGATTTCTATAGAAAAAGACGTGAGGTGTAGAACTATACATTAAGCAATTTTTCCG 13740
Dh 43000 GTGATTTCTATAGAAAAAGACGTGAGGTGTAGAACTATACATTAAGCAATTTTTCCG 43059
Qy 13741 GTTTTGTAAATAGGCAACGAACAGTGTGACTTAATTAAGAGCATTTTATAGAGCG 13800
Dh 43060 GTTTTGTAAATAGGCAACGAACAGTGTGACTTAATTAAGAGCATTTTATAGAGCG 43119

Qy 13801 TGGTGTGATTAAGAAACAGGTGTGAGAGAGCGCTTGGTTAAAGCGCGCTGTTT 13860
Dh 43120 TGGTGTGATTAAGAAACAGGTGTGAGAGAGCGCTTGGTTAAAGCGCGCTGTTT 43179
Qy 13861 CGCAACGATATGATTAACGATTTTGAAGGATTTTGGGATTTATGAGACATGGGCTCAT 13920
Dh 43180 CGCAACGATATGATTAACGATTTTGAAGGATTTTGGGATTTATGAGACATGGGCTCAT 43239
Qy 13921 AAGCTGGGTACGGCTATTAACCAACTCGGAACCTTGGCAATGCCACGCTAACTGG 13980
Dh 43240 AAGCTGGGTACGGCTATTAACCAACTCGGAACCTTGGCAATGCCACGCTAACTGG 43299
Qy 13981 AGCTGGCTCTGTGTGACGAGATATTAATCTCGGCTAATTAAGCGGCGAGTCTACTGTTTC 14040
Dh 43300 AGCTGGCTCTGTGTGACGAGATATTAATCTCGGCTAATTAAGCGGCGAGTCTACTGTTTC 43359
Qy 14041 TTAGTTGTCTGCGCTACCCCTGACCGCGCTGGCTGCTCCCGGGGGCTTTGTTATTA 14100
Dh 43360 TTAGTTGTCTGCGCTACCCCTGACCGCGCTGGCTGCTCCCGGGGGCTTTGTTATTA 43419
Qy 14101 GGGCGCTACGACCTATCAACCGAGATTTATGTTTGTGGCTTGAGATATGGCCACCA 14160
Dh 43420 GGGCGCTACGACCTATCAACCGAGATTTATGTTTGTGGCTTGAGATATGGCCACCA 43479
Qy 14161 GCGTGTGACATTTCTTAATCGTTTAAACAAGAAATGCAATGTTGGGACACCCGG 14220
Dh 43480 GCGTGTGACATTTCTTAATCGTTTAAACAAGAAATGCAATGTTGGGACACCCGG 43539
Qy 14221 TACGTCCGCTTTGTTGCGGTATACACCGGACCACTGCGCATTTGCGCTTTTGACCC 14280
Dh 43540 TACGTCCGCTTTGTTGCGGTATACACCGGACCACTGCGCATTTGCGCTTTTGACCC 43599
Qy 14281 GCGGATTAACATGGAATATGATGTACTTAATTTTAAATGTTATGATCGTAATCAT 14340
Dh 43600 GCGGATTAACATGGAATATGATGTACTTAATTTTAAATGTTATGATCGTAATCAT 43659
Qy 14341 GAAACCAAAAGATTTGGCGCGTGTACCGTGTACATGAATGAGATATTCGTAATTT 14400
Dh 43660 GAAACCAAAAGATTTGGCGCGTGTACCGTGTACATGAATGAGATATTCGTAATTT 43719
Qy 14401 TTGTGCGACGAATCTGTGCGCATTAAGGACGTGCTGTTAGGGCGGACCTGTGTTTAA 14460
Dh 43720 TTGTGCGACGAATCTGTGCGCATTAAGGACGTGCTGTTAGGGCGGACCTGTGTTTAA 43779
Qy 14461 TCGTTTTGTGATCCCTTTCTAATGCGCGGAGAGCGTTCCGATACCCGGGCGCTTGAACC 14520
Dh 43780 TCGTTTTGTGATCCCTTTCTAATGCGCGGAGAGCGTTCCGATACCCGGGCGCTTGAACC 43839
Qy 14521 ACATCCGCGAAGAAACGCTGCGCGGCTTAACAAACAGAAATTAATATACACTTGGCAAC 14580
Dh 43840 ACATCCGCGAAGAAACGCTGCGCGGCTTAACAAACAGAAATTAATATACACTTGGCAAC 43899
Qy 14581 AGTGCCAAAGAGACAGATATACAGATGCCATTAAGGGGAAAGAGTTCCACCAAAATATCC 14640
Dh 43900 AGTGCCAAAGAGACAGATATACAGATGCCATTAAGGGGAAAGAGTTCCACCAAAATATCC 43959
Qy 14641 GTTTTGTGTTGTGACGAGGGGCTTTTGGCAACGTTTCTCTGTGTGAATTTATGCT 14700
Dh 43960 GTTTTGTGTTGTGACGAGGGGCTTTTGGCAACGTTTCTCTGTGTGAATTTATGCT 44019
Qy 14701 GCTCTGCTCCGCACTGACACAGTTCGCTCGTGGCAGAAATGTTGGGCTTCTTACACA 14760
Dh 44020 GCTCTGCTCCGCACTGACACAGTTCGCTCGTGGCAGAAATGTTGGGCTTCTTACACA 44079
Qy 14761 GTGCGATTAAGACAGCTGTAAATTTGTACGGGGGCCACGTAACCGTAATCCGTATGCG 14820
Dh 44080 GTGCGATTAAGACAGCTGTAAATTTGTACGGGGGCCACGTAACCGTAATCCGTATGCG 44139
Qy 14821 CGGATACAGCCCACTGTACGTGCAAGGAGCTCAACCTGTGCCCCCTTATCTGCTG 14880
Dh 44140 CGGATACAGCCCACTGTACGTGCAAGGAGCTCAACCTGTGCCCCCTTATCTGCTG 44199

OY	14881	CGGGGCGGACGGGCGGCGGATGTCGCGGTTTACCGACACGTTAACTCTTTGGGCGTGT	14940
Db	44200	CGGGGCGGACGGGCGGCGGATGTCGCGGTTTACCGACACGTTAACTCTTTGGGCGTGT	44259
OY	14941	CTTTGACCCCAAAAGCCTCCGCCCAAAGTGACCAAGCTGCCTTTAAAAAGAAACCAACGGCC	15000
Db	44260	CTTTGACCCCAAAAGCCTCCGCCCAAAGTGACCAAGCTGCCTTTAAAAAGAAACCAACGGCC	44319
OY	15001	GGTACCGATTAGAGAGCGCCATGTGCGGCGTCACGGCCGAAGGAGCCGAGGTGCMAACCAAC	15060
Db	44320	GGTACCGATTAGAGAGCGCCATGTGCGGCGTCACGGCCGAAGGAGCCGAGGTGCMAACCAAC	44379
OY	15061	TTGCGCTACCGTGGGGCCCTCATTCGCGCGTGGCGGATTTAAGCAGTCGGGTGATGCTATACGG	15120
Db	44380	TTGCGCTACCGTGGGGCCCTCATTCGCGCGTGGCGGATTTAAGCAGTCGGGTGATGCTATACGG	44439
OY	15121	CTGCGCAGAACTTAAAAAGCATCTGCTTACGTTCTTTATTAAGACAGCTCGCACACATCAAC	15180
Db	44440	CTGCGCAGAACTTAAAAAGCATCTGCTTACGTTCTTTATTAAGACAGCTCGCACACATCAAC	44499
OY	15181	GAACTCGGCGCGCGTCGCGGCGTCGCGTACAGATGTTCCGTTTTCTTTATGTTC	15240
Db	44500	GAACTCGGCGCGCGTCGCGGCGTCGCGTACAGATGTTCCGTTTTCTTTATGTTC	44559
OY	15241	AGGTTTCTGCGGAAAAACCAACCTGGAATAGCGTGGGCGATACCTCGGAGAAACGGCATTTG	15300
Db	44560	AGGTTTCTGCGGAAAAACCAACCTGGAATAGCGTGGGCGATACCTCGGAGAAACGGCATTTG	44619
OY	15301	GCGACGTTTGTGTGGGCGACGTAACCCACGTAAGACGTTTTCACACGACAGAGAAGA	15360
Db	44620	GCGACGTTTGTGTGGGCGACGTAACCCACGTAAGACGTTTTCACACGACAGAGAAGA	44679
OY	15361	ACGCTGATTAATGGCGACACAGATCCATGTTTTCCGCTGACGACGGGGGTAAACAAAACG	15420
Db	44680	ACGCTGATTAATGGCGACACAGATCCATGTTTTCCGCTGACGACGGGGGTAAACAAAACG	44739
OY	15421	CTGGCTTCTGCGTTAAACGTCGTAAACAGTGTGTCGCGTGTGTTCAATTAACCAAAAGGT	15480
Db	44740	CTGGCTTCTGCGTTAAACGTCGTAAACAGTGTGTCGCGTGTGTTCAATTAACCAAAAGGT	44799
OY	15481	TGCTTAAACGTGGCAAAATAACGTGCTGTCCTTTCCGGTGCCTTGTATAGCCGATTAATA	15540
Db	44800	TGCTTAAACGTGGCAAAATAACGTGCTGTCCTTTCCGGTGCCTTGTATAGCCGATTAATA	44859
OY	15541	TAAACGTGTGCATGATTAATTGTTTGAAGGGCTCAAGCCAAACAAACCCGGGGACG	15600
Db	44860	TAAACGTGTGCATGATTAATTGTTTGAAGGGCTCAAGCCAAACAAACCCGGGGACG	44919
OY	15601	TAACTCCCATTTAAAAATGACGACAGGTGGCTTAAAAACTGCGGACGTTCTGCATTAACG	15660
Db	44920	TAACTCCCATTTAAAAATGACGACAGGTGGCTTAAAAACTGCGGACGTTCTGCATTAACG	44979
OY	15661	GGGCACTCTAGGAACCTTCGTGGGTGCGCTTGGGCGGATTTGGTATTCATGACTGATCC	15720
Db	44980	GGGCACTCTAGGAACCTTCGTGGGTGCGCTTGGGCGGATTTGGTATTCATGACTGATCC	45039
OY	15721	TTGGCGTTTCCCATTTTGAACCCGACAACTGTTTGTAAAGTAGTTGTGAGTTCCTCG	15780
Db	45040	TTGGCGTTTCCCATTTTGAACCCGACAACTGTTTGTAAAGTAGTTGTGAGTTCCTCG	45099
OY	15781	GTTAAACGGGGCAAGCTAGCGTGGCTAGAGAAATTCGGGGCTTCCCAACGTAAGGGCCGGC	15840
Db	45100	GTTAAACGGGGCAAGCTAGCGTGGCTAGAGAAATTCGGGGCTTCCCAACGTAAGGGCCGGC	45159
OY	15841	ATGGGTTCTTGAACCTGCGGGAATAGCTTGAACATATATCTTAAAAACGAATATATATGCA	15900
Db	45160	ATGGGTTCTTGAACCTGCGGGAATAGCTTGAACATATATCTTAAAAACGAATATATATGCA	45219
OY	15901	TTTAACCGCGGATTAATCTCCCAAGCATGCGGTGGGCGATTCGTCGCTGTGTCGCTTGGCC	15960
Db	45220	TTTAACCGCGGATTAATCTCCCAAGCATGCGGTGGGCGATTCGTCGCTGTGTCGCTTGGCC	45279
OY	15961	GATATATATACGGGGCGGTTGCCGAAACAGTTTTCGCAACACCGCTCCGTGACCAACGGC	16020

Db	45280	GATATATAATACGGGGGGGTTGCCGAACCGTTTGGCAACACCGTCCGTGACACGGCC	45339
QY	16021	AAAGTATATTTGAAAGACGTTCCGGATAGCTGTTAAACAATGTCCTTCAAGTTTTTGTG	16080
Db	45340	AAGTTATTTTGAAGACGTTCCGGATAGCTGTTAAACAATGTCCTTCAAGTTTTTGTG	45399
QY	16081	AATAACGGGACCCCGGAAACGACACGGCGCTTCGTTAAAGCGTTCAGTTACTTTAGAC	16140
Db	45400	AATAACGGGACCCCGGAAACGACACGGCGCTTCGTTAAAGCGTTCAGTTACTTTAGAC	45459
QY	16141	CTGTGTGAACAACACCTCCGGGACAGTTTAAACAGTTGAAACACCTCTTAATAGTTTTCTT	16200
Db	45460	CTGTGTGAACAACACCTCCGGGACAGTTTAAACAGTTGAAACACCTCTTAATAGTTTTCTT	45519
QY	16201	CTGTATCCAAACGTTCTCGCGGAATCGCGCCCGGTTAGAGACTGTCGCAAGCCGGAAGGG	16260
Db	45520	CTGTATCCAAACGTTCTCGCGGAATCGCGCCCGGTTAGAGACTGTCGCAAGCCGGAAGGG	45579
QY	16261	TTTGCATTTGAACACATTCACCTCCCAAACTTAACACGATCAGCGTCTCTGGGGCGA	16320
Db	45580	TTTGCATTTGAACACATTCACCTCCCAAACTTAACACGATCAGCGTCTCTGGGGCGA	45639
QY	16321	TACCTCGACACATGTTAAACAGACGACACGCTCGTTAAGCTAAAGGCAAGTCTCCGAAAT	16380
Db	45640	TACCTCGACACATGTTAAACAGACGACACGCTCGTTAAGCTAAAGGCAAGTCTCCGAAAT	45699
QY	16381	TCACAGGGTGCCCTTGTATTATCTGCCGATATGACACAGGACGAATGTGAGGCGCTCACG	16440
Db	45700	TCACAGGGTGCCCTTGTATTATCTGCCGATATGACACAGGACGAATGTGAGGCGCTCACG	45759
QY	16441	TTAAGGAAAGACACAGTGTGTTAAATGCGCTGTAGAGGGCTTGTCAAATCCCAACACTGTG	16500
Db	45760	TTAAGGAAAGACACAGTGTGTTAAATGCGCTGTAGAGGGCTTGTCAAATCCCAACACTGTG	45819
QY	16501	AAAGGTTAGAGCCCGTGAGATCCTTTACCGCTCAATATGAGGCTCTGTTTACAGTCCCGG	16560
Db	45820	AAAGGTTAGAGCCCGTGAGATCCTTTACCGCTCAATATGAGGCTCTGTTTACAGTCCCGG	45879
QY	16561	TCGTTCTGTCCGGGAACAGAGTGCCTATATGAACGCAATTTTGGTATGAAGGACCCATA	16620
Db	45880	TCGTTCTGTCCGGGAACAGAGTGCCTATATGAACGCAATTTTGGTATGAAGGACCCATA	45939
QY	16621	CTCTTACCGCCACATATGATGATGCCCCCAAAAGACGTAATGACTTTTGTCCATCATGTA	16680
Db	45940	CTCTTACCGCCACATATGATGATGCCCCCAAAAGACGTAATGACTTTTGTCCATCATGTA	45999
QY	16681	ATTAGTAGTGTTAAATTTTATATAGCTGAACGCGGTGGGGGCTTGAAACATCAACCGTCC	16740
Db	46000	ATTAGTAGTGTTAAATTTTATATAGCTGAACGCGGTGGGGGCTTGAAACATCAACCGTCC	46039
QY	16741	CCGCGGTTCCGAGGCGCTCGCGGTTGGGCGCACAGCCATCGCTCGTCCGGGGACGTGGAAGG	16800
Db	46060	CCGCGGTTCCGAGGCGCTCGCGGTTGGGCGCACAGCCATCGCTCGTCCGGGGACGTGGAAGG	46119
QY	16801	GATGACGATACCTGTCTCCGCAAGTGATGTTGTGTCACTGTACACCAACCAACGATACG	16860
Db	46120	GATGACGATACCTGTCTCCGCAAGTGATGTTGTGTCACTGTACACCAACCAACGATACG	46179
QY	16861	ATTTCGATTCATGAAACACACGTGGGGGAGTCAATCGCATTTAAGCGGAGACGCTCCGAGA	16920
Db	46180	ATTTCGATTCATGAAACACACGTGGGGGAGTCAATCGCATTTAAGCGGAGACGCTCCGAGA	46239
QY	16921	TATATTAACGTCTAGTGTCCGGGCTTAACGGGTGCACGAGTCCGGGGAGATTTTGTTTAATC	16980
Db	46240	TATATTAACGTCTAGTGTCCGGGCTTAACGGGTGCACGAGTCCGGGGAGATTTTGTTTAATC	46299
QY	16981	CCCGCTGTACAACATTGAAGGGCTGTAGACATGATTAAGGGAACATGCGCTCGGACGACGC	17040
Db	46300	CCCGCTGTACAACATTGAAGGGCTGTAGACATGATTAAGGGAACATGCGCTCGGACGACGC	46359
QY	17041	TAAAAAAATGTTAATTAATGCGAGCTCGAGTCGGAATCAACAAAAACTGTCCATCTC	17100

Db	46360	TAATAAAATCTTAATTAAAGTCGAGAGCTCGAGTCGGAATATCAACAAAAAATCTCATCTC	46413
Oy	17101	CGTAATTTGACAGGTTTTGGGGCCGACAGTCCCGTGTTTAAACGGCAGATAAAGGAACAG	17160
Db	46420	CGTATTTGACAGGTTTGGGGCCGACAGTCCCGTGTTTAAACGGCAGTAAAGGAACAG	46479
Oy	17161	GGAAATCGCTCGGCTCGTACAAACGCTAAAAAAGAAGACGATTCGGGACCGCTGTGG	17220
Db	46480	GGAAATCGCTCGGCTCGTACAAACGCTAAAAAAGAAGACGATTCGGGACCGCTGTGG	46539
Oy	17221	AACGCTGAACACGTCGCTGCTGAATAAACAAAGCGAATTGGGATTTACTAAAGGGGTTTAA	17280
Db	46540	AACGCTGAACACGTCGCTGCTGCTGAATAAACAAAGCGAATTGGGATTTACTAAAGGGGTTTAA	46599
Oy	17281	CAGAAAAAAATTTGAAGAGTTTGACGCTGTGGCGGACGGCGTTCGCGACTCAAGACGA	17340
Db	46600	CAGAAAAAAATTTGAAGAGTTTGACGCTGTGGCGGACGGCGTTCGCGACTCAAGACGA	46659
Oy	17341	GCTGTACGGGAACGTGAGATTTTAGGTACGCTTGACAAATGAAATCTGTTCCCGTGAAGA	17400
Db	46660	GCTGTACGGGAACGTGAGATTTTAGGTACGCTTGACAAATGAAATCTGTTCCCGTGAAGA	46719
Oy	17401	AGAGTCCCCCAAGSAGAGACATTTTAAAGTGGAAATTGAGCGCTGCGCCAGAGTGTGGC	17460
Db	46720	AGAGTCCCCCAAGSAGAGACATTTTAAAGTGGAAATTGAGCGCTGCGCCAGAGTGTGGC	46779
Oy	17461	CAAAAGCCCTTGATGCCATTTCCCAAGGTTCCAGACTACGCTCGACAGAACAGCATGTGCC	17520
Db	46780	CAAAAGCCCTTGATGCCATTTCCCAAGGTTCCAGACTACGCTCGACAGAACAGCATGTGCC	46839
Oy	17521	ATATTAACCGTCATTTAAACACGTAAGAGATGCCCCACTGAAAGATACCTAACAACTGGG	17580
Db	46840	ATATTAACCGTCATTTAAACACGTAAGAGATGCCCCACTGAAAGATACCTAACAACTGGG	46899
Oy	17581	GCCAGGTATCTACACAGCGSAGCAGCATGGAACCGCGCTGCTCGGACGGGCTGTATGTGG	17640
Db	46900	GCCAGGTATCTACACAGCGSAGCAGCATGGAACCGCGCTGCTCGGACGGGCTGTATGTGG	46959
Oy	17641	TGGTAGAGTCCATGTACTCTGCGCGCTGGGTTAAGCATTTTGGACGCCGCTGAGTTT	17700
Db	46960	TGGTAGAGTCCATGTACTCTCTGCGCGCTGGGTTAAGCATTTTGGACGCCGCTGAGTTT	47019
Oy	17701	TTTACGAGTGCATTTTTTAAACGATATAGTACGCGCTGCCGGGAGAAACATCCCTGAACC	17760
Db	47020	TTTACGAGTGCATTTTTTAAACGATATAGTACGCGCTGCCGGGAGAAACATCCCTGAACC	47079
Oy	17761	GCGGGGGTGACCTATATCTATATGTTTCCCTAGAGACCGCTGCTACCATGTGCGCGCTGATAT	17820
Db	47080	GCGGGGGTGACCTATATCTATATGTTTCCCTAGAGACCGCTGCTACCATGTGCGCGCTGATAT	47139
Oy	17821	TCCGCGAGTTAAACAGGGAATCTGCTAAACCGCGGATTTTAAACACGGAACCCCTGAAGGC	17880
Db	47140	TCCGCGAGTTAAACAGGGAATCTGCTAAACCGCGGATTTTAAACACGGAACCCCTGAAGGC	47199
Oy	17881	TGGCGGTTGAATTTCTCTGAGACTGAGGGAAGCGGTAGTTTCTAAATAATATATGTGCA	17940
Db	47200	TGGCGGTTGAATTTCTCTGAGACTGAGGGAAGCGGTAGTTTCTAAATAATATATGTGCA	47259
Oy	17941	TCGTTACCTGTGACATCAGTCCGAAAAATATACTGATTAAGGGGGAACCTGACAACTGGT	18000
Db	47260	TCGTTACCTGTGACATCAGTCCGAAAAATATACTGATTAAGGGGGAACCTGACAACTGGT	47319
Oy	18001	ACGGGAGACTTATGATCGAGATCTAAGGGTCGCGCTTTTAAACAGGGGAACCCCTTGA	18060
Db	47320	ACGGGAGACTTATGATCGAGATCTAAGGGTCGCGCTTTTAAACAGGGGAACCCCTTGA	47379
Oy	18061	CCGGAGTGAATGTAACCTCCAAACCTCGGGTTGCTGACGACACAGTACATTTTAAAGCAC	18120
Db	47380	CCGGAGTGAATGTAACCTCCAAACCTCGGGTTGCTGACGACACAGTACATTTTAAAGCAC	47439
Oy	18121	CGGCGAGATTTATCTGTAAAGACATTTACCGGCGCTGTCTCTCTTAACGGGTGTGGC	18180
Db	47440	CGGCGAGATTTATCTGTAAAGACATTTACCGGCGCTGTCTCTCTCTTAACGGGTGTGGC	47499

QY	18181	IGTGTGGGGGGGGGGGGGGGAGGCGGATATGCTTAATCAGCGCTTCCAAATCATTCCAC	18240
Db	47500	TGTGTGGGGGGGGGGGGGGGAGGCGATATGCTTAATCAGCGCTTCCAAATCATTCCAC	47559
QY	18241	AACCTGGCTCCAAATGTAGATATGATGCTCCCTGGGTTATAGTTGGTACATGCTTAGA	18300
Db	47560	AACCTGGCTCCAAATGTAGATATGATGCTCCCTGGGTTATAGTTGGTACATGCTTAGA	47619
QY	18301	AATATCTTCAGCCAGCTGACCATTTTCCACAGAGGAGCGTTGGCGAGCGTTCCTCG	18360
Db	47620	AATATCTTCAGCCAGCTGACCATTTTCCACAGAGGAGCGTTGGCGAGCGTTCCTCG	47679
QY	18361	AATCGGCCACCCATTTGTTCTATTGGCGTTGATGTTGGCCAGAGATGATCAGCCGAGA	18420
Db	47680	AATCGGCCACCCATTTGTTCTATTGGCGTTGATGTTGGCCAGAGATGATCAGCCGAGA	47739
QY	18421	TTTTTCTGTGTGCTGGGAGCTTCCACTCGATTTAGCCATTCATCTGCGCACGGCG	18480
Db	47740	TTTTTCTGTGTGCTGGGAGCTTCCACTCGATTTAGCCATTCATCTGCGCACGGCG	47799
QY	18481	CAGCATTTCCCTGAGAGAGGGTACAGCGGGTTTTTCCCAACCACTGATGTTATTAA	18540
Db	47800	CAGCATTTCCCTGAGAGAGGGTACAGCGGGTTTTTCCCAACCACTGATGTTATTAA	47859
QY	18541	GGGGCCAAATACAAAGAGATGGGTTAGAAAAGCATCTCTGGGGGCTGTAACTCAAAAC	18600
Db	47860	GGGGCCAAATACAAAGAGATGGGTTAGAAAAGCATCTCTGGGGGCTGTAACTCAAAAC	47919
QY	18601	TTAAACTAGTTCTCCAGAAAGCTGTTGGTACGGACTACTTTAGTATTGCGGAAACTGG	18660
Db	47920	TTAAACTAGTTCTCCAGAAAGCTGTTGGTACGGACTACTTTAGTATTGCGGAAACTGG	47979
QY	18661	GAGATCATGAGATTTTTTCTCAGATGAGCGGATGGTTCAGAGATGGCGGCTTCGCATTC	18720
Db	47980	GAGATCATGAGATTTTTTCTCAGATGAGCGGATGGTTCAGAGATGGCGGCTTCGCATTC	48039
QY	18721	GATGAGCAGCAGCGGCTCCTCTCGAAAATGAGCTTGGCCACTTTTAAACATGAGCA	18780
Db	48040	GATGAGCAGCAGCGGCTCCTCTCGAAAATGAGCTTGGCCACTTTTAAACATGAGCA	48099
QY	18781	GTAAGGGGGTTTTTATAGCGATTAACAAAAGAAATAGATGCCGGCTATAGCGTTCGAG	18840
Db	48100	GTAAGGGGGTTTTTATAGCGATTAACAAAAGAAATAGATGCCGGCTATAGCGTTCGAG	48159
QY	18841	TATAATTTTTATCTATCTCGCCAGGAGGGAGATTTTTATCGGCAACACCGACGTATCGAT	18900
Db	48160	TATAATTTTTATCTATCTCGCCAGGAGGGAGATTTTTATCGGCAACACCGACGTATCGAT	48219
QY	18901	TTTTTACGTACTTGGCTGTTCAAGGGGAGGGCGCTGACCGGCTGTGCGAAGTGTACGAC	18960
Db	48220	TTTTTACGTACTTGGCTGTTCAAGGGGAGGGCGCTGACCGGCTGTGCGAAGTGTACGAC	48279
QY	18961	GGGTGCTTAAACATGACACCGGAGCATGCAACACAGTGTGTGATTTGATAGAACAGGTC	19020
Db	48280	GGGTGCTTAAACATGACACCGGAGCATGCAACACAGTGTGTGATTTGATAGAACAGGTC	48339
QY	19021	ACGGCGGCCCAAAACATCATCTCTGTGTGGAGCGCTGTGAGGAGCGCATTAATTCGTGC	19080
Db	48340	ACGGCGGCCCAAAACATCATCTCTGTGTGGAGCGCTGTGAGGAGCGCATTAATTCGTGC	48399
QY	19081	TCAAAATTTTCACTGGGCCATTAACCAACAGAAATGCTCCAAAAAAATTTTAAACCGGTGG	19140
Db	48400	TCAAAATTTTCACTGGGCCATTAACCAACAGAAATGCTCCAAAAAAATTTTAAACCGGTGG	48459
QY	19141	CCTATAGTCAACAATCACTTTGTAGACGGGCCGCTCGCTTGTGGACTGTGCGAGGAA	19200
Db	48460	CCTATAGTCAACAATCACTTTGTAGACGGGCCGCTCGCTTGTGGACTGTGCGAGGAA	48519
QY	19201	GTGGTAAAAAGATATCTGGCGACGTTGCTGCATCCAGCGGAGCGCAGCTGTGAAAACTTAC	19260
Db	48520	GTGGTAAAAAGATATCTGGCGACGTTGCTGCATCCAGCGGAGCGCAGCTGTGAAAACTTAC	48579

OY	19261	GGATTTCATGCAGAGATCCTCTCCAAACGGGGTTTGTGGCGTCTCCTTGATTTTGGAAATTAAC	193220
Dd	48580	GGATTTCATGCAGAGATCCTCTCCAAACGGGGTTTGTGGCGTCTCCTTGATTTTGGAAATTAAC	486399
OY	19321	GTCAGGCTCAGACCCAAAGACGGTTTGGAGTTTCAACCAGACGCAAAATCTATGAATA	193801
Dd	48640	GTCAGGCTCAGACCCAAAGACGGTTTGGAGTTTCAACCAGACGCAAAATCTATGAATA	486999
OY	19381	AAATGCCGGTTTAAAGTACACTTTTCCAAAGATGAGTGTACCCGATTTACGCTGCGTAT	194401
Dd	48700	AAATGCCGGTTTAAAGTACACTTTTCCAAAGATGAGTGTACCCGATTTACGCTGCGTAT	487599
OY	19441	GCTAACTTTTATCAGAAAGCCCGACATGACAGCCTTAAGGGTTTTGTACTTCATATCT	195000
Dd	48760	GCTAACTTTTATCAGAAAGCCCGACATGACAGCCTTAAGGGTTTTGTACTTCATATCT	488199
OY	19501	AAACGGCGAGATCGAGTTTGTCCGAGAGAGACAGGCTCCCGAGTAAACGGAGTATCTGTGG	195600
Dd	48820	AAACGGCGAGATCGAGTTTGTCCGAGAGAGACAGGCTCCCGAGTAAACGGAGTATCTGTGG	488799
OY	19561	GCATATGACAAAGAAATGGAGGTGTGTCCGCGGAAAAAGAGACGCTTAACGTCAGTACAC	196200
Dd	48880	GCATATGACAAAGAAATGGAGGTGTGTCCGCGGAAAAAGAGACGCTTAACGTCAGTACAC	489399
OY	19621	CATCTACTTTAAAAAGTGCATGATTCACAACTCTACGGCGCCTTGTGATGTATATTTG	196800
Dd	48940	CATCTACTTTAAAAAGTGCATGATTCACAACTCTACGGCGCCTTGTGATGTATATTTG	489999
OY	19681	TCAGATCCGGAGAGAAACCGGAGGSCCAAATTAATTAAGGTCATGTGAGGSCCAACCTA	197400
Dd	49000	TCAGATCCGGAGAGAAACCGGAGGSCCAAATTAATTAAGGTCATGTGAGGSCCAACCTA	490599
OY	19741	TTTATTAACGTCAGAGCATCCGATTTATATCAAGTGTGCTCCAGTCTCTCCTGTATACG	198000
Dd	49060	TTTATTAACGTCAGAGCATCCGATTTATATCAAGTGTGCTCCAGTCTCTCCTGTATACG	491199
OY	19801	GAGTACATTCAGTCTCTTCCAAAGGGAACCTAAAAATTTGGGAACCCAGAAAACTTTATAGG	198600
Dd	49120	GAGTACATTCAGTCTCTTCCAAAGGGAACCTAAAAATTTGGGAACCCAGAAAACTTTATAGG	491799
OY	19861	ACTGGCTTTTATGAAAAAGGCGAGTTTCAAGACCCGAGGTGCGGCGACGATCGGTAAATTT	199200
Dd	49180	ACTGGCTTTTATGAAAAAGGCGAGTTTCAAGACCCGAGGTGCGGCGACGATCGGTAAATTT	492399
OY	19921	GCCCCGTTGGATCCACACGTAGAGATACGACCCCTTTAATGCTGTGACACCGGCTGATATTT	199800
Dd	49240	GCCCCGTTGGATCCACACGTAGAGATACGACCCCTTTAATGCTGTGACACCGGCTGATATTT	492999
OY	19981	CCCAAGCCTGGCCAAACCAACCACTGTGTGAAGCAGGCGACCGAATTTGGCGCGCTATGCT	200400
Dd	49300	CCCAAGCCTGGCCAAACCAACCACTGTGTGAAGCAGGCGACCGAATTTGGCGCGCTATGCT	493599
OY	20041	CGTGAAGCATTTTCCCGAGCTACCATGAGGAAATTAACCTCTCTGTGTGCAAAAGCCCGACCA	201000
Dd	49360	CGTGAAGCATTTTCCCGAGCTACCATGAGGAAATTAACCTCTCTGTGTGCAAAAGCCCGACCA	494199
OY	20101	ACACCGTAGATGTGAAGGGGGAGCCCATAGATGTATCCAAAGAAATTCGATCTATTTATAG	201600
Dd	49420	ACACCGTAGATGTGAAGGGGGAGCCCATAGATGTATCCAAAGAAATTCGATCTATTTATAG	494799
OY	20161	GAGAGAAAGCAATTTGTCTTGTTTAAGCGCGAGATGGGACTGCCCGCGGCGGCTGTACAAC	202200
Dd	49480	GAGAGAAAGCAATTTGTCTTGTTTAAGCGCGAGATGGGACTGCCCGCGGCGGCTGTACAAC	495399
OY	20221	CCAAACCCAGCCATCCAAACATAAAAACAATTAATGTGCAATTTTGTTTAAGCATTCG	202800
Dd	49540	CCAAACCCAGCCATCCAAACATAAAAACAATTAATGTGCAATTTTGTTTAAGCATTCG	495999
OY	20281	TATCTTTATTTGAGATGGGGGTGATGTGTGGGGTTTGGAAAGGAATGGGATTTGAGGGGAG	203400
Dd	49600	TATCTTTATTTGAGATGGGGGTGATGTGTGGGGTTTGGAAAGGAATGGGATTTGAGGGGAG	496599
OY	20341	GATGAATGCTAGAAATCATATGTATTTTGGATATGCATCTCTGTATGCTACGCTCTCTC	204000

[illegible]

Db 50740 CATAGTCGAAGATAACAGTACTGTTTAAACCAGATAGATAAAGATGAGTCCG 50799
Qy 21481 TGAATTTTCATAGTTCAAGAAATCTGCTCGCGGGTGGCTTGGGCAATAGCATAAA 21540
Db 50800 TGAATTTTCATAGTTCAAGAAATCTGCTCGCGGGTGGCTTGGGCAATAGCATAAA 50859
Qy 21541 TCAGCAAGTGGCTTACATGTTACAGGATTTAAATAGGCTCCGCTTTTAAATATCACATTC 21600
Db 50860 TCAGCAAGTGGCTTACATGTTACAGGATTTAAATAGGCTCCGCTTTTAAATATCACATTC 50919
Qy 21601 GTGCAAGAGTGTGGCCAGCGCAGCAATGAACGCCCGGGAGGTGGCACTCAGCGGACATG 21660
Db 50920 GTGCAAGAGTGTGGCCAGCGCAGCAATGAACGCCCGGGAGGTGGCACTCAGCGGACATG 50979
Qy 21661 TTTTGCACATATCCGTGCATAGCAGCAGCAGCGGAGAAATTAATTAATCTGGCAGTTC 21720
Db 50980 TTTTGCACATATCCGTGCATAGCAGCAGCAGCGGAGAAATTAATTAATCTGGCAGTTC 51039
Qy 21721 ATTTACTGTTATGTCACAAATGCGGAATTCAGGGAGATGCGCATATCTATTTGTCACCG 21780
Db 51040 ATTTACTGTTATGTCACAAATGCGGAATTCAGGGAGATGCGCATATCTATTTGTCACCG 51099
Qy 21781 AAACATTAAAGCAATCTAGTGGGGAATATACGGCGATAAACCGTACAGCAGCTGCA 21840
Db 51100 AAACATTAAAGCAATCTAGTGGGGAATATACGGCGATAAACCGTACAGCAGCTGCA 51159
Qy 21841 TAAATGAGCAGCGCGCTAATATATATGAGTGGGAATCCGTACTGTTAGGGAATCCCA 21900
Db 51160 TAAATGAGCAGCGCGCTAATATATATGAGTGGGAATCCGTACTGTTAGGGAATCCCA 51219
Qy 21901 TCATTCATTTGTTAAAGTCCGAGCGCGGTGCGGTTAACGTAAAGGTCAGCGAGCGGAAT 21960
Db 51220 TCATTCATTTGTTAAAGTCCGAGCGCGGTGCGGTTAACGTAAAGGTCAGCGAGCGGAAT 51279
Qy 21961 TGGTAATGTTGGGGTGGGGAAGAGAGGTGAGTACATCGTGGTGGCGGAGTGGAG 22020
Db 51280 TGGTAATGTTGGGGTGGGGAAGAGAGGTGAGTACATCGTGGTGGCGGAGTGGAG 51339
Qy 22021 CCTATCTTCATTTGGCATACACTATGAGCTTATGTTGATTTGTTGTCGCCAACCC 22080
Db 51340 CCTATCTTCATTTGGCATACACTATGAGCTTATGTTGATTTGTTGTCGCCAACCC 51399
Qy 22081 GCGAATTTTGGTTCTCAGAGATGTTTCTCAGCTGTTTACGTTTCAACATTTGAATTTACC 22140
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Db 51460 TTAACAAACAGGGGGGTTATATCTATAGGGATGAGGCAAGCGAATGCGGAAAGAG 51519
Qy 22201 CGAAGATGGGCAATTTGGGTATCTTGTATATCTTAAATTTGGGAATCTGTGAATATCAAG 22260
Db 51520 CGAAGATGGGCAATTTGGGTATCTTGTATATCTTAAATTTGGGAATCTGTGAATATCAAG 51579
Qy 22261 TTGGCGGGCAGAGTACACCTTGTAGTATGCGCACCGCAACATTTACGTTCTCTGGGTGG 22320
Db 51580 TTGGCGGGCAGAGTACACCTTGTAGTATGCGCACCGCAACATTTACGTTCTCTGGGTGG 51639
Qy 22321 ACGAGGCGTGTATGGAAGAGGGGGCCGCGCGAATTTTAAAGGCGGTGACATATAGT 22380
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Db 51820 GAAAGCGCGAAGGCTGACAGTAAACGGGCGTCCAGAACTCCCAAAAGACAAATTTGGG 51879

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Db 52840 GAGGCACTATGTGTTTTTATGTTGTGTCACAGCGGAGGATACGAGAGTCAAGCGGA 52899
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Dh 55180 GCTGCACACCGCGCAACGGGTCTTCAGGGTGGTCTCGAAGTTGGTCCAGTCCCTTAAGA 55239
Qy 25921 CGTTGTCGTATGTGCACGTCCCAATGCGCTTGTGTACAGGTGTATGAACAGCTGTCTTC 25980
Dh 55240 CGTTGTCGTATGTGCACGTCCCAATGCGCTTGTGTACAGGTGTATGAACAGCTGTCTTC 55299
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Dh 55720 TCTGTCCAGCATCTTACGAGCTTTTGGCTTTAAGACCGCAGCATCAATATATACCGTCA 55779
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Dh 55840 AGTATTTGGCGGTATATGTGACATTTATGAAGAAGGTTATGGCGCAAAACCCCAATGCGA 55899
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Dh 56140 CAACCTTACAAACAGGAGCGCAAAAGAGATATGCTGCTGCGAGAAACAATCTTAACAT 56199
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Qy 27241 ACAAGGGGGCGTCAACCTCACCAACCTCACCGGACCGAGTGGGTGACAAAACCTCT 27300
Dh 56560 ACAAGGGGGCGTCAACCTCACCAACCTCACCGGACCGAGTGGGTGACAAAACCTCT 56619
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Dh 56740 CTTTAAATGGAAGAAAAACAAAATGATGTGGGTTCAGGGGACGTACTTGAATTCGA 56799
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OY 28141 AGGAGGAGCGTTTTCAGAGTGTGCTGTCGGGGGACTATGGGTCACCTCAAAATTAG 28200
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OY 28921 GCCCTCTGCGGTTGATCTAGATATATACCTGACAGGCGGGGAGGCGCCGCGGGA 28980
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OY 29101 CCGGAGACACCAACACGGGATGATGGGCGGGCGGCTCGGTGTGTGGTGGCACCTGT 29160
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OY 29281 GTGCTGTCTCCGATGAGATGATCGGTTTCTGCTGGCCCTTTTGGATAGTGGAGGGGA 29340
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OY 29401 GGGCGGTACCGGCAACCCCGTACGGGACCGGCGGAACAAAAACGTCCTGTTCTTTT 29460
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OY 29461 CCTAGGTGCCCCGGGATGGGAGATCCTGGGAGTGGCGGGGCTTGAGCGGTG 29520
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OY 29521 GGATTAAGAACATAGCCATGGCCGGAACGTTACCTGTAAAGACGACTGCTATCCCGAT 29580
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OY 29581 CAGTTATATTTTCAGTCAACGCGACCCCTCCGATTTCTGACATAGATATGTCACAGT 29640
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OY 29641 TTAATAATGTTGACGCTTGAAGTACGCGGACGAGGAACCGGTTGGCGCGGGGTA 29700
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OY 29701 GCCAGGGAGAGAGATGGCGCCCTTGAGAGACAGATGTCTGTCCGTTATACAGCTG 29760
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OY 29761 GCCTGTCTATAGCCTTTTCTCCCAACAGATATATATATATATATATATATATAT 29820
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OY 29821 AGGAGCTTATATAGTGTGATGAACCAATCCAGGCAAGGTTGAGGTCAGCCCGCC 29880
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OY 29881 TTCCCTCTTTCACCGCTCAGATGTTTAAAGCAGAACTCCCGTTTGCCCAACAG 29940
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59200 TTCCCTCTTTCACCGCTCAGATGTTTAAAGCAGAACTCCCGTTTGCCCAACAG 59259
OY 29941 TCTAAGCACCCGTGAGAGAGAGCGGTGAACCCAGGTATAGTATGCTATCTTTAA 30000
|||||
59260 TCTAAGCACCCGTGAGAGAGAGCGGTGAACCCAGGTATAGTATGCTATCTTTAA 59319
OY 30001 ATATTTTGAAGCTTGAAGATATGATGTGTCGAGAGCAACCTTAAAGGCTAGTCCGGTG 30060
|||||
59320 ATATTTTGAAGCTTGAAGATATGATGTGTCGAGAGCAACCTTAAAGGCTAGTCCGGTG 59379
OY 30061 GCTTACCGCGATGTGTAAGATCTGAGCAAGATCAGACATTAATATCTCCGTTGCG 30120
|||||
59380 GCTTACCGCGATGTGTAAGATCTGAGCAAGATCAGACATTAATATCTCCGTTGCG 59439
OY 30121 CAACATACGACACACATATATTTATCTATGCTGTGATATACAGGTTACGTTGCTC 30180
|||||
59440 CAACATACGACACACATATATTTATCTATGCTGTGATATACAGGTTACGTTGCTC 59499
OY 30181 ATATCCATACGCGGTTACGACGAGACCGGACCTCTGTTTAAATAGGAAGATTT 30240
|||||

Db 5950 ATATCCATAAGCGCTTCAGACAGCCGCAAGCTTCTGTTTAAATAATGAGAAAGATTT 59559
Qy 30241 AAAAATTCAGCCATGAGTCGCTAAGTAGCAAGCTTTGTGTGAGGGTCTTCTAACAAT 30300
Db 59560 AAAAATTCAGCCATGAGTCGCTAAGTAGCAAGCTTTGTGTGAGGGTCTTCTAACAAT 59619
Qy 30301 TCTGTGTGACATTTTACTTCCAAACTATTGTTTAAAGCCAAACCCCTCCATTAATCCCGCGTC 30360
Db 59620 TCTGTGTGACATTTTACTTCCAAACTATTGTTTAAAGCCAAACCCCTCCATTAATCCCGCGTC 59679
Qy 30361 TGGTAATTTACTTACGTATAGCTGAACCTTTGTACTCTGTGTGAGAAATTCACAGAG 30420
Db 59680 TGGTAATTTACTTACGTATAGCTGAACCTTTGTACTCTGTGTGAGAAATTCACAGAG 59739
Qy 30421 GTGGCCGCGTATAGCAGTTCCGCTTCACTACCGTTATGTGAAAGTCTTCAACACGCG 30480
Db 59740 GTGGCCGCGTATAGCAGTTCCGCTTCACTACCGTTATGTGAAAGTCTTCAACACGCG 59799
Qy 30481 CTAAAACTCATCAAGACTATATGCAATTAATTCACAAATGGAAGCTCTCTGGGGA 30540
Db 59800 CTAAAACTCATCAAGACTATATGCAATTAATTCACAAATGGAAGCTCTCTGGGGA 59859
Qy 30541 CACTGTATTTAACTTGTACAAAACTCTATAAAAAGCCCTAAGGTGAATTCATTTA 30600
Db 59860 CACTGTATTTAACTTGTACAAAACTCTATAAAAAGCCCTAAGGTGAATTCATTTA 59919
Qy 30601 CACATATTTCTGTGTAGAGCAGTATCAGCTTATATCGCAATGTGTGTACACAGCCCTG 30660
Db 59920 CACATATTTCTGTGTAGAGCAGTATCAGCTTATATCGCAATGTGTGTACACAGCCCTG 59979
Qy 30661 GACATTAAGCTAAATTTGTTAAATGAAAGAGCAATCTCAACGGCTCCGGAAATATA 30720
Db 59980 GACATTAAGCTAAATTTGTTAAATGAAAGAGCAATCTCAACGGCTCCGGAAATATA 60039
Qy 30721 AGTCACATAGGTGATATTTTACAAATGATTTTACTACAGCCGCTTCAACATATA 30780
Db 60040 AGTCACATAGGTGATATTTTACAAATGATTTTACTACAGCCGCTTCAACATATA 60099
Qy 30781 TTAATAAATAATCCACATGATATTAATTAATTAAGGTATACATCTCTCATGTGTTATA 30840
Db 60100 TTAATAAATAATCCACATGATATTAATTAATTAAGGTATACATCTCTCATGTGTTATA 60159
Qy 30841 CATTAATATGAAAGCTTAATGCTGTATATATATATATATAGAAATTAATGCAATACAGTC 30900
Db 60160 CATTAATATGAAAGCTTAATGCTGTATATATATATATATAGAAATTAATGCAATACAGTC 60219
Qy 30901 ATGGTAGTATATTTTAAAGCATATGCAAAACATTAATATTAACAAAAATGCAGC 30960
Db 60220 ATGGTAGTATATTTTAAAGCATATGCAAAACATTAATATTAACAAAAATGCAGC 60279
Qy 30961 TTCCGATATCCGCCAGCTGTTAACCCGAAATATACGAATGACTACACAAACACACT 31020
Db 60280 TTCCGATATCCGCCAGCTGTTAACCCGAAATATACGAATGACTACACAAACACACT 60339
Qy 31021 GAAACCAATTTTATCTCAACATATGCAACAAATATTTTCAAGGTAAACCATGTTAATAA 31080
Db 60340 GAAACCAATTTTATCTCAACATATGCAACAAATATTTTCAAGGTAAACCATGTTAATAA 60399
Qy 31081 ATACGAGCATGACATTTTAACTAGCTATGCTTCAAGAGACATTTCTCTCATTTATG 31140
Db 60400 ATACGAGCATGACATTTTAACTAGCTATGCTTCAAGAGACATTTCTCTCATTTATG 60459
Qy 31141 ACATCATCAACCTGCGTTTCCGTGTATATGTCGAAATATATGATCCAGATACCTCTGCT 31200
Db 60460 ACATCATCAACCTGCGTTTCCGTGTATATGTCGAAATATATGATCCAGATACCTCTGCT 60519
Qy 31201 CATCGCACAATAATTAATTCAGGCGTTGTAATAATATCATCAAGTATCAAGCTCTATG 31260
Db 60520 CATCGCACAATAATTAATTCAGGCGTTGTAATAATATCATCAAGTATCAAGCTCTATG 60579
Qy 31261 TCAGAGATGTTGTTTCTAATTTTAAAGCCATTCAAATGATGAGTGGTGAACATTTGGAC 31320
Db 60580 TCAGAGATGTTGTTTCTAATTTTAAAGCCATTCAAATGATGAGTGGTGAACATTTGGAC 60639

Qy 31321 AAGACCCCGTAAATTTGGCAGCTCCACACAAACGGAAGGATGATTTGATCGTTCAGA 31380
Db 60640 AAGACCCCGTAAATTTGGCAGCTCCACACAAACGGAAGGATGATTTGATCGTTCAGA 60699
Qy 31381 GGGGACGATATTTATTTTATTAACATCAGAAACCGGACCCGTCATGACGACATATGT 31440
Db 60700 GGGGACGATATTTATTTTATTAACATCAGAAACCGGACCCGTCATGACGACATATGT 60759
Qy 31441 CCAATTAAGATTTGGAGTGTGACACATGTTGAATTTGAGCGTGAATAAATATGATTCGT 31500
Db 60760 CCAATTAAGATTTGGAGTGTGACACATGTTGAATTTGAGCGTGAATAAATATGATTCGT 60819
Qy 31501 CACATGCGTAACTATTTTAAACACAGAGGCGGAATTAACAGGGTCCCGCGCTAA 31560
Db 60820 CACATGCGTAACTATTTTAAACACAGAGGCGGAATTAACAGGGTCCCGCGCTAA 60879
Qy 31561 GGGCGTGAATGCGGACGACAGGCTCATTTCCATTTCCAGATTTGTTAAATCTGTTGAA 31620
Db 60880 GGGCGTGAATGCGGACGACAGGCTCATTTCCATTTCCAGATTTGTTAAATCTGTTGAA 60939
Qy 31621 CATACGATCTAAATTAAGTATTAACAGAGCAAGTTCAACAGAGCAACGGCGCTGG 31680
Db 60940 CATACGATCTAAATTAAGTATTAACAGAGCAAGTTCAACAGAGCAACGGCGCTGG 60999
Qy 31681 TTTCCACCCGAGATCCCGCTCACAACCCGAACTCTTAGAAACGACATCAAAAGCT 31740
Db 61000 TTTCCACCCGAGATCCCGCTCACAACCCGAACTCTTAGAAACGACATCAAAAGCT 61059
Qy 31741 TCAGACAAATTCGGAACCCGAAACCTAGTCTGAGACACCATCTGTTAATACTCGG 31800
Db 61060 TCAGACAAATTCGGAACCCGAAACCTAGTCTGAGACACCATCTGTTAATACTCGG 61119
Qy 31801 TTTAAGAGAGAGGGGCCACACAGTGTGTGAGAGATTCAGTTTGTGAGGCGCTGAGG 31860
Db 61120 TTTAAGAGAGAGGGGCCACACAGTGTGTGAGAGATTCAGTTTGTGAGGCGCTGAGG 61179
Qy 31861 CTTGCTGACAGGCCCGTAGTGTGCTGCGGCGCTCGGCAACCTTTGACAGCCGACCA 31920
Db 61180 CTTGCTGACAGGCCCGTAGTGTGCTGCGGCGCTCGGCAACCTTTGACAGCCGACCA 61239
Qy 31921 GTTCAGAGCGAGGACAGAACGCTCTTTCAGAGTGGCCCATATCTCGGCCATAGAGATT 31980
Db 61240 GTTCAGAGCGAGGACAGAACGCTCTTTCAGAGTGGCCCATATCTCGGCCATAGAGATT 61299
Qy 31981 CGCTCGGATCTTTTAAAGGATATATCTGTTGGGTAACAAACCTCACCTCCGTA 32040
Db 61300 CGCTCGGATCTTTTAAAGGATATATCTGTTGGGTAACAAACCTCACCTCCGTA 61359
Qy 32041 AAAGGGGAATTAAGTCCGCTCTTCTATGCTTTTCTGATCTATAGTTACATCTTTAA 32100
Db 61360 AAAGGGGAATTAAGTCCGCTCTTCTATGCTTTTCTGATCTATAGTTACATCTTTAA 61419
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Db 61420 GTATTAACCAAGAGCGTAAAAACCCAGATGTCGACACCTTTAAAAATTCGCAAAAGCG 61479
Qy 32161 ACGGATGAGCTATCCGCGTTCCATGTCGTTCAAGGTAAGTACAGATGGATCCAGT 32220
Db 61480 ACGGATGAGCTATCCGCGTTCCATGTCGTTCAAGGTAAGTACAGATGGATCCAGT 61539
Qy 32221 TAGACTCTGCTCCCTTTAAACACCTTAATCTGGAATGGAAGAGCCATGACACCTGAA 32280
Db 61540 TAGACTCTGCTCCCTTTAAACACCTTAATCTGGAATGGAAGAGCCATGACACCTGAA 61599
Qy 32281 CTTCTGATGTCCTTAAATTAACCCGGAACAGACTTAATTAACATGATCTGACCC 32340
Db 61600 CTTCTGATGTCCTTAAATTAACCCGGAACAGACTTAATTAACATGATCTGACCC 61659
Qy 32341 CTACCCCAAGCAGCGCCCGCTACTATTTAACCAGGCTGATACCGCTATCTTTAA 32400
Db 61660 CTACCCCAAGCAGCGCCCGCTACTATTTAACCAGGCTGATACCGCTATCTTTAA 61719

32401 AACCACATCGTGGATTTGTAGAGTAACACAGCTCGTATATTTACAGACGCTGTCATA 32460
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Db 61720 AACCACATCGTGGATTTGTAGAGTAACACAGCTCGTATATTTACAGACGCTGTCATA 61779
32461 AATGGATCCGACGACATCAGTATTAACCTTTTATTTCAAGATTCAGAGAGCG 32520
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Db 61780 AATGGATCCGACGACATCAGTATTAACCTTTTATTTCAAGATTCAGAGAGCG 61839
32521 TGTTTACAGTGTGTAGTGGAGCATATCTGCCAATGGGAATGGCTGATGAATCCACA 32580
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Db 61840 TGTTTACAGTGTGTAGTGGAGCATATCTGCCAATGGGAATGGCTGATGAATCCACA 61899
32581 CTTAGGCTCGGATAGAGTGTGTGTGTCTTACTAGTGGCGAATGAACCTAAATTTGGC 32640
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Db 61900 CTTAGGCTCGGATAGAGTGTGTGTGTCTTACTAGTGGCGAATGAACCTAAATTTGGC 61959
32641 GTGTTAGTGTGTACCAACCAAAAACTCGGCTCGCTCTTTTGAAGCTCTATGCAA 32700
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Db 61960 GTGTTAGTGTGTACCAACCAAAAACTCGGCTCGCTCTTTTGAAGCTCTATGCAA 62019
32701 GCTTTATCGTGTCCAAATAGCTTGTCTTTAAAAATGCAACTGTGTATCTTTATGACA 32760
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Db 62020 GCTTTATCGTGTCCAAATAGCTTGTCTTTAAAAATGCAACTGTGTATCTTTATGACA 62079
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Db 62080 GTGTGTCCAAAAAACAAGATTTAAAAACAGTTAACTGGGTGCTGTAGTCCGAGTCCG 62139
32821 TATATTAACCTCTCAACAAGAAAAATTTTAAACCAACTCGCAGTACTGAAACGAT 32880
|||||
Db 62140 TATATTAACCTCTCAACAAGAAAAATTTTAAACCAACTCGCAGTACTGAAACGAT 62199
32881 GGTAGGAGACAGTGTGAAAAAGTGTCTATCATCTCTTACCTCCCTTTGAAGTTTGG 32940
|||||
Db 62200 GGTAGGAGACAGTGTGAAAAAGTGTCTATCATCTCTTACCTCCCTTTGAAGTTTGG 62259
32941 GTTACACGACCATGTGATAGGACACAGCTCAGGGGGAGGTGCGATCGAGAGGGGT 33000
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Db 62260 GTTACACGACCATGTGATAGGACACAGCTCAGGGGGAGGTGCGATCGAGAGGGGT 62319
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62320 AACCAATCGTGGCGGTGGGGGTACTCTCAGTTTATAGGATCTCGGAGAGGACGGCTAG 62379
33061 TCTTGTCAAAATCTACGACGCGCATCCACAGGGGAGTACTGATTAATAGTCCC 33120
62380 TCTTGTCAAAATCTACGACGCGCATCCACAGGGGAGTACTGATTAATAGTCCC 62439
33121 CGAATTCATCTGTGTATTTTGTGAGAGCTCTTTAGACAGTAAACATGTTGGTCGA 33180
62440 CGAATTCATCTGTGTATTTTGTGAGAGCTCTTTAGACAGTAAACATGTTGGTCGA 62499
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62560 GACAGATATAGGCCCCGTTCACCTCTAAGGGTTGCCGTGTGTAGACGCGATTTGGGGCA 62619
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33361 TACATATGATTTAAAAAGATGTCTTCCGTAATGGCGACTATGTCGTTTAAAGCT 33420
62680 TACATATGATTTAAAAAGATGTCTTCCGTAATGGCGACTATGTCGTTTAAAGCT 62739
33421 TCACAGGGGTAAAAAACTGAAAGTCTGCGTGAGACACTTTTGGGACTCTCCGAA 33480
62740 TCACAGGGGTAAAAAACTGAAAGTCTGCGTGAGACACTTTTGGGACTCTCCGAA 62799
33481 CCGCTCAGAGGATTAACCTGTACACGCGGTGCTTCTTATAAAGAAAGCATACTCAAAAA 33540

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Db 62800 CCGCTCAGGAGATTAAGCTGTACACGCGGTGCTTCTTATTAACGAAGCATACTCAAAAA 62859
33541 CATGACCCAGTGTACTTAATAATAGCTCACAGAAAGAGTCTGTGATGTATTTAGGAA 33600
62860 CATGACCCAGTGTACTTAATAATAGCTCACAGAAAGAGTCTGTGATGTATTTAGGAA 62919
33601 TGTGCTCCCTGGGTCCCATCTCCGGGCTCATCGCGGATCTGAATCTTTTAACTGTTT 33660
62920 TGTGCTCCCTGGGTCCCATCTCCGGGCTCATCGCGGATCTGAATCTTTTAACTGTTT 62979
33661 TGCCTCTACCGGGGTTCCCGGGTTAAAAACCGCGGGGCCGACCTGTAACTCCCGTGC 33720
62980 TGCCTCTACCGGGGTTCCCGGGTTAAAAACCGCGGGGCCGACCTGTAACTCCCGTGC 63039
33721 GCAGAAATGCGCCAGGAGCATCTGAGAAATTCACAGAGAGGCCCTTGTGTACCGAA 33780
63040 GCAGAAATGCGCCAGGAGCATCTGAGAAATTCACAGAGAGGCCCTTGTGTACCGAA 63099
33781 AAGATGTATATAGCTGTGCTGTGACAGCGGGGTCTTATACGCCCATGTTGGCAGAGTT 33840
63100 AAGATGTATATAGCTGTGCTGTGACAGCGGGGTCTTATACGCCCATGTTGGCAGAGTT 63159
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63160 CTGCACGACGCTACGCGGAAATGAAGGCAAGTGTGGGGGCGTGGCGTCTCATTA 63219
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33961 GATGCCAGAGGAAATGGAACCTTAGACATCAAGCAAGCAAGTGAACCTGTTTCAACC 34020
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34081 GACAAATATTTTACATCACCGGTAACGCGGAGGAAAGGCGCTGTGCTGATGAAAT 34140
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63700 ATGACACGATGGAAGAGCGGTGCACAGAGCATTTACACAGACAGAGCGCTATTTTGG 63759
34441 GCCGCCGACTAACCGGTTGCAATCTGCGGCGCTTGGCGCGCATGCGATGTTTCCCA 34500
63760 GCCGCCGACTAACCGGTTGCAATCTGCGGCGCTTGGCGCGCATGCGATGTTTCCCA 63819
34501 GTTGGCGGACGCTCTCCGAGGTGGAAGGTTCCGGGGGCGTGTGATTTGGGGAACACAGA 34560
63820 GTTGGCGGACGCTCTCCGAGGTGGAAGGTTCCGGGGGCGTGTGATTTGGGGAACACAGA 63879
34561 TGCCTTCGACGCGCGCTTACCGGCCAATGTCGCCGCAAGAGATGAAACGGTATACA 34620

Dh 63880 TGGCTTCCGAGCCCCGGCTTACCGCCCAATGTCCCGCCCAAGAGATGAAACGGTAGCA 63939
Qy 34621 CAGTTGGGAAGAGCTCCCGTAAAGAAAGCTGCACATCGAGAGCCGCGTATACGCTCACTG 34680
Dh 63940 CAGTTGGGAAGAGCTCCCGTAAAGAAAGCTGCACATCGAGAGCCGCGTATACGCTCACTG 63939
Qy 34681 GTTAATATACCAATTAATAGACTTAACGTCCTCCGTCAGAGTCCGGCCAGAGTCCGGCCGAT 34740
Dh 64000 GTTAATATACCAATTAATAGACTTAACGTCCTCCGTCAGAGTCCGGCCAGAGTCCGGCCGAT 64059
Qy 34741 ATGGCCAACTCAGAGTCCCGCATGCGCGGCTCTCCGCTTCCGCGGAACCGCC 34800
Dh 64060 ATGGCCAACTCAGAGTCCCGCATGCGCGGCTCTCCGCTTCCGCGGAACCGCC 64119
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Dh 64120 GCAACGTCCTCCGTCAGAGAAAGCAGCAGCGAGAGCGTGGCAGACAAAGACTGAG 64179
Qy 34861 GGGGAGCTTGGGGCGCGGCAACAGTAACACCTTTCCCGGAGCCGTCGGGATGCGC 34920
Dh 64180 GGGGAGCTTGGGGCGCGGCAACAGTAACACCTTTCCCGGAGCCGTCGGGATGCGC 64239
Qy 34921 GTTCGCGAGAGGGCTTATTCGATTTATGAAAGCTCCAGAGTATTAACCGGCAACGCA 34980
Dh 64240 GTTCGCGAGAGGGCTTATTCGATTTATGAAAGCTCCAGAGTATTAACCGGCAACGCA 64299
Qy 34981 TCTGAGACCCAAAGAGCAGCAGCATGCTAGCGGCTTATTCGAGAGCTGTATGACTA 35040
Dh 64300 TCTGAGACCCAAAGAGCAGCAGCATGCTAGCGGCTTATTCGAGAGCTGTATGACTA 64359
Qy 35041 CAGTCCCGCCCGGCGATGATTCCTCCCGCAGCACTCGGAGCAATGAGAGATATTTCGA 35100
Dh 64360 CAGTCCCGCCCGGCGATGATTCCTCCCGCAGCACTCGGAGCAATGAGAGATATTTCGA 64419
Qy 35101 G 35101
Dh 64420 G 64420

RESULT 2

AAC64754
ID AAC64754 standard; DNA: 133719 BP.

AC AAC64754;

DT 28-FEB-2001 (first entry)

DE Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1.

XX Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
KM genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;
IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
KM cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
KM lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
KM splenomegaly; hypergammaglobulinemia; autoimmune haemolytic anaemia;
ds.

XX Macaca mulatta rhadinovirus 17577.

XX W0200028040-42.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-US26260.

XX 06-NOV-1998; 98US-0107507.

XX 20-NOV-1998; 98US-0109409.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Wong SM, Axthelm MK, Searles RP;

XX WPI: 2000-376552/32.

XX New rhesus rhadino virus for producing non-human primate model useful
PT for testing potential treatments and efficacy of the candidate vaccine
PT for conditions associated with RRV infection -
PS Claim 2; Page 83-122; 141pp; English.

XX The present invention describes a novel rhesus macaque rhadinovirus
CC called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
CC RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
CC encoded by the genome sequence. The present invention also specifically
CC claims the individual open reading frame (ORF) nucleotide sequences from
CC the genome which encode the individual proteins, but these sequences are
CC not given. A non-human animal infected with RRV can be used for testing
CC the efficacy of drug in the treatment of condition associated with
CC infection with RRV such as Kaposi's sarcoma, lymphoproliferative
CC disorder, B-cell hyperplasia, lymphadenopathy, splenomegaly,
CC hypergammaglobulinemia or autoimmune hemolytic anaemia, by
CC administering the drug to a immuno-compromised non-human primate
CC preferably Rhesus macaque monkey obtained by as a result of infection
CC by Simian immunodeficiency Virus (SIV). RRV is useful for producing
CC non-human primate model for testing potential treatments for conditions
CC associated with RRV infection. It is also useful for testing the
CC efficacy of the candidate vaccine against RRV infection or conditions
CC associated with its infection by administering the vaccine to the
CC subject capable of infection with RRV, inoculating the subject with RRV
CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
CC to AAB53213 represent sequence used in the exemplification of the
CC present invention.

XX SQ Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;

XX Query Match 86.6%; Score 30381; DB 21; Length 133719;

XX Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

XX Matches 35101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCTAAGGTGGTGSTAAATTTCTAAGCAAAATTTATATATTAATTAATACATGAC 60
Dh 34900 ACACCTAAGGTGGTGSTAAATTTCTAAGCAAAATTTATATATTAATTAATACATGAC 34959
Qy 61 ACCAAATACAGTGAATTTATCAGCTAACCAACATTTAGCGGATGTAATACATG 120
Dh 34960 ACCAAATACAGTGAATTTATCAGCTAACCAACATTTAGCGGATGTAATACATG 35019
Qy 121 TATGAAGTTTAAACAAATTAATTAATTAAGCTCAGATTCCTGTTTATCCGTAT 180
Dh 35020 TATGAAGTTTAAACAAATTAATTAATTAAGCTCAGATTCCTGTTTATCCGTAT 35079
Qy 181 ATATTGTTCACTCATGTGTATATATGATAGATATCATATATGATTAATCAATGCA 240
Dh 35080 ATATTGTTCACTCATGTGTATATATGATAGATATCATATATGATTAATCAATGCA 35139
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Dh 35140 AAGCCCATGACATCACCATATTTCCGCTGTTTCCGCTGTTTATTAAGCTTAAGTTT 35199
Qy 301 GATTAGATGAAGAAACAGATACGATCCGAGCAGCAGCAGATCAAAAGAACGGCTCG 360
Dh 35200 GATTAGATGAAGAAACAGATACGATCCGAGCAGCAGCAGATCAAAAGAACGGCTCG 35259
Qy 361 GAACCTGCACAAAGAGGCTGTGTTTGGCGGCTGTGTCACGCTTTCACGCCAGCGCT 420
Dh 35260 GAACCTGCACAAAGAGGCTGTGTTTGGCGGCTGTGTCACGCTTTCACGCCAGCGCT 35319
Qy 421 ATAACGAGTTTTCAGTCATTAATTTGACAGAGTGGCATGGAAGCAAGTAACGCCCTG 480
Dh 35320 ATAACGAGTTTTCAGTCATTAATTTGACAGAGTGGCATGGAAGCAAGTAACGCCCTG 35379
Qy 481 ATGCCGCTTACGAACATCAGTACATTAAGCTCCGTGCGCCCTGATCAAGCTCGGCTT 540
Dh 35380 ATGCCGCTTACGAACATCAGTACATTAAGCTCCGTGCGCCCTGATCAAGCTCGGCTT 35439
Qy 541 TACGAGGTTTCGAGAGTGTCTTAAACAGCGCGATGTTGTCTCGCGCTTATCAAAAT 600


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Db 35440 TACGAGTTTCGAGGTGTTCTTACACGCGAGTTGTCTCGCCGCTTAATCCAAAT 35499
QY 601 TGTTCATTTTACACCGCCGGTACCGCCCTACACATCCGATATTGTATAACTTTCC 660
|||||
Db 35500 TGTTCATTTTACACCGCCGGTACCGCCCTACACATCCGATATTGTATAACTTTCC 35559
QY 661 GCGCCGAGATATAGATGTCCGCTGTGTATTTGATTGTTTGAAGCTATGATGAAACAG 720
35560 GCGCCGAGATATAGATGTCCGCTGTGTATTTGATTGTTTGAAGCTATGATGAAACAG 35619
Db 721 GGACTACAGACCATGATGTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 780
35620 GGACTACAGACCATGATGTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 35679
QY 781 TATTCCTCTTTTGTACACAGATATTTTCATATCCATTTATTTGTGTATTAAGCAAC 840
|||||
Db 35680 TATTCCTCTTTTGTACACAGATATTTTCATATCCATTTATTTGTGTATTAAGCAAC 35739
QY 841 GGTACCGTGTGGAATTTGGGGATTTGTACAGAACACGCACTAGTCTATGCAATTA 900
|||||
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QY 901 GATTTCCTTTTATTGGAACAATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 960
35800 GATTTCCTTTTATTGGAACAATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 35859
QY 961 CTGGCCTAAACTGTTAATTAACGTAATAAACTTTAAAGGTTGTCCCTTTCTTTTGG 1020
35860 CTGGCCTAAACTGTTAATTAACGTAATAAACTTTAAAGGTTGTCCCTTTCTTTTGG 35919
Db 1021 ATGGTTACCGGGGAGCTGAGATTAGCGAGAACCTCGGATAGAGCGTGGCCGTACATAT 1080
QY 35920 ATGGTTACCGGGGAGCTGAGATTAGCGAGAACCTCGGATAGAGCGTGGCCGTACATAT 35979
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35980 GATTCATACACCTCGCGCACTGGAATGGCAGCTCGATTTTGGGAGAGAAACAT 36039
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36040 AAAAAATATTTGTCGGTCCGGTTAATAATCGCTCGAGAGCCGCGACAAACCTGAA 36099
Db 1201 TCCCTCTGAAATCGTGGGACCTATGAGGTTTAAACAAACACCATGCTTCCAGGCGC 1260
QY 36100 TCCCTCTGAAATCGTGGGACCTATGAGGTTTAAACAAACACCATGCTTCCAGGCGC 36159
Db 1261 TGTTTTACGCGGAGAGCATGATTCGAAGTATCTCTGTATACGGGCGCGCCGCTTA 1320
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QY 1321 CACGATTTGCGGTATAGCATTTTAAAGTGAAACAGAAATATTTCCAAACCCAAAGCTGC 1380
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QY 36460 GACTGTACATTTGACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36519
Db 1621 TTATCCGCGGAGGCGCTCATTAAGGCGGTGCGGATTTGATGCTGATTTCTTGCGTG 1680
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QY 1681 GTGTTTCCAGCTCGTTATGTTATCTGTTTATTTGTAAGGTTACCGGTGGGCTC 1740
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36640 TTGACGCTGCCGGGACGGAATAATGGCTTCGAGTGTCAAAAAAAGAGATTACTCCGATTC 36699
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36700 ACTAATTTTGAATTAACGTAATGTTGTCGCTCAAGATGCAACTTCTAATTTACTGGG 36759
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36760 TCTGTGAACATGATACGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36819
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Db 2461 GATGGCTTTTGAAGTCAACAGTACCAAGCGGCGGCGGCTCAGGGCTCCAGATC 2520
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.Db	38740	ATTGATGATAACAGCTGCCGATCAAGTGTTCGGCAGTGTGCGCGTAAAGCAGCAAAACA	3879
QY	3901	TTCCGCAAGTTCCTCAATATTTAGGTAAACGACAGAGATTCGAAACAATGGCTTGATATTT	3960
Db	38800	TTCTCTGATTTCCCAATTTTAAAGGTAAACGACAGAGATTCGAAACAATGGCTTGATATTT	3885
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Db	38980	GATATGGGAAATGTACATCCGATACATCAATCAATTAATTAACCGCGTCCCGGTACTC	3903
QY	4141	GTTACCGGCTTTGGCAACGATACCAACCTTGGCGGTGTATAAAGGTATAGTCCCTCTCC	4200
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QY	4201	CAATACACAGACCGCGGAGCGGACGCGTAAAGGTGTCTCTTTGGCATAGCCCT	4260
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QY	4441	GGTACGACCTTCATATATTTAGGCGACGAGGCAATCTGTTGCTCAATAGAAAGATC	4500
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QY	4621	TCTGGAAACGTGCGTACGCGGTTCGGGTAAACACGAGTTTAAAGACCTCAACGAAT	4680
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QY	4741	GCGGGCCCAAAACAAAAACAATATTCATATCATGAAGGCGTCAATAGCATTCATATTTGG	4800
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QY	4801	TGCGGAGATAGAGCTGTGCACTGATGATAGACTGCTATTCATTACACAGAAACCC	4860
Db	39700	TGCGGAGATAGAGCTGTGCACTGATGATAGACTGCTATTCATTACACAGAAACCC	3975
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Db	39760	ACTGATATTACACAGAAATACGCGGGGGCGTAAACAGATTAACCGGCTCTCCAGTTTGG	3981
QY	4921	CGTGGACCGCTGTGAGAGGGGCTGTGATATACCGTATTTGAATTTAAAGTTAGTTAGTTCGGC	4980

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Db 44320 GTTCTATATTTAACTCTGGCCCGCAGATTTACGTTTACGCTTCTCATCGACAGAA 44379
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Db 44500 ACACGAGACGACAGAGCGATGATTTATACCTTAAGACCAACCTTAAGCAAGAGC 44559
OY 9661 GCGCGACGTTGTTAAGAGGCTTTGATACGAAACCCAGTGGACATTTGAAGCAAA 9720
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OY 9781 ATTTTATTTGAGTACGCTGTGCTTGTCTCTCTCTCTACTTGGCAGTTAAACCGTACA 9840
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Db 44800 TACCCGACCCGCTATTTGCGGTAGGTTGTGGGGCAGAGCGCATCTGAAGACTGTA 44859
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Db 45100 TGTGTGCAACGATTCATGAAAAAACTCTGTGCGCCCACTGGAATGATTAATTAACA 45159
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OY 10321 TAGTGTCTTAATGATGATGATGAGAAACATTAACGATTTCCAGACGACTTCAATGACGTT 10380
Db 45220 TAGTGTCTTAATGATGATGATGAGAAACATTAACGATTTCCAGACGACTTCAATGACGTT 45279
OY 10381 GTTTTATTTGCTGTGAAGTATTAACGATTAATGGAGGTTCCGCTGGTGGCTTAAG 10440
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QY	15961	GATATTAATAACGGGGGGTTGGCCAAACAGTTTTCGCAACACGCGTCCGTGACACGGCC	16020
Db	50860	GATATTAATAACGGGGGGTTGGCCAAACAGTTTTCGCAACACGCGTCCGTGACACGGCC	50919
QY	16021	AAGTTATTTTGAAGAGCTTCGCGATAGCTGGTTAACACATCTTCCCTTCAAGTTTCTTG	16080
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QY	16081	AATPAACGGGACCCCGGAACGGAACGCGCTTCGTTAAAGGCGTTCACTTACCTTTAGAC	16140
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QY	16201	CTGGTATCCAAACGTTCTGGCCGAATCGCCCGGTTAGAGACTGTCCGACGCGGAAGG	16260
Db	51100	CTGGTATCCAAACGTTCTGGCCGAATCGCCCGGTTAGAGACTGTCCGACGCGGAAGG	51159
QY	16261	TTTGTACTTTGACACATTCACCTCCCAAACTPAACAGCATCAGCGTCTCTGGGGCGA	16320
Db	51160	TTTGTACTTTGACACATTCACCTCCCAAACTPAACAGCATCAGCGTCTCTGGGGCGA	51219
QY	16321	TACGGCAGCATGTPTTAAACAGACGACAGCTGGTTAACTPAAGGCAAGTTCCTCGAT	16380
Db	51220	TACGGCAGCATGTPTTAAACAGACGACAGCTGGTTAACTPAAGGCAAGTTCCTCGAT	51279
QY	16381	TCACAGGGTCCCTGTGTTTTATCTGCGCGTATGACACAGACGAATGGAAATTTGGCGTCAAG	16440
Db	51280	TCACAGGGTCCCTGTGTTTTATCTGCGCGTATGACACAGACGAATGGAAATTTGGCGTCAAG	51339
QY	16441	TTTAAGGAAGAACAAGTTGGTTAAATAGCGCTGTAGAGGCTTGTCAATCCCAACGACTGG	16500
Db	51340	TTTAAGGAAGAACAAGTTGGTTAAATAGCGCTGTAGAGGCTTGTCAATCCCAACGACTGG	51399
QY	16501	AAAGGTTTAGAGCCCGCTGATCCCTTACGCGTCATATGCGCTTCTGTTTACGCTTCCGG	16560
Db	51400	AAAGGTTTAGAGCCCGCTGATCCCTTACGCGTCATATGCGCTTCTGTTTACGCTTCCGG	51459
QY	16561	TCGTTCTGTGCGGAACACAGAGTCCCTATATGAACGCAATTTTGGATGAAGGAGCCATA	16620
Db	51460	TCGTTCTGTGCGGAACACAGAGTCCCTATATGAACGCAATTTTGGATGAAGGAGCCATA	51519
QY	16621	CTCTTACCGCCACATATGTATGCGCCCCCAAAAGAGCATATGACTTTTGTCCATCATGTGA	16680
Db	51520	CTCTTACCGCCACATATGTATGCGCCCCCAAAAGAGCATATGACTTTTGTCCATCATGTGA	51579
QY	16681	ATTTAAGTACGTTTAAATTTTATACGTGAAGCGCGGGGGGCTTGAACCTGAACCGTCC	16740
Db	51580	ATTTAAGTACGTTTAAATTTTATACGTGAAGCGCGGGGGGCTTGAACCTGAACCGTCC	51639
QY	16741	CCGCGCTTGAAGGCGCTCGCGGTTGGCGCAGCCATCGTCTCGGGAGCTGGAAGCG	16800
Db	51640	CCGCGCTTGAAGGCGCTCGCGGTTGGCGCAGCCATCGTCTCGGGAGCTGGAAGCG	51699
QY	16801	GATGAGCCATACCTGTCCGGAAGTGCATGTTGTGCACTGTGACAAAGAAACATATACG	16860
Db	51700	GATGAGCCATACCTGTCCGGAAGTGCATGTTGTGCACTGTGACAAAGAAACATATACG	51759
QY	16861	ATTTCGATTCATGTAACACACAGTGGGCGAGTATGCATTTAAGGCGAGACGCTCGAGA	16920
Db	51760	ATTTCGATTCATGTAACACACAGTGGGCGAGTATGCATTTAAGGCGAGACGCTCGAGA	51819
QY	16921	TATTAATAACGCTATAGTGTTCGGGCTCAACGGTGCAGAGTCCGGGAGATTTTGTTTTAATC	16980
Db	51820	TATTAATAACGCTATAGTGTTCGGGCTCAACGGTGCAGAGTCCGGGAGATTTTGTTTTAATC	51879

QY	16961	CCCCGTACACACATTGGAAGGCGTCTGTAAGCATGATATAGGAAACATATGCGCTCGGACAGAC	17040
Db	51880	CCCCGTACACACATTGGAAGGCGTCTGTAAGCATGATATAGGAAACATATGCGCTCGGACAGAC	51939
QY	17041	TAATAAATAATGTAATAATTAAGTCGAGCTCGACATCGGAAATCAACAAAAAACTGTCATCTC	17100
Db	51940	TAATAAATAATGTAATAATTAAGTCGAGCTCGACATCGGAAATCAACAAAAAACTGTCATCTC	51999
QY	17101	CGTATTTGACAGGTTTGGGGCCGACAGTGCCTGTTTAAACGGCGCACTATATAGGAAACAG	17160
Db	52000	CGTATTTGACAGGTTTGGGGCCGACAGTGCCTGTTTAAACGGCGCACTATATAGGAAACAG	52059
QY	17161	GGAAATCGCTGGCGTCTGTACACACAGCTTAATAAAGAAAGACGATCTTGCGACCGTTTGCG	17220
Db	52060	GGAAATCGCTGGCGTCTGTACACACAGCTTAATAAAGAAAGACGATCTTGCGACCGTTTGCG	52119
QY	17221	AACGCTACAAACGTCGCTGCGTGGAAAAACAAGGCGAATTGGGATTCTTAAGGGGTTTAA	17280
Db	52120	AACGCTACAAACGTCGCTGCGTGGAAAAACAAGGCGAATTGGGATTCTTAAGGGGTTTAA	52179
QY	17281	CAGGAAAAAAATGGAAGAGTTTGGACGCTGTGGCGAGCGGCTTCCGACCTCAAGAGCGA	17340
Db	52180	CAGGAAAAAAATGGAAGAGTTTGGACGCTGTGGCGAGCGGCTTCCGACCTCAAGAGCGA	52239
QY	17341	GCTGTACGAGACATCGAGATTTCTTAGTACGCTTGACAAATGAATCTGTTCCGCTGGAAGA	17400
Db	52240	GCTGTACGAGACATCGAGATTTCTTAGTACGCTTGACAAATGAATCTGTTCCGCTGGAAGA	52299
QY	17401	AGAGTCCCCCAAGGACGACATTTATATAGTGGAAATTGGAGCGCTCTCCAGATGTGGCC	17460
Db	52300	AGAGTCCCCCAAGGACGACATTTATATAGTGGAAATTGGAGCGCTCTCCAGATGTGGCC	52359
QY	17461	CAAAAGCCCTTGATCCCATTTCCCAAGGTTCAAGCTGACCTCGACAGACAGATCTGTTCC	17520
Db	52360	CAAAAGCCCTTGATCTCCCATTTCCCAAGGTTCAAGCTGACCTCGACAGACAGATCTGTTCC	52419
QY	17521	ATATACCGCTCATTTAAACACGTAATAGACGATGCGCCCACTGAAGATACCTAACACTGG	17580
Db	52420	ATATACCGCTCATTTAAACACGTAATAGACGATGCGCCCACTGAAGATACCTAACACTGG	52479
QY	17581	GCCATGTATGATACACGAGGAGGAGGACTGACCGCGCTGCTCGGAGCGGCTGCTATGGTG	17640
Db	52480	GCCATGTATGATACACGAGGAGGAGGACTGACCGCGCTGCTCGGAGCGGCTGCTATGGTG	52539
QY	17641	TGCTGAGGTCCATGTCCTCTCGGCGCGCTGCGTTAAGCATTTTGGACGCGCGTAGATTTT	17700
Db	52540	TGCTGAGGTCCATGTCCTCTCGGCGCGCTGCGTTAAGCATTTTGGACGCGCGTAGATTTT	52599
QY	17701	TTTACGAGTCATTTTAAACGAT	17760
Db	52600	TTTACGAGTCATTTTAAACGAT	52659
QY	17761	GCGGGGGTACCGCTATCTATCTCTAGACCGCGCTACACATCTCGCGCCCTGATAT	17820
Db	52660	GCGGGGGTACCGCTATCTATCTCTAGACCGCGCTACACATCTCGCGCCCTGATAT	52719
QY	17821	TCGCCACAGTTAACAGGAATCTGCTAAACGCGGATCTTAAACACGTAACCCCTGAAACGCG	17880
Db	52720	TCGCCACAGTTAACAGGAATCTGCTAAACGCGGATCTTAAACACGTAACCCCTGAAACGCG	52779
QY	17881	TGGCGGTGAATTTCTCTGAGCTGAGGAGGAGCGTTATGTTTTCTAAATATATATGTGGCA	17940
Db	52780	TGGCGGTGAATTTCTCTGAGCTGAGGAGGAGCGGTATGTTTTCTAAATATATATGTGGCA	52839
QY	17941	TGCTTACAGTCACATCACTCCAGAAAAATATATCTGATTAAGGGGGAACGTACAACTGCGT	18000
Db	52840	TGCTTACAGTCACATCACTCCAGAAAAATATATCTGATTAAGGGGGAACGTACAACTGCGT	52899
QY	18001	ACGGAGAGCTTATGATTCGAGACTTATAGGCTCGCGCTTCTTACACAGGGGAACCCCTTGG	18060
Db	52900	ACGGAGAGCTTATGATTCGAGACTTATAGGCTCGCGCTTCTTACACAGGGGAACCCCTTGG	52959
QY	18061	CCGAGTGAATGTGACCTTCAAACTCGGGTCTGTGACGACACATTTTAAAGGCAC	18120

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Db 52960 CCGGAGTGTGATGACCTCAACCTCGGTTGTGAGCAGACGATCAATTTAAAGGCAC 53019
|||||
Oy 18121 CGGAGAGATTTATCTGTAAAGACATTTTACGGCCGCTGTCTCTCTAACCCTGTCTGC 18180
|||||
Db 53020 CGGACAGATTTATCTGTAAAGACATTTTACGGCCGCTGTCTCTCTAACCCTGTCTGC 53079
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Oy 18181 TGTCTGTGCGCGGGGGGGGGCGGACGGGCGCATGTCTAAATACGCCGTTCCAAATCCCTCAC 18240
53080 TGTCTGTGCGCGGGGGGGGGCGGACGGGCGCATGTCTAAATACGCCGTTCCAAATCCCTCAC 53139
Oy 18241 AACTCGGTCTCAATTTGACATATGTCCTCGGTTATGTTTGTAGATGCTAGAGAA 18300
53140 AACTCGGTCTCAATTTGACATATGTCCTCGGTTATGTTTGTAGATGCTAGAGAA 53199
Db 18301 AATATCTTCAGCCAGCTGACCCATTTCCACAGGAGCGTTGGCGGACGCTTCCTCGG 18360
53200 AATATCTTCAGCCAGCTGACCCATTTCCACAGGAGCGTTGGCGGACGCTTCCTCGG 53259
Oy 18361 AATCGCGCCAGCCAGCTGTTCTATTTGCGTTGATGTCGCAAGAGATGATCATGCCGAGAA 18420
53260 AATCGCGCCAGCCAGCTGTTCTATTTGCGTTGATGTCGCAAGAGATGATCATGCCGAGAA 53319
Oy 18421 TTTTTCGTGTGCTGGAGCGTTCACATGATTTTGGCATTTGACATCATGTGCGCACGGGC 18480
53320 TTTTTCGTGTGCTGGAGCGTTCACATGATTTTGGCATTTGACATCATGTGCGCACGGGC 53379
Db 18481 CAGCTATTTCCCTGAGAGAGCGTACAGGCGGTTTTTTCGCAACGATGATGTTATATA 18540
53380 CAGCTATTTCCCTGAGAGAGCGTACAGGCGGTTTTTTCGCAACGATGATGTTATATA 53439
Oy 18541 GGGCCCATATCAAAAGAGATGGGTTAGAAAAGCATCCTCGCGGCTGTGTAACTCAAAAC 18600
53440 GGGCCCATATCAAAAGAGATGGGTTAGAAAAGCATCCTCGCGGCTGTGTAACTCAAAAC 53499
Oy 18601 TTAACATGTTCTCCAGAAAGCTGTGTGTCAGGAGCTACTTGTATGTCGGAAGAACTGCG 18660
53500 TTAACATGTTCTCCAGAAAGCTGTGTGTCAGGAGCTACTTGTATGTCGGAAGAACTGCG 53559
Db 18661 GAGATCATGAGATTTTTTCTCAGATGAGCGGATGTTTCAGAGAGATGGCGTTCTCGACATC 18720
53560 GAGATCATGAGATTTTTTCTCAGATGAGCGGATGTTTCAGAGAGATGGCGTTCTCGACATC 53619
Oy 18721 GATGAGCAGACGGGCTCCTCTCGAAATATGACCTGGCCCACTTTTAAACATAGAGCA 18780
53620 GATGAGCAGACGGGCTCCTCTCGAAATATGACCTGGCCCACTTTTAAACATAGAGCA 53679
Oy 18781 GTAAAGGCGTTTTTATAGGATTAACAAAAGAAATAGCATCCGGCTATACGGTTCTGTG 18840
53680 GTAAAGGCGTTTTTATAGGATTAACAAAAGAAATAGCATCCGGCTATACGGTTCTGTG 53739
Oy 18841 TATATTTTTTATCTATTTGCGCAAGGTGGAGATTTTATCGGCAACCGAGCTGTACAT 18900
53740 TATATTTTTTATCTATTTGCGCAAGGTGGAGATTTTATCGGCAACCGAGCTGTACAT 53799
Db 18901 TTTTACGTCACCTGGCTGTTCAGAGGGAGCGGCTGAGCGGCTGTGCGAAGTGTACAC 18960
53800 TTTTACGTCACCTGGCTGTTCAGAGGGAGCGGCTGAGCGGCTGTGCGAAGTGTACAC 53859
Oy 18961 GCGTGTCTTAAACATGACCCGACGATGACACACAGTGTGTGATTAAGAAAGGTC 19020
53860 GCGTGTCTTAAACATGACCCGACGATGACACACAGTGTGTGATTAAGAAAGGTC 53919
Oy 19021 ACGCGGGCCAAACATCAATCTGTGTGGAGCGCTGTAGGAGACGATATATTTCTGTG 19080
53920 ACGCGGGCCAAACATCAATCTGTGTGGAGCGCTGTAGGAGACGATATATTTCTGTG 53979
Db 19081 TCAAAATTTTCACTGGGCGATTAACACAGAAATTCGTCACAAAATTTTAAACCCGTGG 19140
53980 TCAAAATTTTCACTGGGCGATTAACACAGAAATTCGTCACAAAATTTTAAACCCGTGG 54039
Oy 19141 CCTATGTCACAACTATTTGTAGCGGGCGGCTGTGAGCTGCTGTGCGAGAA 19200
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Db 54040 CCTATGTCACAACTATTTGTAGCGGGCGGCTGTGAGCTGCTGTGCGAGAA 54099
Oy 19201 GTGGTTAAAAAGATACTGGCGAGCTGTGTGTCATCCAGGAGCGCAGTGTAAAACTAC 19260
54100 GTGGTTAAAAAGATACTGGCGAGCTGTGTGTCATCCAGGAGCGCAGTGTAAAACTAC 54159
Oy 19261 GCATTCATGCAAGTCCTCTCAACGGGGTTTTTGGCGTCTCTGTGATTTTGAATTAAC 19320
54160 GCATTCATGCAAGTCCTCTCAACGGGGTTTTTGGCGTCTCTGTGATTTTGAATTAAC 54219
Oy 19321 GTGAGGTGTGACCCAAAAGAGCGTTTGGATTTCAACCCAGCATGCAAAATCTATGAATA 19380
54220 GTGAGGTGTGACCCAAAAGAGCGTTTGGATTTCAACCCAGCATGCAAAATCTATGAATA 54279
Db 19381 AATGCGCGTTTAACTATCACTTTTCCAGATGAGTGTGACCCGATTTTACGCTCGAT 19440
54280 AATGCGCGTTTAACTATCACTTTTCCAGATGAGTGTGACCCGATTTTACGCTCGAT 54339
Oy 19441 GCTAAACTTTATCAGAAAGCCGACATGACAGCGCTTAAGGGTTTTTGTACTCCATATCT 19500
54340 GCTAAACTTTATCAGAAAGCCGACATGACAGCGCTTAAGGGTTTTTGTACTCCATATCT 54399
Oy 19501 AAACGGCGATCGAGTTTGTGAG 19560
54400 AAACGGCGATCGAGTTTGTGAG 54459
Oy 19561 GCATATGACAAAGAAATGGGAGGTGTGTCCGCGAAAAAGAGAGAGAGAGAGAGAGAGAG 19620
54460 GCATATGACAAAGAAATGGGAGGTGTGTCCGCGAAAAAGAGAGAGAGAGAGAGAGAGAG 54519
Oy 19621 CATCTAGTTTAAAAAGTGCATGATTTACAACTCTACGGCGCTTCTGTGATGTATATTTG 19680
54520 CATCTAGTTTAAAAAGTGCATGATTTACAACTCTACGGCGCTTCTGTGATGTATATTTG 54579
Oy 19681 TCAGATCCGACAGAAAGCGAGAGCGCAAAATTAATTAAGCTCATCTGAGCCCAACCTA 19740
54580 TCAGATCCGACAGAAAGCGAGAGCGCAAAATTAATTAAGCTCATCTGAGCCCAACCTA 54639
Db 19741 TTTATTAACGTCAGGCTATCTATTTATTAATCAAGTGTGTCTCAAGTCTCTGTGTACAG 19800
54640 TTTATTAACGTCAGGCTATCTATTTATTAATCAAGTGTGTCTCAAGTCTCTGTGTACAG 54699
Oy 19801 GAGTACATCAGTCTCTCCAGAGGAACTAAATTTTGGGAAACCCAGAAACTTTATAGG 19860
54700 GAGTACATCAGTCTCTCCAGAGGAACTAAATTTTGGGAAACCCAGAAACTTTATAGG 54759
Oy 19861 ACTGCGTTTTTATAGAAAGCGAGTTTTCAAGACCCGAGCTGTGACGATGCGTAATTT 19920
54760 ACTGCGTTTTTATAGAAAGCGAGTTTTCAAGACCCGAGCTGTGACGATGCGTAATTT 54819
Oy 19921 GCCCGTTGATCAACAGCTAGAGATACCGACCTTTTATATCTGACACCCGGTATATTT 19980
54820 GCCCGTTGATCAACAGCTAGAGATACCGACCTTTTATATCTGACACCCGGTATATTT 54879
Db 19981 CCCAGCGTGGCCAAACACCACTGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 20040
54880 CCCAGCGTGGCCAAACACCACTGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 54939
Oy 20041 CGTGAAGCATTTCCGAGCTACCATGGGATTTATCTCTGTGTGCAAAAGCCGCCACCA 20100
54940 CGTGAAGCATTTCCGAGCTACCATGGGATTTATCTCTGTGTGCAAAAGCCGCCACCA 54999
Oy 20101 ACACCGTATGTGAAGGGGGAGCCCATAGATGATTCAAAAGAAATTCATCTATATATAG 20160
55000 ACACCGTATGTGAAGGGGGAGCCCATAGATGATTCAAAAGAAATTCATCTATATATAG 55059
Oy 20161 GAGAAAGAAAGATTTCTTTTAAAGCGAGATGGGACGCGCCGCGCGGTGTACAAAC 20220
55060 GAGAAAGAAAGATTTCTTTTAAAGCGAGATGGGACGCGCCGCGCGGTGTACAAAC 55119
Db 20221 CCAAAACCAACGATCAACATATAAAATTAATTTGATTTTGTAAAGATTCG 20280
55120 CCAAAACCAACGATCAACATATAAAATTAATTTGATTTTGTAAAGATTCG 55179

OY	20281	TATCTTAAATGAGATGGGGTGGATGCTGTGGGGTTGGGAAAGGAATGGATTGAGGGAG	20340
Db	55180	TATCTTAAATGAGATGGGGTGGATGCTGTGGGGTTGGGAAAGGAATGGATTGAGGGAG	55239
OY	20341	GATGAATAGCTAGAAATCATATGTAATTTTGGATATGCATCTCTCGTAATCCGTACAGCTTC	20400
Db	55240	GATGAATAGCTAGAAATCATATGTAATTTTGGATATGCATCTCTCGTAATCCGTACAGCTTC	55299
OY	20401	TTCTGTTTCATATTAACCGCTTCAGTTCGGGGAGTACTTAACCTTTTGTCTCTCTCTT	20460
Db	55300	TTCTGTTTCATATTAACCGCTTCAGTTCGGGGAGTACTTAACCTTTTGTCTCTCTCTT	55359
OY	20461	AGGCCCTTGAAGAAAGGGGTGCTATTCGGCGCATTTTGGCGACATTTTCCAAATCGTTTCT	20520
Db	55360	AGGCCCTTGAAGAAAGGGGTGCTATTCGGCGCATTTTGGCGACATTTTCCAAATCGTTTCT	55419
OY	20521	GATTAATCTTAAATGAGTGGCTAGATGCAAGATGATGGAAATCATTAAGATGTTTCAACGGC	20580
Db	55420	GATTAATCTTAAATGAGTGGCTAGATGCAAGATGATGGAAATCATTAAGATGTTTCAACGGC	55479
OY	20581	TATGACTTGTGACAGCTGGGAGATATGAATACCTTGTCTGATTCGAACGAGCGGAGAAAG	20640
Db	55480	TATGACTTGTGACAGCTGGGAGATATGAATACCTTGTCTGATTCGAACGAGCGGAGAAAG	55539
OY	20641	CAGAAATCAGTAACTGACAAAAACGCCACAGTGAATCCGATCTGTGTAGTACTT	20700
Db	55540	CAGAAATCAGTAACTGACAAAAACGCCACAGTGAATCCGATCTGTGTAGTACTT	55599
OY	20701	TACTAGAAATAGTTCTGTGTGATATPACCAAGCTATTGTAAAGCAAAAAACAAGTTAT	20760
Db	55600	TACTAGAAATAGTTCTGTGTGATATPACCAAGCTATTGTAAAGCAAAAAACAAGTTAT	55659
OY	20761	TGAACCAAAACAATATCGAAAGAGCATATAGAAACTGTTTCCAAATAGCCATCATCGT	20820
Db	55660	TGAACCAAAACAATATCGAAAGAGCATATAGAAACTGTTTCCAAATAGCCATCATCGT	55719
OY	20821	TCCGAGGAGAAATCTAAACATCTCCATGCGCTATTAAAGACAGATTAATGGGCCAAT	20880
Db	55720	TCCGAGGAGAAATCTAAACATCTCCATGCGCTATTAAAGACAGATTAATGGGCCAAT	55779
OY	20881	CGGTTTTCCGTAACGCAACAGGGGTCTAGCAAGCTATTCTCAGAGTAATCTGCTCTTAA	20940
Db	55780	CGGTTTTCCGTAACGCAACAGGGGTCTAGCAAGCTATTCTCAGAGTAATCTGCTCTTAA	55839
OY	20941	GACGCGTAGAGACCAAGGTGGCCGAATTGACAGATATCATAGCCGTGACGTCGTAACGA	21000
Db	55840	GACGCGTAGAGACCAAGGTGGCCGAATTGACAGATATCATAGCCGTGACGTCGTAACGA	55899
OY	21001	TAGGCAAAAATGTAATPACGTAATACAAAGAGGCTTAAAGAGTATGTTTGAACGACAAAC	21060
Db	55900	TAGGCAAAAATGTAATPACGTAATACAAAGAGGCTTAAAGAGTATGTTTGAACGACAAAC	55959
OY	21061	GTGAATAAATTAAGTATGATGTCCACAGCCTCAAAATAGACATAAATACTACAGTGGGA	21120
Db	55960	GTGAATAAATTAAGTATGATGTCCACAGCCTCAAAATAGACATAAATACTACAGTGGGA	56019
OY	21121	GCCTATGAGACAGATCCATGTCTGAGAGCTGTGCAATTTGTGTGCGCTGACAGCGCTTGGC	21180
Db	56020	GCCTATGAGACAGATCCATGTCTGAGAGCTGTGCAATTTGTGTGCGCTGACAGCGCTTGGC	56079
OY	21181	CTTGAAATTTGGCCAGATAGGCGCCACGATAGTAACACAGACGATATCCGTCCACAAAAA	21240
Db	56080	CTTGAAATTTGGCCAGATAGGCGCCACGATAGTAACACAGACGATATCCGTCCACAAAAA	56139
OY	21241	CGCCACAGAGATGAGACAAACATTTCTGTGTCTTCCAAAAACAAGTGGCGTCAGATG	21300
Db	56140	CGCCACAGAGATGAGACAAACATTTCTGTGTCTTCCAAAAACAAGTGGCGTCAGATG	56199
OY	21301	TTTAAAGCAAACTTGTGACCGTTAGGTTTAAACGCGCTGTAGTTGAACCAAGTGTAAAGTA	21360
Db	56200	TTTAAAGCAAACTTGTGACCGTTAGGTTTAAACGCGCTGTAGTTGAACCAAGTGTAAAGTA	56259
OY	21361	GCACGGAAATCCAAAGTCCCGGGAATGCGGATCTAGTGGCAATACCGATTAATTA	21420
Db	56260	GCACGGAAATCCAAAGTCCCGGGAATGCGGGAATGCGGGAATGCGGGAATGCGGGAAT	56319
OY	21421	CATTAAGTCCAAAGATTAACGAGTATGTTTCCCATGACGATTAAGATTAACGATTCGCTCG	21480
Db	56320	CATTAAGTCCAAAGATTAACGAGTATGTTTCCCATGACGATTAAGATTAACGATTCGCTCG	56379
OY	21481	TGAATAATTTTCATAGTTCAAAAGAAATGCTGCGGGGTGCTTTCGGCAAACTAGCAATAAA	21540
Db	56380	TGAATAATTTTCATAGTTCAAAAGAAATGCTGCGGGGTGCTTTCGGCAAACTAGCAATAAA	56439
OY	21541	TCAGCAAGTGGCTTACATGTTTACGATTTTAAATAGGCTCCGCTTTTAAATATCACATTC	21600
Db	56440	TCAGCAAGTGGCTTACATGTTTACGATTTTAAATAGGCTCCGCTTTTAAATATCACATTC	56499
OY	21601	GTGCAAAAGAGTTGAGCCACGCGCACCATTAAGACCGCGGAGGTGGGACATCACGGGACATG	21660
Db	56500	GTGCAAAAGAGTTGAGCCACGCGCACCATTAAGACCGCGGAGGTGGGACATCACGGGACATG	56559
OY	21661	TTTTGCATATTCGCTGATAGCACGACGACGAGCGGAGAAATTAATCTGGACGTTT	21720
Db	56560	TTTTGCATATTCGCTGATAGCACGACGACGAGCGGAGAAATTAATCTGGACGTTT	56619
OY	21721	ATTTACTTGTATGTCAACAATCGGAAATTCAGGGAGATCCCGCATATCTATTGTTCACCG	21780
Db	56620	ATTTACTTGTATGTCAACAATCGGAAATTCAGGGAGATCCCGCATATCTATTGTTCACCG	56679
OY	21781	AAACATTAAGCAATATGACTGAGGAAATATACGGCGATTAACGTCACGACCGTCCA	21840
Db	56680	AAACATTAAGCAATATGACTGAGGAAATATACGGCGATTAACGTCACGACCGTCCA	56739
OY	21841	TAAATGAGACGCGCGTAAATTAATATGACGTGGAACTCCGTACTGCTTTACGAAATCCA	21900
Db	56740	TAAATGAGACGCGCGCGTAAATTAATATGACGTGGAACTCCGTACTGCTTTACGAAATCCA	56799
OY	21901	TCATTCAAATTTGTAATGTGCGCAGCCCGGGGGGTTTAAGCTAAGGGTCACGAGCGGAATA	21960
Db	56800	TCATTCAAATTTGTAATGTGCGCAGCCCGGGGGGTTTAAGCTAAGGGTCACGAGCGGAATA	56859
OY	21961	TGGTAATAGTGGGCTCGCAACGAGCTTGGATCTACTGCTTCCGTTCCGTTCCGCTGACGTGAG	22020
Db	56860	TGGTAATAGTGGGCTCGCAACGAGCTTGGATCTACTGCTTCCGTTCCGTTCCGCTGACGTGAG	56919
OY	22021	CCATATCTTCAATGCGATATCCACTATGAGCACTTATAGTTGGATTCGTGTGCCAACCC	22080
Db	56920	CCATATCTTCAATGCGATATCCACTATGAGCACTTATAGTTGGATTCGTGTGTGCCAACCC	56979
OY	22081	GCGAATTTGGTCTCAGAGATGTTTTCACGCTTATCTTCCAAAC	22140
Db	56980	GCGAATTTGGTCTCAGAGATGTTTTCACGCTTATCTTCCAAAC	57039
OY	22141	TTTAAACAAACGGGCGGTTATATCATTAAGGGCATCGAGTCCACGCAATCCGAAAAAGGG	22200
Db	57040	TTTAAACAAACGGGCGGTTATATCATTAAGGGCATCGAGTCCACGCAATCCGAAAAAGGG	57099
OY	22201	CGAAGATGGCGCATTTGGGTATTTCTTGATATCTTTAATTGCGAATCTGCGAAATACAG	22260
Db	57100	CGAAGATGGCGCATTTGGGTATTTCTTGATATCTTTAATTGCGAATCTGCGAAATACAG	57159
OY	22261	TTGCGGGGAGAAAGTACCTTGAGATGAGTGGCCACGCAACATTTTCACTGCTGCGGTTGG	22320
Db	57160	TTGCGGGGAGAAAGTACCTTGAGATGAGTGGCCACGCAACATTTTCACTGCTGCGGTTGG	57219
OY	22321	ACGAGCGTGTATGTGGAACGGGGCGCTTGCCGAATTTTATAGGGCGCTGACAAATAGT	22380
Db	57220	ACGAGCGTGTATGTGGAACGGGGCGCTTGCCGAATTTTATAGGGCGCTGACAAATAGT	57279
OY	22381	TGTTTCGGCAGCGGGAGGCGTATGCGCCACAGCTTAACTGATGCTGTGTCGGGGCGCACCTC	22440
Db	57280	TGTTTCGGCAGCGGGAGGCGTATGCGCCACAGCTTAACTGATGCTGTGTCGGGGCGCACCTC	57339
OY	22441	CGAGGGAATCCCTTCCCTTCCCTTATTTTTCGCGGTTTCCACACTCCCGCTGCTGTTTG	22500

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Db 57340 CGAGGGAACCCCTTCCCCCTTCTTCCGCTTCCACACCTCCGCTGTGTGG 57399
OY 22501 GAAGACCGGAAGGCTCGAGTAACCGCGCTCCAGAACTCCAAAAGCAAAATGCGG 22560
Db 57400 GAAGACCGGAAGGCTCGAGTAACCGCGCTCCAGAACTCCAAAAGCAAAATGCGG 57459
OY 22561 TACATGCGCCCCGTTTAAAGATTCATCTTAGGGATCAGCTTCTCATCTGCGCATTT 22620
Db 57460 TACACTGGCCCCGTTTAAAGATTCATCTTAGGGATCAGCTTCTCATCTGCGCATTT 57519
OY 22621 CACCTAAAAGCAGGTACCGTACCGCTGTTGGCGCTTGGGGGAGGATGTAACT 22680
Db 57520 CACCTAAAAGCAGGTACCGTACCGCTGTTGGCGCTTGGGGGAGGATGTAACT 57579
OY 22681 TGAAGTCTCGAGAGACAGAGAAAGGTTGCCGCACTAGTCGACCCACATTCATAGTAA 22740
Db 57580 TGAAGTCTCGAGAGACAGAGAAAGGTTGCCGCACTAGTCGACCCACATTCATAGTAA 57639
OY 22741 TCATAAATTTTCATCATCTGTTGTGCGACACCTAAATATGCAACGCTGCTTGTAAAA 22800
Db 57640 TCATAAATTTTCATCATCTGTTGTGCGACACCTAAATATGCAACGCTGCTTGTAAAA 57699
OY 22801 ATGAGTTAGATACATAGCAACCATCTGTTCAGAGGACCTGGCTTCATCCAAAGAG 22860
Db 57700 ATGAGTTAGATACATAGCAACCATCTGTTCAGAGGACCTGGCTTCATCCAAAGAG 57759
OY 22861 AATACAAACCGGTTACTTGGCCACATTTTTCAGTGGGCGCGGAGACGGGTATACCTGGG 22920
Db 57760 AATACAAACCGGTTACTTGGCCACATTTTTCAGTGGGCGCGGAGACGGGTATACCTGGG 57819
OY 22921 CGGCCATTGATAAACACAGATATTCATAGAGCTCCCAAGCTCAGCGACGCTGTAACTG 22980
Db 57820 CGGCCATTGATAAACACAGATATTCATAGAGCTCCCAAGCTCAGCGACGCTGTAACTG 57879
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Db 57880 GTTTCGCCATCAGTAATATGTTGGCGTAGGAACAAATGTTACGAAGTTTAAAAATAC 57939
OY 23041 AGTTCATTTCTTTTCACAGAAACAGCAAAAGTCTGACCCGCTTTGAGCGCATTTTGGG 23100
Db 57940 AGTTCATTTCTTTTCACAGAAACAGCAAAAGTCTGACCCGCTTTGAGCGCATTTTGGG 57999
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OY 23161 GTCCGTGTTTAAAAAATACAGCGCGGGTGTATGACGGGAGCTGCAAGAGACCCAC 23220
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Db 58120 CAGGGAACGAAACGGGACTGTCGCTGAGCTGTCTAGTAGAAGCGCGAGCTTGTGCT 58179
OY 23281 TAAACAATCAGTGTACGATGAGGAGGCGGTGGCGGGATCTTAACCAACCTTTTGGCAA 23340
Db 58180 TAAACAATCAGTGTACGATGAGGAGGCGGTGGCGGGATCTTAACCAACCTTTTGGCAA 58239
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OY 23521 GGAGGACTATGTGTTTGTAGTGTGTCAACGGGAGGATGAGAGATCACGCGA 23580
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Db 58420 GGAGGACTATGTGTTTGTAGTGTGTGTCCAAACGGGAGGATGAGAGATCACGCGA 58479
OY 23581 CAATATACGACAATTAAGAAAGTTTAAAAAGTACTATGTTTAAATTAACAGACTCTG 23640
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Db 58900 GGCCCGGTCAACCGCGGAGATTAATATAGGGGGGCTATGCTATTTTCCAGCAT 58959
OY 24061 AGAAGAAATGACAGAGAGTTCGTTACGCTCCGCTCCGCGGCTTAAACAGCTGCACGCG 24120
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Db 59500 TTATGTAGCTAAACGGGCTTAAGAAATGAAACCGTGTCTGCAAGAGGATGCTGCG 59559
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Qy	29161	CGAAGTATGACGGTAGGTAGCCCGCGCTCTG	CGCGGCTGTTGGCCACTAACACCGCACGG	29220
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Qy	29221	CGGATCTATTTAGTGGGGAGAGACCGCGGCT	CGCGGCTGTTGGCCACTAACACCGCACGG	29280
Db	64120	CGGATCTATTTAGTGGGGAGAGACCGCGGCT	CGCGGCTGTTGGCCACTAACACCGCACGG	64179
Qy	29281	GTCCCTGTTCCGGAATGAGTGGTGGTGGTGG	CGCGGCTGTTGGCCACTAACACCGCACGG	29340
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Qy	29341	ATCTTGGTCAAAAAATCCTCAGGTGCACTAT	CGCGGCTGTTGGCCACTAACACCGCACGG	29400
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Qy	29401	GGCGGGTACCGGGACACCCCGTACGGGAC	CGCGGCTGTTGGCCACTAACACCGCACGG	29460
Db	64300	GGCGGGTACCGGGACACCCCGTACGGGAC	CGCGGCTGTTGGCCACTAACACCGCACGG	64359
Qy	29461	CCTAGGTGCCCCGGGAATCGGCAGATCCTG	CGCGGCTGTTGGCCACTAACACCGCACGG	29520
Db	64360	CCTAGGTGCCCCGGGAATCGGCAGATCCTG	CGCGGCTGTTGGCCACTAACACCGCACGG	64419
Qy	29521	GGATTAAGAACTAGCCATGCGCCGGAAGCT	CGCGGCTGTTGGCCACTAACACCGCACGG	29580
Db	64420	GGATTAAGAACTAGCCATGCGCCGGAAGCT	CGCGGCTGTTGGCCACTAACACCGCACGG	64479
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Db	64480	CAGTTAATATTTCCAGTCAACGGGACCCCT	CGCGGCTGTTGGCCACTAACACCGCACGG	64539
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Qy	29701	GGCAGGGGAGCGGATGGCGCGCTTAGAG	CGCGGCTGTTGGCCACTAACACCGCACGG	29760
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Qy	29761	GGCTTGTCTATAGGCTTTCTTCCCGACAG	CGCGGCTGTTGGCCACTAACACCGCACGG	29820
Db	64660	GGCTTGTCTATAGGCTTTCTTCCCGACAG	CGCGGCTGTTGGCCACTAACACCGCACGG	64719
Qy	29821	AGGCAAGCTTATATGATAGCTGTAACCAAT	CGCGGCTGTTGGCCACTAACACCGCACGG	29880
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Qy	29881	TTCCCTCTTTCCACCGTCAGATGTTTAAAG	CGCGGCTGTTGGCCACTAACACCGCACGG	29940
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Qy	29941	TCTAAGACCCCGTGAAGAGGCGGTGAAC	CGCGGCTGTTGGCCACTAACACCGCACGG	30000
Db	64840	TCTAAGACCCCGTGAAGAGGCGGTGAAC	CGCGGCTGTTGGCCACTAACACCGCACGG	64899
Qy	30001	ATATTTTGAAGCTTGAAGGATATCTAGT	CGCGGCTGTTGGCCACTAACACCGCACGG	30060
Db	64900	ATATTTTGAAGCTTGAAGGATATCTAGT	CGCGGCTGTTGGCCACTAACACCGCACGG	64959
Qy	30061	GCTTGACCGCATGTAAGATCTCTGGCAAG	CGCGGCTGTTGGCCACTAACACCGCACGG	30120
Db	64960	GCTTGACCGCATGTAAGATCTCTGGCAAG	CGCGGCTGTTGGCCACTAACACCGCACGG	65019

|||||
Db 66100 CATGCCCAATTAATTCAGGGCTGTAAATATCATCCAGTAATACGTGCTAATG 66159
Qy 31261 TCAAGAGATGTTGTTCTAATTTTAAAGCCATCCAAATGAGTGGGTACACTTTGGGAC 31320
Db 66160 TCAAGAGATGTTGTTCTAATTTTAAAGCCATCCAAATGAGTGGGTACACTTTGGGAC 66219
Qy 31321 AAGACCCCGTAAATTTGGCAGCTCCACAAAGGAGATGATTTGATGCTTCAGCA 31380
Db 66220 AAGACCCCGTAAATTTGGCAGCTCCACAAAGGAGATGATTTGATGCTTCAGCA 66279
Qy 31381 GGGGAGCATATTTTATTTTAAATACATGAGAACCGGACCGGTCAATGACGACATATG 31440
Db 66280 GGGGAGCATATTTTATTTTAAATACATGAGAACCGGACCGGTCAATGACGACATATG 66339
Qy 31441 CCATTAGATTTGAGTCTGTGACACTGTTGATTTGACGGTGAATAAATGATATTCGT 31500
Db 66340 CCATTAGATTTGAGTCTGTGACACTGTTGATTTGACGGTGAATAAATGATATTCGT 66399
Qy 31501 CACATGCGTAATATTTTAAACACACAGAGGGCGGAATTAACGGTCCCGGCGTAA 31560
Db 66400 CACATGCGTAATATTTTAAACACACAGAGGGCGGAATTAACGGTCCCGGCGTAA 66459
Qy 31561 GGCGGTGATGGGAGGACAGGCGTCAATGGCATTTCCAGATTTGTTAAATCTGTTGAA 31620
Db 66460 GGCGGTGATGGGAGGACAGGCGTCAATGGCATTTCCAGATTTGTTAAATCTGTTGAA 66519
Qy 31621 CATACGAGTCTAAATCAAGTATAACACAGACAAAGTTCAAAAGGAGCAACGCGCTGG 31680
Db 66520 CATACGAGTCTAAATCAAGTATAACACAGACAAAGTTCAAAAGGAGCAACGCGCTGG 66579
Qy 31681 TTTCCACCCGGACATCCCGGCTCAGCAAAACCCGAATCTCTAGAGACGACATCAAAAGGT 31740
Db 66580 TTTCCACCCGGACATCCCGGCTCAGCAAAACCCGAATCTCTAGAGACGACATCAAAAGGT 66599
Qy 31741 TCAGACAAATTCGGAACCAAAACCCAGTCTAGAGACCATCGTTATTAATCTGGAG 31800
Db 66640 TCAGACAAATTCGGAACCAAAACCCAGTCTAGAGACCATCGTTATTAATCTGGAG 66699
Qy 31801 TTAAGAGACGAGCGGACACACATGCTGTTGTAGAGATTCAGCTTAGTGGGCTGCAGG 31860
Db 66700 TTAAGAGACGAGCGGACACACATGCTGTTGTAGAGATTCAGCTTAGTGGGCTGCAGG 66759
Qy 31861 CTGCTGACAGGCGGCTAGCTGCTGAGGCGGCTGCGGACCTTTGAAGCGGACGCA 31920
Db 66760 CTGCTGACAGGCGGCTAGCTGCTGAGGCGGCTGCGGACCTTTGAAGCGGACGCA 66819
Qy 31921 GTTCAGAGCAGCAGAGGAGGCTGTTGACAGTCGCGCATATCTCGGCAATAGAGAT 31980
Db 66820 GTTCAGAGCAGCAGAGGAGGCTGTTGACAGTCGCGCATATCTCGGCAATAGAGAT 66879
Qy 31981 CGCTGCGGTATCTTTTAGTGATATATCTGTTGGGTAACAAACTCACTCCCTGTA 32040
Db 66880 CGCTGCGGTATCTTTTAGTGATATATCTGTTGGGTAACAAACTCACTCCCTGTA 66939
Qy 32041 AAAAGGGAATAGGTCCTTTCTATCGTTTCTCGAATCTATATGATCTTTAA 32100
Db 66940 AAAAGGGAATAGGTCCTTTCTATCGTTTCTCGAATCTATATGATCTTTAA 66999
Qy 32101 GTATACCAAGAGCGTAAACCAACAGATGTTGACACCTTTAAATAATGCAAAACG 32160
Db 67000 GTATACCAAGAGCGTAAACCAACAGATGTTGACACCTTTAAATAATGCAAAACG 67059
Qy 32161 ACCGAGATGCTATCCGCGTTTCCATGCTTCAAAAGTAGTCAGATGATCTCCAGT 32220
Db 67060 ACCGAGATGCTATCCGCGTTTCCATGCTTCAAAAGTAGTCAGATGATCTCCAGT 67119
Qy 32221 TAGACTGCTCTCCCTGTTAAACCCCTTAAGTGAATGAAACGCAATGACCCGTGA 32280
Db 67120 TAGACTGCTCTCCCTGTTAAACCCCTTAAGTGAATGAAACGCAATGACCCGTGA 67179
Qy 32281 CTTCCTGATGCTCTTAATTAACCCGGAAGAGATTAATCCATGATGCTGCACCC 32340
|||||

Db 67180 CTTCCTGATGCTCTTAATTAACCCGGAAGAGATTAATACCAATGATGCTGCACC 67239
Qy 32341 CTACCCCAAGCCAGCCCGGCTACTATTAGACAGGAGTGAATACACGCTATCCCTTAA 32400
Db 67240 CTACCCCAAGCCAGCCCGGCTACTATTAGACAGGAGTGAATACACGCTATCCCTTAA 67299
Qy 32401 AAACCCATACGTTGGAGTTTGTAAAGTAAACAGCTGTGTATTTTCAACGCTGTCTATA 32460
Db 67300 AAACCCATACGTTGGAGTTTGTAAAGTAAACAGCTGTGTATTTTCAACGCTGTCTATA 67359
Qy 32461 AAATGATACGACACATCAATCAGTAATTAACCTTTTATTAATCAAGATTCAGAGGCG 32520
Db 67360 AAATGATACGACACATCAATCAGTAATTAACCTTTTATTAATCAAGATTCAGAGGCG 67419
Qy 32521 TGTTTACAGTGTGTAGTGGAGCATCTCCGCCAATGGGAATGGCTGATGATCACA 32580
Db 67420 TGTTTACAGTGTGTAGTGGAGCATATCTCCGCCAATGGGAATGGCTGATGATCACA 67479
Qy 32581 CTTAGTGTGCGATAGGTGCTCTGTACTTTACTAGTGGCGGATGAACCTTAATTTGGC 32640
Db 67480 CTTAGTGTGCGATAGGTGCTCTGTACTTTACTAGTGGCGGATGAACCTTAATTTGGC 67539
Qy 32641 GTGTTAGTGTGTACCAACCAAAACCTGCGGCTGCGCTTTTGAAGCTCTATGCA 32700
Db 67540 GTGTTAGTGTGTACCAACCAAAACCTGCGGCTGCGCTTTTGAAGCTCTATGCA 67599
Qy 32701 GCTTTAATGTTGCCAATAGCTGTCTTTAAATATCAATCTGTGATCTTTATGACA 32760
Db 67600 GCTTTAATGTTGCCAATAGCTGTCTTTAAATATCAATCTGTGATCTTTATGACA 67659
Qy 32761 GTGGTCCAAAAAAGATTTTAAACACGTTAAATCGTGTGCTGGATGCTCG 32820
Db 67660 GTGGTCCAAAAAAGATTTTAAACACGTTAAATCGTGTGCTGGATGCTCG 67719
Qy 32821 TATATACCTCTCTCAACAGAAAAATTTTAAACCAACTCGCAGGTACTGAACGAT 32880
Db 67720 TATATACCTCTCTCAACAGAAAAATTTTAAACCAACTCGCAGGTACTGAACGAT 67779
Qy 32881 GGTACGACAGTGTGTAAGAGTCTATCATCTCTTCCACTCCCTTTGAAGTTTGG 32940
Db 67780 GGTACGACAGTGTGTAAGAGTCTATCATCTCTTCCACTCCCTTTGAAGTTTGG 67839
Qy 32941 GTTACAGCAGCATGATGATAGCAGCAGGTCAGGGGAGGTGGATGCGAGGGGT 33000
Db 67840 GTTACAGCAGCATGATGATAGCAGCAGGTCAGGGGAGGTGGATGCGAGGGGT 67889
Qy 33001 AAACATTCGTGGGCTGTGGGGTACTCCAGTTTAAAGATCTCCGAGGACGCTACAGT 33060
Db 67900 AAACATTCGTGGGCTGTGGGGTACTCCAGTTTAAAGATCTCCGAGGACGCTACAGT 67959
Qy 33061 TCTTCGTCAATCTCAGCAGCCGATCCACACAGGGCAGTACTGATTAATAGTCC 33120
Db 67960 TCTTCGTCAATCTCAGCAGCCGATCCACACAGGGCAGTACTGATTAATAGTCC 68019
Qy 33121 CGAATTCATGTTGCTTAATTTTGGAGGTCCTTAAACGTAACCATGTTGCTCGCA 33180
Db 68020 CGAATTCATGTTGCTTAATTTTGGAGGTCCTTAAACGTAACCATGTTGCTCGCA 68079
Qy 33181 CACTGCGGTAGAGTAACCGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 33240
Db 68080 CACTGCGGTAGAGTAACCGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 68139
Qy 33241 GACAGATATAGGCGGCTTCCACTTAAGGTTGCCGTTGGTGAAGCGATTTGGGGCA 33300
Db 68140 GACAGATATAGGCGGCTTCCACTTAAGGTTGCCGTTGGTGAAGCGATTTGGGGCA 68199
Qy 33301 TTGACGTCATGTTGTTTATTTCAACCGCTATCATGCGGAGTGGCGGATATGGAACCTG 33360
Db 68200 TTGACGTCATGTTGTTTATTTCAACCGCTATCATGCGGAGTGGCGGATATGGAACCTG 68259
Qy 33361 TACATATGATTTAAAGATGTTTCCCGTAATGAGCAGCTCATGCTGTGTTTAAGT 33420
Db 68260 TACATATGATTTAAAGATGTTTCCCGTAATGAGCAGCTCATGCTGTGTTTAAGT 68319
|||||

QY 33421 TCACAGGGGTGTTAAAAAACTCAGAGGTCCTGCTGACACATTTTGGGAGCTCCGAA 33480
 Db 68820 TCACAGGGGTGTTAAAAAACTCAGAGGTCCTGCTGACACATTTTGGGAGCTCCGAA 68879
 QY 33481 CCGCTCAGGGATTAAGCTGTACACAGCGGTGCTTTTAAACGAAGCATACGTCAAAAA 33540
 Db 68830 CCGCTCAGGGATTAAGCTGTACACAGCGGTGCTTTTAAACGAAGCATACGTCAAAAA 68839
 QY 33541 CATACCCACGCTGACCTTAATAAAGCTCAGACAGAGCTGTGATGATGTAATGAA 33600
 Db 68440 CATACCCACGCTGACCTTAATAAAGCTCAGACAGAGCTGTGATGATGTAATGAA 68499
 QY 33601 TGTGCTCCTCCCTGGGATCCCATCTCGGGGCTCATCCGGATCTGAATCTCTTAACCTGTC 33660
 Db 68500 TGTGCTCCTCCCTGGGATCCCATCTCGGGGCTCATCCGGATCTGAATCTCTTAACCTGTC 68559
 QY 33661 TGCCTTACCGGGGTTCCTCCGGTTAAAAACCCGGGGGCGCCACCTGTAAACGTCCTGTC 33720
 Db 68560 TGCCTTACCGGGGTTCCTCCGGTTAAAAACCCGGGGGCGCCACCTGTAAACGTCCTGTC 68619
 QY 33721 GCACAAATGCGCCGAGGCGATGTAAGATTTCTACCCGAGAGGCGCTTTGTTGTAACGAA 33780
 Db 68620 GCACAAATGCGCCGAGGCGATGTAAGATTTCTACCCGAGAGGCGCTTTGTTGTAACGAA 68679
 QY 33781 AAGATGTTCAATAGCGTCGCTGCGAGCGGGGTCGTTATACCGCCCAAGTTGGCCAGAGTT 33840
 Db 68680 AAGATGTTCAATAGCGTCGCTGCGAGCGGGGTCGTTATACCGCCCAAGTTGGCCAGAGTT 68739
 QY 33841 CTGCACGACGCTTACGCGGGAATGAAGGCCAAGTGTGGGGCGTGGCGTCTCATTA 33900
 Db 68740 CTGCACGACGCTTACGCGGGAATGAAGGCCAAGTGTGGGGCGTGGCGTCTCATTA 68799
 QY 33901 TGTGACGGGGGCTATCATGGCTATGTGCGAGCTGCGCTGCTGACTTAATAACCTG 33960
 Db 68800 TGTGACGGGGGCTATCATGGCTATGTGCGAGCTGCGCTGCTGACTTAATAACCTG 68859
 QY 33961 GATCCGAGGGGAAAACTGGAATTAAGACTAAAGCACTGTGCAAACTGTTTTCACACC 34020
 Db 68860 GATCCGAGGGGAAAACTGGAATTAAGACTAAAGCACTGTGCAAACTGTTTTCACACC 68919
 QY 34021 ATCTTTCTTCAAGAAATCTTAAGCCCTATGCACTACTGCGCAACGGGAGAGTGTCT 34080
 Db 68920 ATCTTTCTTCAAGAAATCTTAAGCCCTATGCACTACTGCGCAACGGGAGAGTGTCT 68979
 QY 34081 GACAAATTAATTTTACCATCAGCGGTACGCGGAGGAAGGGCGCTGTGCTGACTGGAAGT 34140
 Db 68980 GACAAATTAATTTTACCATCAGCGGTACGCGGAGGAAGGGCGCTGTGCTGACTGGAAGT 69039
 QY 34141 ACTAGCGGGATGACGTGTCCGGGAAGCAGCCTGTGCCGATTCCTTAATCCTGCAGTA 34200
 Db 69040 ACTAGCGGGATGACGTGTCCGGGAAGCAGCCTGTGCCGATTCCTTAATCCTGCAGTA 69099
 QY 34201 TGCACACCGGGGCTTTCGCCGCAACCCCTGCTGACCTCAATATGTTTGAANAATCCA 34260
 Db 69100 TGCACACCGGGGCTTTCGCCGCAACCCCTGCTGACCTCAATATGTTTGAANAATCCA 69159
 QY 34261 GAATATCATCTCAGCGCGCCACCCCTGAGTAATTTGTCACACAAACAGCACCCCGAGT 34320
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 QY 34321 CTGCTCAGTCAGTCAGATTAATTAAGCCCAACGAGGCGTGTTCGCCGCAATGTTTT 34380
 Db 69220 CTGCTCAGTCAGTCAGATTAATTAAGCCCAACGAGGCGTGTTCGCCGCAATGTTTT 69279
 QY 34381 ATGACACAGTGAAGAGGGGTGTCAAGAGCATTCACACGAGGACAGCCCTATTTTG 34440
 Db 69280 ATGACACAGTGAAGAGGGGTGTCAAGAGCATTCACACGAGGACAGCCCTATTTTG 69339
 QY 34441 GCCCGCGCACTAACCGGTTGACATCTGCGGCCCTGGCCCGCATATGCAATGTTCCCA 34500
 Db 69340 GCCCGCGCACTAACCGGTTGACATCTGCGGCCCTGGCCCGCATATGCAATGTTCCCA 69399

QY 34501 GTTGCCGGCAGCTCTCGGACAGTGAAGGGTTCGCGGGGCGTTCGATTTGGGGAAACAGCA 34560
 Db 69400 GTTGCCGGCAGCTCTCGGACAGTGAAGGGTTCGCGGGGCGTTCGATTTGGGGAAACAGCA 69459
 QY 34561 TGCCTTCGACAGCCCGGCTTAACCGCCCAATGTCCCGCCAAAGAGAGTGAACGGTACCA 34620
 Db 69460 TGCCTTCGACAGCCCGGCTTAACCGCCCAATGTCCCGCCAAAGAGAGTGAACGGTACCA 69519
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 Db 69520 CAGTTGGGAAAGCGTCCCGTAAAGGTCACATTCGAGGCGCGCTGTACGTCACATG 69579
 QY 34681 GTTAATATACCAATTAATAGACTTAACGTCCTCCGTCAGGGTCCGGCCAGAGTCCGGCGAT 34740
 Db 69580 GTTAATATACCAATTAATAGACTTAACGTCCTCCGTCAGGGTCCGGCCAGAGTCCGGCGAT 69639
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 Db 69700 GCACGGTTCGCGCTAAGAGAAAGCAGCAGCGGAGGAGCGTGGCAGCAAAAAGCTGAG 69759
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 Db 69760 GCGCAGCTTCGCGGCGCGCAACAGTAACCAACCTTTCCCGGAGACGTCCTCCGGATGCGC 69819
 QY 34921 GTTGCGGACAGGGGCTTAATTTGATTTAATGCAAAAGCTTCACGATTAACCGGACGCA 34980
 Db 69820 GTTGCGGACAGGGGCTTAATTTGATTTAATGCAAAAGCTTCACGATTAACCGGACGCA 69879
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 Db 69880 TCTGAGCCCAAAAAGCAGCAGCATGCTAGCGGCTATCTTACAGGACCTGTATGAGACTA 69939
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 Db 69940 CAGTCCCGCCCGGCATCGATTCCTCCCTCCAGCAACTGCAATGAGAGATATTTCGA 69999
 QY 35101 G 35101
 Db 70000 G 70000

RESULT 3
 ID AA164297 standard; DNA; 524 BP.
 AA164297;
 22-APR-2002 (first entry)
 JMW Orf24 nucleotide sequence from cosmid 3 fragment 3 SP6.
 RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 JMW; cytostatic; antiallergic; antiallergic; dermatological;
 KW; vulnereary; gene therapy; leucopenia; thrombocytopenia;
 KW; inflammatory disease; asthma; allergy; dermatitis; ds.
 OS Japanese macaque herpesvirus.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 3..524
 FT /tag= a
 FT /partial
 FT /note= "no start or stop codon present"
 PN MO200188203-A1.
 XX 22-NOV-2001.
 XX 17-MAY-2001; 2001WO-US16274.
 PF

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XX 18-MAY-2000; 2000US-205652P.
PR (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Wong SW, Axthelm MK;
PI
XX MPI: 2002-075323/10.
DR P-PSDB; AAG78385.
XX
XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
PT reading frames in virus, useful for producing animal models for
PT assessing efficacy of drugs for treatment or prevention of multiple
PT sclerosis
XX
XX Claim 9; Page 68-69; 175pp; English.
XX
XX The invention relates to an isolated virus (Japanese macaque virus (JMHV)
CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
CC primate models infected with the new virus are useful for testing the
CC efficacy of a drug for treating a condition associated with JMHV,
CC preferably a drug used to treat multiple sclerosis. This involves
CC administering the drug to a non-human primate infected with JMHV and
CC observing the non-human primate to determine if the drug prevents or
CC reduces the presentation of one or more symptoms associated with JMHV
CC infection. Methods of the invention are also useful for testing the
CC efficacy of candidate vaccine against JMHV infection, or conditions
CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
CC invention are useful for diagnosing the presence of JMHV or a related
CC virus in a biological specimen. JMHV genome possesses an interleukin
CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
CC to induce stimulation of haematopoietic stem cells to enhance
CC proliferation, differentiation and terminal maturation of erythroid
CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
CC and platelets, and for the inhibition of tumour growth and for treating
CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHVorf21 nucleotide sequence from cosmid 3 fragment 3 SP6. The function
CC of Orf 24 is unknown.
XX
XX Sequence 524 BP; 157 A; 134 C; 104 G; 129 T; 0 other;
SQ
XX
XX Query Match 0.2%; Score 66; DB 24; Length 524;
XX Best Local Similarity 100.0%; Pred. No. 5,3e-17;
XX Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3118 GCACGTATTTGGTATTAATACATATTTGTAAGAAACGAGATTTGAAGTTGTCG 3177
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 203 GCACGTATTTGGTATTAATACATATTTGTAAGAAACGAGATTTGAAGTTGTCG 144
QY 3178 TAAACT 3183
DB ||||||
XX 143 TAAACT 138
XX
XX RESULT 4
XX ABL59513
XX ID ABL59513 standard; cDNA; 1606 BP.
XX AC ABL59513;
XX 16-JUL-2002 (first entry)

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XX Human glycerol-3-phosphate dehydrogenase cDNA SEQ ID NO:13.
DE
XX
XX Human; glycerol-3-phosphate dehydrogenase; enzyme;
KW tumour; lipid associated gene; lipid metabolism; lipid synthesis;
XX chromosome 2q24.1; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200227028-A1.
PN
XX
XX 04-APR-2002.
PD
XX
XX 27-SEP-2001; 2001MO-US30366.
PF
XX
XX 28-SEP-2000; 2000US-0676052.
PR
XX
XX (ATAI-) ATAIRGIN TECHNOLOGIES INC.
PA
XX Skinner MK, Patton JL, Chaudhary J;
PI
XX
XX MPI: 2002-402054/43.
DR
XX
XX Identifying tumor characteristics in a tissue sample taken from a
PT patient, involves determining the copy number or expression level of
PT genes associated with lipid metabolism, synthesis or action
XX
XX Example 1; Page 72; 113pp; English.
PS
XX
XX The present invention describes a method for identifying tumour
CC characteristics, comprising measuring a copy number or expression level
CC of at least two genes associated with lipid metabolism, synthesis, or
CC action in cells from a patient tissue sample, and comparing the results
CC with a copy number or expression level of the genes in a normal cell.
CC Also described is an array of nucleic acid polymers immobilised on a
CC solid support, comprising a solid support, at least two different nucleic
CC acid polymers which are each specific for a different gene associated
CC with lipid metabolism, synthesis or action, where each nucleic acid
CC polymer is located at a predetermined position on the solid support, and
CC the array comprises nucleic acid polymers which are specific for less
CC than 100 genes other than the selected genes. The method is useful for
CC determining tumour characteristics in a tissue sample taken from a
CC patient. The present sequence represents a human lipid-associated gene
CC related cDNA sequence, which is used in the exemplification of the
CC present invention.
XX
XX Sequence 1606 BP; 402 A; 372 C; 449 G; 383 T; 0 other;
SQ
XX
XX Query Match 0.1%; Score 24; DB 24; Length 1606;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 8723 GCTGGCTCTGGGGAACCTGTGCTC 8746
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 98 GCTGGCTCTGGGGAACCTGTGCTC 121
QY
XX
XX RESULT 5
XX AAD42098/c
XX ID AAD42098 standard; DNA; 29793 BP.
XX AC AAD42098;
XX
XX 04-NOV-2002 (first entry)
DE
XX Poly adenosine diphosphate-ribose glycohydrolase (PARG) gene.
XX
XX Poly adenosine diphosphate-ribose glycohydrolase; PARC; enzyme;
KW ADP-ribose; neoplastic disorder; genotoxic oxidative stress; neurotoxic;
KW cardiac disorder; neuronal disorder; reperfusion injury; neurotoxicity;
KW Alzheimer's disease; Huntington's disease; Parkinson's disease; cardiac;
KW cytosolic; vasotropic; neuroprotective; anticonvulsant; gene therapy;
KW antisense therapy; gene; ds.

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XX OS Caenorhabditis elegans.
XX Key Location/Qualifiers
XX CDS 3591..9540
FT /*tag= a
FT /*product= "CepARG"
FT exon 3591..3635
FT /*tag= b
FT /*number= 1
FT intron 3636..3680
FT /*tag= c
FT exon 3681..4121
FT /*tag= d
FT /*number= 2
FT intron 4122..5064
FT /*tag= e
FT exon 5065..5235
FT /*tag= f
FT /*number= 3
FT intron 5236..5929
FT /*tag= g
FT exon 5930..6152
FT /*tag= h
FT /*number= 4
FT intron 6153..6199
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FT /*tag= j
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FT intron 6268..7245
FT /*tag= k
FT exon 7246..7338
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FT intron 7339..7385
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FT exon 7386..7553
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FT exon 8153..8435
FT /*tag= r
FT /*number= 9
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FT /*tag= s
FT exon 8487..8610
FT /*tag= t
FT intron 8611..8661
FT /*tag= u
FT exon 8662..8952
FT /*tag= v
FT /*number= 11
FT intron 8953..9382
FT /*tag= w
FT exon 9383..9540
FT /*tag= x
FT /*number= 12
XX US6395543-B1.
XX PN 28-MAY-2002.
XX PD 23-FEB-2000; 2000US-0511507.
XX PE 01-MAY-1998; 98US-083768P.
PR

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PR 30-APR-1999; 99US-0302812.
XX
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX
XX Jacobson MK, Jacobson EL, Ame J, Lin W;
XX WPI: 2002-535641/57.
XX P-PSDB: AAE25633.
XX
XX New nucleic acid molecule encoding bovine poly adenosine
XX phosphate-ribose glycohydrolase involved in cellular response to DNA
XX damage. Inhibition of which is useful for treating neoplastic disorders
XX and neurodegenerative diseases
XX
XX Example 14; Column 89-116; 77pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule which encodes
XX a bovine poly (adenosine diphosphate (ADP)-ribose) glycohydrolase (bPARG)
XX which catalyzes release of ADP-ribose from an ADP ribose polymer. The
XX invention is useful as probes and primer molecules that can used in
XX hybridisation assays and polymerase chain reaction (PCR) amplification.
XX The knowledge of the nucleotide sequence of the PARG gene permits the
XX preparation of antisense therapeutics containing sequences complementary
XX to the mRNA of PARG gene. The antisense therapeutics are useful to treat
XX neoplastic disorders and conditions caused by genotoxic oxidative stress
XX e.g., cardiac disorders, neuronal disorders, reperfusion injury,
XX neurotoxicity, Alzheimer's disease, Huntington's disease and Parkinson's
XX disease. The invention is useful in gene therapy and antisense therapy.
XX The present sequence is CepARG gene.
XX
XX Sequence 29793 BP; 9945 A; 4952 C; 5003 G; 9893 T; 0 other;
XX
XX Query Match 0.1%; Score 24; DB 24; Length 29793;
XX Best Local Similarity 100.0%; Pred. No. 15;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 11807 AGTAAAAAACTAGTGTGATTGTCA 11830
XX Db 21745 AGTAAAAAACTAGTGTGATTGTCA 21722
XX
XX RESULT 6
XX ABK14930/C
XX ID ABK14930 standard; DNA: 29793 BP.
XX AC ABK14930;
XX XX
XX DT 08-MAY-2002 (first entry)
XX
XX Worm poly(ADP-ribose) glycohydrolase (PARG) sequence from cosmid F20C5.
XX DE
XX KW Worm: poly(ADP-ribose) glycohydrolase; PARG; PARG modulator;
XX ADP-ribose; adenosine diphosphate-ribose; DNA repair; apoptosis;
XX neoplasia; inherited genetic disease; myocardial infarction; cancer;
XX vascular stroke; aging; neurodegeneration; Huntington's disease;
XX Parkinson's disease; Alzheimer's disease; neurotoxicity; gene; ds.
XX KW
XX XX
XX OS Caenorhabditis elegans.
XX
XX Key Location/Qualifiers
XX CDS 3591..9540
FT /*tag= a
FT /*product= "Worm poly(ADP-ribose) glycohydrolase (PARG)"
FT exon 3591..3635
FT /*tag= b
FT /*number= 1
FT intron 3636..3680
FT /*tag= c
FT exon 3681..4121
FT /*tag= d
FT /*number= 2
FT intron 4122..5064
FT

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[illegible]

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FT	/number= 4
FT	6153..6199
FT	Intron
FT	/tag= i
FT	/number= 1
FT	exon
FT	6200..6267
FT	/tag= j
FT	/number= 5
FT	Intron
FT	6268..7245
FT	/tag= k
FT	/number= 5
FT	exon
FT	7246..7338
FT	/tag= l
FT	/number= 6
FT	Intron
FT	7339..7385
FT	/tag= m
FT	/number= 6
FT	exon
FT	7386..7553
FT	/tag= n
FT	/number= 7
FT	Intron
FT	7554..7737
FT	/tag= o
FT	/number= 7
FT	exon
FT	7738..7853
FT	/tag= p
FT	/number= 8
FT	Intron
FT	7854..8152
FT	/tag= q
FT	/number= 8
FT	exon
FT	8153..8435
FT	/tag= r
FT	/number= 9
FT	Intron
FT	8436..8486
FT	/tag= s
FT	/number= 9
FT	exon
FT	8487..8610
FT	/tag= t
FT	/number= 10
FT	Intron
FT	8611..8661
FT	/tag= u
FT	/number= 10
FT	exon
FT	8662..8952
FT	/tag= v
FT	/number= 11
FT	Intron
FT	8953..9382
FT	/tag= w
FT	/number= 11
FT	exon
FT	9383..9540
FT	/tag= x
FT	/number= 12
XX	US637202-B1.
PN	
XX	08-JAN-2002.
PD	
XX	23-FEB-2000; 2000US-0511477.
PE	
XX	01-MAY-1998; 98US-083768P.
PR	30-APR-1999; 99US-030281Z.
XX	
PA	(KENT) UNIV KENTUCKY RES FOUND.
XX	
P1	Jacobson MK, Jacobson EL, Ame J, Lin W;
XX	
DR	WPI: 2002-163240/21.
XX	
XX	Novel Isolated and purified poly(ADP-ribose) glycohydrolase protein
PT	which catalyses release of ADP-ribose from ADP ribose polymer. useful
PT	for treating neoplastic and neurological disorders, heart attack and
PT	stroke -
XX	
PS	Example 14; Column 91-116; 81pp; English.
XX	

CC	The present invention relates to a new poly(ADP-ribose) glycohydrolase
CC	(PARG) protein which catalyses release of ADP-ribose from an ADP
CC	(adenosine diphosphate)-ribose polymer. The PARC molecule of the
CC	invention is useful for generating antibodies and can be inhibited or
CC	activated for diagnosing and treating neoplastic disorders such as
CC	adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma,
CC	teratocarcinoma, hyperplasia and hypertrophy, reperfusion following
CC	ischæmia, heart attack, stroke, neurodegenerative diseases,
CC	neurological disorders including Alzheimer's, Huntington's and
CC	Parkinson's diseases, and related conditions. PARC levels may be
CC	enhanced to suppress DNA repair and increase the cell's susceptibility
CC	to chemotherapy drugs. Antagonists of PARC are administered to treat or
CC	prevent neoplastic disorders. The present nucleic acid sequence
CC	represents the worm PARC DNA sequence of the invention. This sequence
CC	was isolated from cosmid F20C5.
SQ	Sequence 29793 BP; 9945 A; 4952 C; 5003 G; 9893 T; 0 other;
Query Match	0.1%; Score 24; DB 24; Length 29793;
Best Local Similarity	100.0%; Pred. No. 15;
Matches 24; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	11807 AGTAAANAACAGTAGATTGTGCA 11830
Dd	21745 AGTAANAACAGTAGATTGTGCA 21722
RESULT 8	
ABX14494/C	
ID.	ABX14494 standard; DNA; 29793 BP.
XX	
AC	ABX14494;
XX	
DT	13-MAR-2003 (first entry)
XX	
DE	Cosmid F20C5 containing C. elegans PARC genomic DNA.
XX	
KM	Poly(ADP-ribose) glycohydrolase; PARC; PARC expression;
KW	cellular response; DNA damage; neoplastic disorder inducing agent;
KW	oxidative stress; neoplastic disorder; myocardial infarction;
KW	vascular stroke; neurodegenerative disorder; Alzheimer's disease;
KW	Parkinson's disease; Huntington's disease; Inborn genetic error;
KW	reperfusion; Ischaemia; aging; neurotoxicity; PARC activity;
KW	cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiant;
KW	vasotrophic; anticonvulsant; cerebroprotective; gene; cosmid F20C5; ds.
XX	
OS	Caenorhabditis elegans.
OS	Synthetic.
XX	
PN	US2002132328-A1.
XX	
PD	19-SEP-2002.
XX	
PF	09-OCT-2001; 2001US-0973451.
XX	
PR	01-MAY-1998; 98US-083768P.
XX	
PR	30-APR-1999; 99US-0302812.
XX	
PA	(JACO/) JACOBSON M K.
PA	(JACO/) JACOBSON E L.
PA	(AMEJ/) AME J.
PA	(LINW/) LIN W.
XX	
PI	Jacobson MK, Jacobson EL, Ame J, Lin W;
XX	
DR	WPI; 2003-155895/15.
PT	New nucleic acid molecule encoding a polypeptide with poly(ADP-ribose)
PT	glycohydrolase activity, for preventing, treating, or ameliorating a
PT	disease condition, e.g. neoplastic disorder, myocardial infarction or
PT	vascular stroke -
XX	
PS	Example 14; Page 49-62; 86pp; English.

XX The present invention relates to the isolation of poly(ADP-ribose) CC
 CC glycohydrolase (PARG) from several species, and the polynucleotide CC
 CC sequences encoding them. Methods for inhibiting PARG expression or CC
 CC overexpressing PARG are also disclosed. PARG is involved in the CC
 CC cellular response to DNA damage, and is associated with the body's CC
 CC response to neoplastic disorder inducing agents and oxidative stress. CC
 CC The polynucleotide sequences encoding PARG and PARG modulators are CC
 CC useful for preventing, treating, or ameliorating diseases such as CC
 CC neoplastic disorders, myocardial infarction, vascular stroke, CC
 CC neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's CC
 CC disease or Huntington's disease), inborn genetic errors, reperfusion CC
 CC following ischemia, aging, and neurotoxicity. The polynucleotide CC
 CC sequences are also useful in gene therapy. The methods are useful CC
 CC for identifying an agent that modulates PARG activity, identifying a CC
 CC mutant PARG allele in an individual, or screening candidate molecules CC
 CC for PARG modulating activity. The present DNA sequence represents CC
 CC cosmid F2005 (Genbank Accession number Z68161) which contains CC
 CC Caenorhabditis elegans PARG genomic DNA. CC
 XX

Sequence 29793 BP; 9945 A; 4952 C; 5003 G; 9893 T; 0 other;
 Query Match 0.1%; Score 24; DB 25; Length 29793;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11807 AGTAAACACTGATTGATTGCA 11830
 DB 21745 AGTAAACACTGATTGATTGCA 21722
 |||||||||||||||||||||
 |||||||||||||||||||||

RESULT 9
 ID AAT30688 standard; DNA; 918 BP.
 XX AAT30688;
 XX
 DT 11-SEP-1996 (first entry)
 XX
 DE Kaposi's sarcoma associated herpesvirus ORF26.
 XX
 KW Kaposi's sarcoma associated herpesvirus; KSHV; gamma-2 herpesvirus;
 KM therapy; diagnosis; antisense; triplex; vaccine; AIDS; ss.
 XX
 OS Kaposi's sarcoma associated herpesvirus.
 OS
 XX
 PN WO9615779-A1.
 XX
 PD 30-MAY-1996.
 XX
 PE 21-NOV-1995; 95WO-US15138.
 XX
 PR 11-APR-1995; 95US-0420235.
 PR 21-NOV-1994; 94US-0343101.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Chang Y, Moore PS;
 XX
 DR WPI; 1996-268320/27.
 DR P-PSDB; AAR97836.
 XX
 PT Herpes virus associated with Kaposi's sarcoma - also definitive DNA
 PT sequences; useful for diagnosis of and to develop prods. for
 PT treatment of Kaposi's sarcoma
 XX
 PS Claim 17; Page 213-215; 277pp; English.
 XX
 CC Lambda clone KS5 (AAT30681) has 17 protein-coding regions (AAT30682-98),
 CC 15 of which are complete ORFs, including ORF26 (AAT30688) (nts 11913-
 CC 12830), which codes for virion polypeptide VP23 (AAR97836). KS5 is a
 CC fragment of a newly identified human gamma-2 herpesvirus associated
 CC with Kaposi's sarcoma (KS). The ORFs were identified by sequence and

CC positional homology to known herpesvirus sequences. Probes that bind CC
 CC specifically to the KS associated herpesvirus can be used for KS CC
 CC diagnosis. Antisense or triplex oligonucleotides are useful for CC
 CC prophylaxis or treatment of KS, and the protein products (see also CC
 CC AAR97830-46) of the 17 open reading frames are useful as vaccines. CC
 XX

Sequence 918 BP; 204 A; 258 C; 229 G; 227 T; 0 other;
 Query Match 0.1%; Score 23; DB 17; Length 918;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9414 AGCTCAGTCTCATATTATCT 9436
 DB 823 AGCTCAGTCTCATATTATCT 845
 |||||||||||||||||||||
 |||||||||||||||||||||

RESULT 10
 ID AAT16818 standard; DNA; 918 BP.
 XX AAT16818;
 XX
 DT 25-MAR-2003 (updated)
 DT 13-AUG-1996 (first entry)
 XX
 DE Kaposi's sarcoma associated herpesvirus ORF26.
 XX
 KW Kaposi's sarcoma; KSHV; lymphoma; AIDS; vaccine; diagnosis; therapy;
 KM virion polypeptide; ss.
 XX
 OS Kaposi's sarcoma associated herpesvirus.
 OS
 XX
 PN WO9606159-A1.
 XX
 PD 29-FEB-1996.
 XX
 PE 11-AUG-1995; 95WO-US10194.
 XX
 PR 18-AUG-1994; 94US-0292365.
 PR 21-NOV-1994; 94US-0343101.
 PR 11-APR-1995; 95US-0420235.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PA (GRAN/) GRANT D E.
 PA (VIEL/) VIELE L.
 XX
 PI Chang Y, Moore PS, Grant DE, Viele L;
 XX
 DR WPI; 1996-151362/15.
 DR P-PSDB; AAR93612.
 XX
 PT Herpesvirus DNA associated with Kaposi's sarcoma - also associated
 PT vectors and proteins, used in detection and vaccination.
 XX
 PS Claim 17; Page 226-228; 305pp; English.
 XX
 CC Kaposi's sarcoma associated herpes virus (KHSV) clone KS5 (AAT16806),
 CC obtd. from a KS lesion genomic library, includes 15 complete ORFs and
 CC 2 incomplete ORFs (AAT16807-23) named according to their herpesvirus
 CC salmieri positional homologues. ORF26 (AAT16818) codes for the virion
 CC polypeptide (AAR93612). KSHV DNA may be incorporated into a
 CC vector and expressed in host cells to produce peptides useful in
 CC vaccines or for raising antibodies. The DNA may itself be used to
 CC immunise a subject, or used to design therapeutic antisense and
 CC triplex molecules or diagnostic probes, or to raise transgenic
 CC animals.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC
 CC Sequence 918 BP; 204 A; 258 C; 229 G; 227 T; 0 other;
 CC
 XX

Query Match 0.1%; Score 23; DB 17; Length 918;
 Best Local Similarity 100.0%; Pred. No. 52;


```
XX 29-FEB-1996.
XX
XX 11-AUG-1995; 95MO-US10194.
XX
XX 18-AUG-1994; 94US-0292365.
XX 21-NOV-1994; 94US-0343101.
XX 11-APR-1995; 95US-0420235.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX (GRAN/) GRANT D E.
XX (VIE/) VIELE L.
XX
XX Chang Y, Moore PS, Grant DE, Viele L;
XX WPI; 1996-151362/15.
XX
XX Herpesvirus DNA associated with Kaposi's sarcoma - also associated
XX PT vectors and proteins, used in detection and vaccination.
XX
XX Claim 16; Page 177-188; 305pp; English.
XX
XX Representational difference analysis was used to identify unique
XX CC DNA sequences in Kaposi's sarcoma (KS) tissue. An isolated sequence.
XX CC KS330Bam (AAT16824), was used to screen a KS lesion genomic library. A
XX CC lambda phage, KS5, was identified and the sequence of its insert
XX CC (AAT16808) was detd. This represents a novel infectious agent
XX CC associated with AIDS-KS, Kaposi's sarcoma associated herpesvirus (KSHV).
XX CC The KS5 fragment has 15 complete ORFs and 2 incomplete ORFs (see also
XX CC AAT16807-23). Portions of the sequence may be incorporated into a
XX CC vector and expressed in host cells to produce peptides (see also
XX CC AAR91601-117) useful in vaccines or for raising antibodies. The DNA may
XX CC itself be used to immunise a subject, or used to design therapeutic
XX CC antisense and triplex molecules or diagnostic probes, or to raise
XX CC transgenic animals.
XX CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SO Sequence 20710 BP; 4628 A; 5526 C; 5666 G; 4890 T; 0 other:
XX
XX Query Match 0.1%; Score 23; DB 17; Length 20710;
XX Best Local Similarity 100.0%; Pred. No. 40;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 9414 AGCTCAGTCTCATATTATCT 9436
XX 111111111111111111111111
XX DB 12735 AGTCTCAGTCTCATATTATCT 12757
XX
XX RESULT 13
XX AAV73803
XX ID AAV73803 standard; DNA: 35100 BP.
XX
XX AC AAV73803;
XX
XX DT 25-FEB-1999 (first entry)
XX
XX DE KSHV LUR DNA (nucleotides 35,101-70,200).
XX
XX Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;
XX KM dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis;
XX KM diagnosis; treatment; HHV8; thymidine kinase; glycoprotein H;
XX KM capsid protein; packaging protein; helicase primase; glycoprotein M;
XX KM viral protein kinase; alkaline exonuclease; virion assembly protein;
XX KM uracil DNA glycosylase; UDG; glycoprotein L; ds.
XX
XX Kaposi's sarcoma-associated herpesvirus.
XX
XX OS
XX PN US5849564-A.
XX
XX PD 15-DEC-1998.
XX
XX PF 29-NOV-1996; 96US-0770379.
XX
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PR 29-NOV-1996; 96US-0770379.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
XX WPI; 1999-069741/06.
XX
XX Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
XX PT dihydrofolate reductase and is useful for treatment, prophylaxis
XX PT or diagnosis of Kaposi's sarcoma
XX
XX Disclosure; Column 97-126; 109pp; English.
XX
XX This sequence is a fragment of the Kaposi's sarcoma-associated
XX CC herpesvirus (KSHV) LUR (long unique region). This fragment contains
XX CC coding regions for ORF20, ORF21 which encodes thymidine kinase, ORF22
XX CC which encodes glycoprotein H, ORF23, ORF24, ORF25 which encodes the
XX CC major capsid protein, ORF26 which encodes capsid protein II, ORF27,
XX CC ORF28, ORF29b which encodes packaging protein II, ORF30, ORF31, ORF32,
XX CC ORF33, ORF29a which encodes packaging protein I, ORF34, ORF35, ORF36
XX CC which encodes viral protein kinase, ORF37 which encodes alkaline
XX CC exonuclease, ORF38, ORF39 which encodes glycoprotein M, ORF40 which
XX CC encodes helicase primase subunit I, ORF41 which encodes helicase primase
XX CC subunit II, ORF42, ORF43 which encodes capsid protein III, ORF44 which
XX CC encodes helicase primase subunit III, ORF45 which encodes the virion
XX CC assembly protein, ORF46 which encodes uracil DNA glycosylase (UDG),
XX CC ORF47 which encodes glycoprotein L. KSHV is a new human Herpesvirus
XX CC (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common
XX CC form of neoplasm occurring in persons with acquired immune deficiency
XX CC syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis,
XX CC diagnosis and treatment of a subject with Kaposi's sarcoma and for
XX CC detecting expression of a DNA virus associated with Kaposi's sarcoma in a
XX CC cell.
XX
XX SO Sequence 35100 BP; 8016 A; 9231 C; 9477 G; 8376 T; 0 other:
XX
XX Query Match 0.1%; Score 23; DB 20; Length 35100;
XX Best Local Similarity 100.0%; Pred. No. 38;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 9414 AGCTCAGTCTCATATTATCT 9436
XX 111111111111111111111111
XX DB 12655 AGTCTCAGTCTCATATTATCT 12677
XX
XX RESULT 14
XX AAV19941
XX ID AAV19941 standard; DNA: 137507 BP.
XX
XX AC AAV19941;
XX
XX DT 03-AUG-1998 (first entry)
XX
XX DE KSHV long unique coding region and terminal repeat.
XX
XX KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II;
XX KM interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis;
XX KM complement-binding protein; glycoprotein; capsid protein IV; infection;
XX KM immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
XX KM lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides;
XX KM HIV immune status; anti-inflammatory agent; therapy; ds.
XX
XX Kaposi's sarcoma-associated herpes virus.
XX
XX OS
XX FH Key Location/Qualifiers
XX FT CDS 1142..2794
XX FT /*tag= a
XX FT /product= complement-binding protein
XX FT 8699..11236
XX FT /*tag= b
XX FT /product= glycoprotein B
XX FT complement (17261..17875)
XX
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FT      CDS      /tag- c
FT      CDS      /product- interleukin 6
FT      CDS      complement (21548..21832)
FT      CDS      /tag- d
FT      CDS      /product- macrophage inflammatory protein II
FT      CDS      complement (27137..27424)
FT      CDS      /tag- e
FT      CDS      /product- interferon regulatory factor 1
FT      CDS      28661..29741
FT      CDS      /tag- f
FT      CDS      /product- protein T1.1
FT      CDS      complement (38976..60175)
FT      CDS      /tag- g
FT      CDS      /product- glycoprotein M
FT      CDS      complement (69412..69915)
FT      CDS      /tag- h
FT      CDS      /product- glycoprotein L
FT      CDS      complement (88410..88910)
FT      CDS      /tag- i
FT      CDS      /product- interferon regulatory factor 2
FT      CDS      89600..90541
FT      CDS      /tag- j
FT      CDS      /product- interferon regulatory factor 3
FT      CDS      90173..90643
FT      CDS      /tag- k
FT      CDS      /product- glycoprotein X
FT      CDS      complement (93636..94127)
FT      CDS      /tag- l
FT      CDS      /product- interferon regulatory factor 4
FT      CDS      complement (111931..112443)
FT      CDS      /tag- m
FT      CDS      /product- capsid protein IV
FT      CDS      complement (123808..127296)
FT      CDS      /tag- n
FT      CDS      /product- immediate early protein
FT      CDS      W09804576-A1.
FT      CDS      05-FEB-1998.
FT      CDS      22-JUL-1997; 97WO-US13346.
FT      CDS      29-NOV-1996; 96US-0757669.
FT      CDS      25-JUL-1996; 96US-0688243.
FT      CDS      25-JUL-1996; 96US-0686349.
FT      CDS      25-JUL-1996; 96US-0686350.
FT      CDS      25-JUL-1996; 96US-0687253.
FT      CDS      25-JUL-1996; 96US-0688814.
FT      CDS      05-SEP-1996; 96US-0708678.
FT      CDS      10-OCT-1996; 96US-0728323.
FT      CDS      13-NOV-1996; 96US-0747887.
FT      CDS      13-NOV-1996; 96US-0748640.
FT      CDS      (UYCO ) UNIV COLUMBIA NEW YORK.
FT      CDS      PA
FT      CDS      PI Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
FT      CDS      WPI; 1998-130615/12.
FT      CDS      XX
FT      CDS      DR WPI; 1998-130615/12.
FT      CDS      XX
FT      CDS      PT New nucleic acid encoding Kaposi's sarcoma associated herpes virus
FT      CDS      proteins - useful for, e.g. detecting levels of HHV8 in, and
FT      CDS      preparation of vaccines for treatment of, HIV patients
FT      CDS      XX
FT      CDS      PS Example 2; Page 135-203; 230pp; English.
FT      CDS      XX
FT      CDS      CC This sequence represents the long unique region and terminal repeat of
FT      CDS      the Kaposi's sarcoma associated herpes virus (KSHV). KSHV is also known
FT      CDS      as human herpes virus 8 (HHV8). This sequence contains the DNAs of the
FT      CDS      invention which encode KSHV polypeptides selected from: (a) viral
FT      CDS      macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6);
FT      CDS      (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;
FT      CDS      (d) capsid protein IV encoded by ORF55, and (e) immediate early protein
FT      CDS      encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded

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CC      by it, and antibodies (Ab) specific for the proteins are useful for
CC      detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body
CC      fluids or tissue samples. HHV8 infections can be treated with antisense
CC      or triplex forming molecules or agents that bind specifically to the
CC      protein. Ab may be used for prophylaxis or treatment of HHV8 infection,
CC      while the protein can be used in protective vaccines. Ab may also be used
CC      to differentiate between lymphomas, and HHV8 may be implicated in many
CC      other lymphoproliferative diseases such as lymphomas, leukaemia,
CC      splenomegaly and mycosis fungoides. Cells and animals containing the
CC      nucleic acid are useful for drug screening. HHV8-derived peptides can be
CC      used as targets for antiviral drugs, e.g. dihydropyridate reductase gene
CC      can be inhibited with methotrexate. These can also be used to determine
CC      the immune status of a patient infected with HIV. HHV8 derived protein
CC      viral MIP III may be used as an anti-inflammatory agent for,
CC      e.g. treating rheumatoid arthritis. This sequence is stated as containing
CC      81 open reading frames.
CC      SQ
CC      Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
CC      Query Match 0.1%; Score 23; DB 19; Length 137507;
CC      Best Local Similarity 100.0%; Pred. No. 34;
CC      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC      QY 9414 AGCTCAGTCTATATTATCT 9436
CC      DB 47755 AGCTCAGTCTATATTATCT 47777
CC      RESULT 15
CC      AAC59414/C
CC      ID AAC59414 standard; CDNA: 1060 BP.
CC      XX
CC      AC AAC59414;
CC      XX
CC      DT 02-FEB-2001 (first entry)
CC      XX
CC      DE Human secreted protein CDNA #23.
CC      XX
CC      KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
CC      KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;
CC      KW vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
CC      KW cardiant; gene therapy; cancer; Immune disorder; cardiovascular disorder;
CC      KW neurological disease; infection; human; secreted protein; ss.
CC      XX
CC      OS Homo sapiens.
CC      XX
CC      PN W0200056765-A1.
CC      XX
CC      PD 28-SEP-2000.
CC      XX
CC      PF 16-MAR-2000; 2000WO-US06823.
CC      XX
CC      PR 19-MAR-1999; 99US-0125364.
CC      PR 08-DEC-1999; 99US-0169623.
CC      XX
CC      PA (HDMA-) HDMA GENOME SCI INC.
CC      XX
CC      PI Rosen CA, Ruben SM, Komatsoulis G;
CC      XX
CC      DR WPI; 2000-602215/57.
CC      DR P-PSDB: AAB33984.
CC      XX
CC      PT Nucleic acid molecules encoding human secreted proteins, used in
CC      PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
CC      PT Parkinson's diseases and cancers -
CC      PT
CC      PS Claim 1; Page 341; 410pp; English.
CC      XX
CC      CC The invention relates to the isolation of genes AAC59392-C59439 encoding
CC      CC 48 human secreted proteins AAB33963-B34006. The genes can be used to
CC      CC generate fusion proteins by linking to the gene for the human
CC      CC immunoglobulin G Fc portion (SGRID) for increasing the stability of
CC      CC the fusion protein as compared to the human protein only. The genes and

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CC proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated
 CC from a range of human tissues disclosed in the specification. The
 CC nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d)
 CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

SQ Sequence 1060 BP; 316 A; 212 C; 217 G; 311 T; 4 other;

Query Match 0.1%; Score 22; DB 21; Length 1060;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21007 AAAAAATGATACGATATACAAAC 21028
 |||||||||||||||||||
 Db 367 AAAAAATGATACGATATACAAAC 346

RESULT 16
 ABR63559
 ID ABR63559 standard; cDNA; 1451 BP.
 XX
 AC ABR63559;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Rat sequence differentially expressed in response to a hepatotoxin #1466.
 XX
 KM Rat; ss: hepatotoxin; expressed sequence tag; EST; drug screening;
 XX differential expression; centrilobular necrosis; steatosis.
 XX
 OS Rattus norvegicus.
 XX
 PN M0200210453-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US23872.
 XX
 PR 31-JUL-2000; 2000US-222040P.
 PR 02-NOV-2000; 2000US-244880P.
 PR 11-MAY-2001; 2001US-280029P.
 PR 15-MAY-2001; 2001US-280645P.
 PR 22-MAY-2001; 2001US-292336P.
 PR 06-JUN-2001; 2001US-295798P.
 PR 13-JUN-2001; 2001US-297457P.
 PR 19-JUN-2001; 2001US-298884P.
 PR 09-JUL-2001; 2001US-303459P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendlick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 XX
 DR WPI; 2002-241625/29.
 XX
 PT Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells -
 XX
 PS Claim 1; Seq ID No 1466; 239pp; English.
 XX
 CC The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the

CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression.
 CC The method can also be used to identify an agent which modulates the
 CC toxic response and predict cellular pathways that a compound modulates
 CC in a cell. The methods utilise a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.

SQ Sequence 1451 BP; 386 A; 374 C; 379 G; 312 T; 0 other;

Query Match 0.1%; Score 22; DB 24; Length 1451;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25967 GAACAGCTGCTTCCAAAGATC 25988
 |||||||||||||||||||
 Db 1367 GAACAGCTGCTTCCAAAGATC 1388

RESULT 17
 ABA01689
 ID ABA01689 standard; mRNA; 2526 BP.
 XX
 AC ABA01689;
 XX
 DT 08-FEB-2002 (first entry)
 XX
 DE Mouse fibroblast growth factor receptor 1 mRNA SEQ ID NO:5.
 XX
 KM Fibroblast growth factor receptor 1; FGFR1; antisense oligonucleotide;
 XX phosphorothioate; diagnosis; ss.
 XX
 OS Mus sp.
 XX
 PN JP2001252085-A.
 XX
 PD 18-SEP-2001.
 XX
 PF 15-MAR-2000; 2000JP-0072741;
 XX
 PR 15-MAR-2000; 2000JP-0072741.
 XX
 PA (TOAG) TOA GOSSEI CHEM IND LTD.
 XX
 DR WPI; 2002-029661/04.
 XX
 PT An antisense nucleic acid compound used as a diagnostic and therapeutic
 PT agent -
 XX
 PS Example; Page 7-8; 10pp; Japanese.
 XX
 CC The present invention describes an antisense nucleic acid compound (I),
 CC used as a diagnostic and therapeutic agent. (I) comprises:

CC (1) an antisense nucleic acid compound (II) having the base sequence
CC TTGGGTTT;
CC (11) an antisense nucleic acid compound (III) having the above base
CC sequence in which the base number is expressed by a base sequence
CC between 10 and 60; and
CC (111) an antisense nucleic acid molecule (IV) comprising one of the 3
CC sequences given in ABA01686 to AAB01688, all comprising of 20 nucleic
CC acids, and that inhibit the expression of fibroblast growth factor
CC receptor 1 (FGFR1). (I) is useful as a treating agent, a diagnostic
CC agent and a research reagent. The present sequence represents mouse
CC FGFR1 mRNA, which is given in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 2526 BP; 576 A; 710 C; 712 G; 528 U; 0 other;

Query Match 0.1%; Score 22; DB 24; Length 2526;
Best Local Similarity 77.3%; Pred. No. 1.3e+02;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 25967 GAACAGCTGCTCTCCAAAGATC 25988
DB 1834 GAACAGCTGCTCTCCAAAGATC 1855
|||||:|:|:|:|:|:|

RESULT 18
AAV44041
ID AAV44041 standard; DNA; 3503 BP.
XX
AC AAV44041;
XX
XX 25-MAR-2003 (updated)
DT 01-OCT-1998 (first entry)
XX
XX Mouse bFGF receptor DNA.
XX
XX Basic fibroblast growth factor receptor; bFGF; heparin binding; murine;
KM antitumour agent; inhibitor; wound healing; ss.
XX
OS Mus sp.
XX
XX
FH Key Location/Qualifiers
FT CDS 282..2744
FT /tag= a
FT /product= bFGF receptor
FT /note= "basic fibroblast growth factor receptor"
XX
XX
XX US5789182-A.
XX
XX
XX 04-AUG-1998.
XX
XX
XX 14-DEC-1993; 93US-0166717.
XX
XX 20-DEC-1990; 90US-0631717.
XX
XX 14-DEC-1993; 93US-0166717.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX (HARD) HARVARD COLLEGE.
XX
XX
XX Flanagan JG, Klagsbrun M, Leder P, Ornitz DM, Yayon A;
XX WPI; 1998-446074/38.
XX
XX P-PSDB; AAM63844.
XX
XX Assays for high-affinity heparin-binding growth factor receptor
PT ligands - using receptor-overexpressing cells or cell-free system
XX
XX
XX Disclosure: Fig 9; 38pp; English.
XX
XX
XX This sequence encodes a murine basic fibroblast growth factor (bFGF)
CC which is a member of the heparin-binding growth factor receptor family.
CC This protein is used in a method which assays the ability of a substance
CC to bind to a high-affinity heparin-binding growth factor (bFGF) receptor.
CC The assay screens for potential antitumour agents that inhibit binding of

CC HBGF to high-affinity receptors, or for potential wound healing agents
CC that promote such binding.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 3503 BP; 797 A; 995 C; 972 G; 730 T; 9 other;

Query Match 0.1%; Score 22; DB 19; Length 3503;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25967 GAACAGCTGCTCTCCAAAGATC 25988
DB 2052 GAACAGCTGCTCTCCAAAGATC 2073
|||||:|:|:|:|:|:|

RESULT 19
ABL33920/C
ID ABL33920 standard; DNA; 12590 BP.
XX
XX
XX ABL33920;
XX
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX
DE Human immune system associated gene SEQ ID NO: 1893.
XX
XX
XX Human immune system disease; cytosine methylation; antiasthmatic;
KM antihypertensive; antiasthmatic; antianemic; cytostatic; nootropic;
KM neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KM antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KM antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KM acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KM neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KM gene; ds.
XX
XX
XX Homo sapiens.
XX
XX WO200200928-A2.
XX
XX 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07537.
XX
XX 30-JUN-2000; 2000DE-1032529.
XX
XX 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
XX
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation
XX
XX
XX Claim 1; SEQ ID NO 1893; 32pp + Sequence Listing; German.
XX
XX
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
XX
XX Sequence 12590 BP; 2516 A; 310 C; 3233 G; 6531 T; 0 other;

Query Match 0.1%; Score 22; DB 24; Length 12590;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28429 TCATCTACTAATAATAATAAAA 28450

```

DB      5900 TCATCTACTAAATTAATTAATAA 5879
      |||
RESULT 20
AAH71549/c
ID      AAH71549 standard; cDNA; 752 BP.
XX
XX      AAH71549;
AC
XX      19-SEP-2001 (first entry)
DT
XX      Human cervical cancer marker nucleic acid 2823.
DE
XX      Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX      Homo sapiens.
OS
XX      WO200142467-A2.
PN
XX      14-JUN-2001.
PD
XX      08-DEC-2000; 2000WO-US33312.
PF
XX      08-DEC-1999; 99US-0169681.
PR      21-DEC-1999; 99US-0171350.
PR      14-MAR-2000; 2000US-0189315.
PR      12-MAY-2000; 2000US-0203791.
PR      09-JUN-2000; 2000US-0210600.
PR      21-JUL-2000; 2000US-0220114.
XX
XX      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX      PI      Schlegel R, Deeds J, Berger A, Zhao X;
XX      WPI: 2001-375006/39.
XX
XX      New isolated nucleic acid for diagnosing and treating cervical cancer
XX      and for assessing and detecting compounds for treating the cancer -
XX
XX      Claim 1; Page 579; 1051pp; English.
XX
XX      The invention relates to novel genes (AAH68727-AAH73383) associated with
XX      cervical cancer with cytostatic activity. The nucleic acids and encoded
XX      polypeptides are useful: to assess if a patient is afflicted with
XX      cervical cancer or has a pre-malignant condition; to monitor the
XX      progression of cervical cancer or a premalignant condition in a patient;
XX      and to select and/or assess the efficacy of a compound or therapy for
XX      inhibiting cervical cancer in a patient. The nucleic acids may also be
XX      useful for gene therapy.
XX
SQ      Sequence 752 BP; 219 A; 161 C; 189 G; 181 T; 2 other;
      Query Match      0.1%; Score 21; DB 22; Length 752;
      Best Local Similarity 100.0%; Pred. No. 3.7e+02;
      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      14343 AACCAAAAGATTGGCCCGT 14363
DB      483 AACCAAAAGATTGGCCCGT 463
      |||
RESULT 21
AAH04342/c
ID      AAH04342 standard; DNA; 1536 BP.
XX
XX      AAH04342;
AC
XX      13-APR-1999 (first entry)
DT
XX      Human secreted protein gene 32 clone HTLDQ11.
DE
XX      Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX

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KW      diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
KW      developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW      immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW      inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW      cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW      osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW      endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX      Homo sapiens.
OS
XX      WO9856804-A1.
PN
XX      17-DEC-1998.
PD
XX      11-JUN-1998; 98WO-US12125.
PF
XX      02-OCT-1997; 97US-0061060.
PR      13-JUN-1997; 97US-0049547.
PR      13-JUN-1997; 97US-0049548.
PR      13-JUN-1997; 97US-0049549.
PR      13-JUN-1997; 97US-0049550.
PR      13-JUN-1997; 97US-0049606.
PR      13-JUN-1997; 97US-0049607.
PR      13-JUN-1997; 97US-0049608.
PR      13-JUN-1997; 97US-0049609.
PR      13-JUN-1997; 97US-0049610.
PR      13-JUN-1997; 97US-0049611.
PR      13-JUN-1997; 97US-0050566.
PR      13-JUN-1997; 97US-0050901.
PR      13-JUN-1997; 97US-0052989.
PR      08-JUL-1997; 97US-0051919.
PR      18-AUG-1997; 97US-0055284.
PR      12-SEP-1997; 97US-0058665.
PR      12-SEP-1997; 97US-0058668.
PR      12-SEP-1997; 97US-0058669.
PR      12-SEP-1997; 97US-0058750.
PR      12-SEP-1997; 97US-0058751.
PR      12-SEP-1997; 97US-0058752.
PR      12-SEP-1997; 97US-0058753.
PR      02-OCT-1997; 97US-0060834.
PR      02-OCT-1997; 97US-0060841.
PR      02-OCT-1997; 97US-0060844.
PR      02-OCT-1997; 97US-0060865.
PR      02-OCT-1997; 97US-0061059.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      PI      Brewer LA, Edner R, Ferris AM, Feng P, Greene JM, Lafleur DW;
XX      Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
XX      Xu GL;
XX      WPI: 1999-080881/07.
XX      P-PSDB; AAW78157.
XX
XX      New isolated human genes and the secreted polypeptides they encode -
XX      useful for diagnosis and treatment of e.g. cancers, neurological
XX      disorders, immune diseases, inflammation or blood disorders
XX
XX      Claim 1; Page 197-198; 380pp; English.
XX
XX      This sequence represents a nucleic acid molecule which encodes a
XX      secreted human protein. The gene number, and the clone it is derived
XX      from, are detailed in the descriptor line. The gene can be used to
XX      generate fusion proteins by linking to the gene to a human immunoglobulin
XX      Fc portion (e.g. AAH04302) for increasing the stability of the fused
XX      protein as compared to the human protein only.
XX      The invention relates to 86 novel genes and their fragments (nucleic
XX      acid sequences: AAH03311-X04410; amino acid sequences: AAW78126-W78225)
XX      which are useful for preventing, treating or ameliorating medical
XX      conditions e.g. by protein or gene therapy. Also, pathological
XX      conditions can be diagnosed by determining the amount of the new
XX      polypeptides in a sample or by determining the presence of mutations in
XX      the new polynucleotides. Specific uses are described for each of the 86

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CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAX04311 for described uses).

SO Sequence 1536 BP; 359 A; 382 C; 312 G; 469 T; 14 other;

Query Match 0.18; Score 21; DB 20; Length 1536;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10475 GGAAATAGCTGTAATAGT 10495
 DB 649 GGAAATAGCTGTAATAGT 629

RESULT 22
 ABA88869
 ID ABA88869 standard; DNA: 1557 BP.

AC ABA88869;

DT 11-FEB-2002 (first entry)

DE Escherichia coli polynucleotide SEQ ID NO 324.

KW Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
 KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
 KW systemic infection; non-diarrhoeal infection; septicaemia;
 KW pyelonephritis; antibiotic resistance; ds.

OS Escherichia coli.

PN WO20016572-A2.

PD 13-SEP-2001.

PF 12-MAR-2001; 2001WO-EP03445.

PR 10-MAR-2001; 2000FR-0003145.

PR 02-FEB-2001; 2001FR-0001449.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Blingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;

DR WPI; 2001-550253/61.

PT A library of DNA fragments of Escherichia coli strains for the
 PT phylogenic determination of a given strain comprises polynucleotides of
 PT nature B2/D+ A- -
 PS Exemple 6; Fig 6; 646pp; English.

CC The invention relates to a library of DNA fragments of Escherichia coli
 CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533)
 CC and encoded proteins (ABBS2459-ABBS2919 and ABBS2954-ABBS3094) of nature
 CC B2/D+-. The polynucleotides have potential antiinflammatory,
 CC antibacterial and immunosuppressive activity as part of pharmaceutical
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli
 CC infections. The polypeptides are useful for determining the phylogenic
 CC group of a given E. coli strain. These polypeptides can detect and treat
 CC an undesired development of E. coli, particularly an extra-intestinal
 CC infection that include systemic and non-diarrhoeal infections such as
 CC septicaemia, pyelonephritis and meningitis this is particularly
 CC advantageous as bacterial resistance is increasing with the more
 CC frequent use of broad spectrum antibiotics.

XX Sequence 1557 BP; 446 A; 337 C; 407 G; 367 T; 0 other;

Query Match 0.18; Score 21; DB 22; Length 1557;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23363 CTGCTGCCACGCCGTGGTA 23383

DB 530 CTGCTGCCACGCCGTGGTA 550
 ||||||||||||||||||

RESULT 23
 ABZ09971/c
 ID ABZ09971 standard; DNA: 3628 BP.

AC ABZ09971;

DT 16-JAN-2003 (first entry)

DE Haematopoietic cell proliferation disorder related DNA sequence #111.

KW Human; haematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; gene; ds.

OS Homo sapiens.

PN WO20027272-A2.

PD 03-OCT-2002.

PF 26-MAR-2002; 2002WO-EP03401.

PR 26-MAR-2001; 2001US-278333P.

PA (EPIC-) EPICENOMICS AG.

PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
 PI Pelet C, Schwabe I, Ziebarth H;

DR WPI; 2003-018942/01.

PT Detecting and differentiating between haematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent
 PT that distinguishes between methylated and non-methylated CpG
 PT dinucleotides -

PS Claim 28; SEQ ID 111; 117pp; English.

CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related
 CC DNA sequences. The nucleotide sequences from the present invention can
 CC also be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables
 CC a highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients.

XX Sequence 3628 BP; 734 A; 246 C; 1028 G; 1620 T; 0 other;

Query Match 0.18; Score 21; DB 25; Length 3628;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28433 CTACTAAATTAATAAACAA 28453
|||||
DB 1013 CTACTAAATTAATAAACAA 993

RESULT 24

AB210117/C
ID AB210117 standard; DNA; 3628 BP.

XX AB210117;

DT 16-JAN-2003 (first entry)

XX Haematopoietic cell proliferation disorder related DNA sequence #257.

DE Human; haematopoietic cell proliferation disorder; cytostatic;

KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

KM cytosine methylation state; gene; ds.

XX Homo sapiens.

XX WO20027272-A2.

XX 03-OCT-2002.

XX 26-MAR-2002; 2002MO-EP03401.

XX 26-MAR-2001; 2001US-278333P.

XX (EPIC-) EPIGENOMICS AG.

XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;

PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Len E;

PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;

PI Pelet C, Schwope I, Ziebarth H;

XX WPI; 2003-018942/01.

XX DR 2003-018942/01.

XX PT Detecting and differentiating between hematopoietic cell proliferative

PT disorders, comprises contacting a target nucleic acid with a reagent

PT that distinguishes between methylated and non-methylated CpG

PT dinucleotides -

XX Claim 28; SEQ ID 257; 117pp; English.

XX The present invention describes a method for detecting and

CC differentiating between haematopoietic cell proliferative disorders

CC associated with at least 1 gene and/or their regulatory regions in a

CC subject. The method comprises contacting a target nucleic acid in a

CC biological sample obtained from the subject with at least 1 reagent,

CC which distinguishes between methylated and non-methylated CpG

CC dinucleotides within the target nucleic acid. AB209861 to AB211118

CC represent specifically claimed nucleotide sequences from the present

CC invention. Oligonucleotides from the present invention can be used: for

CC differentiating between healthy haematopoietic cells and proliferative

CC disorder haematopoietic cells: for differentiating between acute

CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for

CC determining the cytosine methylation state and/or single nucleotide

CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder

CC related sequences and their complements; and as primers for the

CC amplification of haematopoietic cell proliferation disorder related

CC DNA sequences. The nucleotide sequences from the present invention can

CC also be used for detecting a predisposition to, differentiation between

CC subclasses, diagnosis, prognosis, treatment and/or monitoring of

CC haematopoietic cell proliferative disorders. The present method enables

CC a highly specific classification of haematopoietic cell proliferative

CC disorders allowing for improved and informed treatment of patients.

XX Sequence 3628 BP; 734 A; 0 C; 1028 G; 1866 T; 0 other;

SO Query Match 0.1%; Score 21; DB 25; Length 3628;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28433 CTACTAAATTAATAAACAA 28453
|||||
DB 1013 CTACTAAATTAATAAACAA 993

RESULT 25

ABL32593/C
ID ABL32593 standard; DNA; 6127 BP.

XX ABL32593;

DT 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 566.

DE Human; immune system disease; cytosine methylation; antiasthmatic;

KW antileukemic; anti-HIV; anticonvulsant; ophthalmological;

KW antineoplastic; antineoplastic; antidiabetic; antipsoriatic;

KW antineoplastic; antineoplastic; antidiabetic; antipsoriatic;

KW acute myeloid leukaemia; cancer; eye disease; arteriosclerosis; anaemia;

KW acute myeloid leukaemia; cancer; eye disease; arteriosclerosis; anaemia;

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

KW gene; ds.

XX Homo sapiens.

XX WO200200928-A2.

XX 03-JAN-2002.

XX 02-JUL-2001; 2001MO-EP07537.

XX 30-JUN-2000; 2000DE-1032529.

XX 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.

XX Berlin K, Piepenbrock C, Berlin K;

PI Olek A, Piepenbrock C, Berlin K;

PI WPI; 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful

PT for diagnosis and treatment of diseases associated with abnormal

PT cytosine methylation -

XX Claim 1; SEQ ID NO 566; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated

CC genes which are modified by the methylation of cytosines. The sequences

CC can be used in the diagnosis and treatment of immune system disorders,

CC including eye diseases such as retinopathy, neovascular glaucoma and

CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel

CC diseases. The present sequence is a gene of the invention.

XX Sequence 6127 BP; 1578 A; 67 C; 1387 G; 3095 T; 0 other;

SO Query Match 0.1%; Score 21; DB 24; Length 6127;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 26

ABST79028

ID ABST79028 standard; DNA; 7636 BP.

XX ABST79028;

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XX 17-DEC-2002 (first entry)
XX
XX E. coli CFT073 genomic sequence #195.
DE
XX Pathogenic; Escherichia coli CFT073 infection; livestock; pyelonephritis;
XX urinary tract infection; open reading frame; ORF; uropathogenic;
XX antibacterial; atrophic; nephrotropic; gene; ds.
XX
XX Escherichia coli.
XX
XX WO200259320-A2.
XX
XX 01-AUG-2002.
XX
XX 19-OCT-2001; 2001WO-US46833.
XX
XX 19-OCT-2000; 2000US-242412P.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Blatner FR, Welch RA, Burland VD:
XX
XX WPI; 2002-691532/74.
XX
XX New DNA sequences of the pathogenic Escherichia coli CFT073 strain,
XX useful for preventing or treating E. coli CFT073 infection in humans or
XX livestock.
XX
XX Claim 1; Page 587-591; 765pp; English.
XX
XX The present invention relates to polynucleotide sequences from the
XX genome of the pathogenic Escherichia coli strain CFT073. Almost all
XX the sequences present in E. coli CFT073 are absent in the previously
XX sequenced laboratory strain K-12. The polynucleotide sequences of
XX the invention are useful for preventing, diagnosing or treating
XX E. coli CFT073 infection in humans or livestock. The polynucleotide
XX sequences are useful for preventing urinary tract infections and
XX pyelonephritis. Likewise, the polypeptides encoded by the different
XX open reading frames (ORF1-5) are useful for generating a vaccine
XX against uropathogenic E. coli strains. AB578834-AB579085 represent
XX genomic sequences from E. coli strain CFT073.
XX
XX Sequence 7636 BP; 2087 A; 1619 C; 1684 G; 2246 T; 0 other;
SQ
Query Match 0.1%; Score 21; DB 24; Length 7636;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23363 CTGCTGCCACGCGCGTGGGTA 23383
DB 6380 CTGCTGCCACGCGCGTGGGTA 6400
RESULT 27
ABA88864
ID ABA88864 standard; DNA; 7646 BP.
XX
XX ABA88864;
AC
XX
XX 11-FEB-2002 (first entry)
XX
XX Escherichia coli polynucleotide SEQ ID NO 315.
DE
XX
XX Escherichia coli; B2/D+A-; antinflammatory; antibacterial;
XX immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
XX systemic infection; non-diarrhoeal infection; septicaemia;
XX pyelonephritis; antibiotic resistance; ds.
XX
XX Escherichia coli.
XX
XX WO200166572-A2.
XX

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PD 13-SEP-2001.
XX
XX 12-MAR-2001; 2001WO-EP03445.
XX
XX 10-MAR-2000; 2000FR-0003145.
XX
XX 02-FEB-2001; 2001FR-0001449.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;
XX
XX WPI; 2001-550253/61.
XX
XX A library of DNA fragments of Escherichia coli strains for the
XX phylogenetic determination of a given strain comprises polynucleotides of
XX nature B2/D+ A- -
XX
XX Example 6; Fig 6; 646pp; English.
XX
XX The invention relates to a library of DNA fragments of Escherichia coli
XX strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533)
XX and encoded proteins (AB52459-AB52919 and AB52954-AB53094) of nature
XX B2/D+A-. The polynucleotides have potential antinflammatory,
XX antibacterial and immunosuppressive activity as part of pharmaceutical
XX compositions used to treat, palliate or prevent extra-intestinal E. coli
XX infections. The polypeptides are useful for determining the phylogenic
XX group of a given E. coli strain. These polypeptides can detect and treat
XX an undesired development of E. coli, particularly an extra-intestinal
XX infection that include systemic and non-diarrhoeal infections such as
XX septicaemia, pyelonephritis and meningitis this is particularly
XX advantageous as bacterial resistance is increasing with the more
XX frequent use of broad spectrum antibiotics.
XX
XX Sequence 7646 BP; 2089 A; 1619 C; 1686 G; 2252 T; 0 other;
SQ
Query Match 0.1%; Score 21; DB 22; Length 7646;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23363 CTGCTGCCACGCGCGTGGGTA 23383
DB 6381 CTGCTGCCACGCGCGTGGGTA 6401
RESULT 28
AAQ90132/C
ID AAQ90132 standard; DNA; 8083 BP.
XX
XX AAQ90132;
AC
XX
XX 25-MAR-2003 (updated)
XX
XX 11-NOV-1995 (first entry)
XX
XX Plasmid pBHVKex-3::p53.
XX
XX Plasmid pBHVKex-3::p53; vector; bovine viral diarrhoea virus 2724;
XX gp53 protein; major glycoprotein; cytomegalo virus promoter;
XX bovine somatotropin polyadenylation signal; attenuation;
XX recombinant vaccine; ds.
XX
XX Bovine viral diarrhoea virus (2724).
XX
XX WO9512682-A2.
XX
XX 11-MAY-1995.
XX
XX 31-OCT-1994; 94WO-US12198.
XX
XX 05-NOV-1993; 93US-0147810.
XX
XX (UPJO ) UPJOHN CO.
XX
XX Haanes EJ, Wardley RC;
XX

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XX WPI: 1995-185781/24.
XX A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
PS Claim 23; Page 22-25; 60pp; English.
XX
CC The sequence corresponds to plasmid PBHVKex-3::gp53, which contains
CC a bovine viral diarrhoea virus (BVDV) major glycoprotein gp53 gene
CC inserted between a cytomegalovirus promoter and a bovine
CC somatotropin gene polyadenylation signal from plasmid
CC pHAS4-delta-Bxex-3, with no added signal peptide sequence. The
CC original gp53 gene has been inserted without site-directed
CC mutagenesis. The plasmid may be used to produce a replicating
CC non-pathogenic virus for use as a safe attenuated recombinant
CC vaccine against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8083 BP; 1833 A; 2215 C; 2247 G; 1788 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8083;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7319 GTGACGCCCTGCGGCCAG 7339
DB 904 GTGACGCCCTGCGGCCAG 884
|||||

RESULT 29
AAO90134/C
ID AAO90134 standard; DNA; 8135 BP.
XX
AC AAO90134;
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1995 (first entry)
XX
DE Plasmid PBHVKex-1::gIII/p53.
XX
KM Plasmid PBHVKex-1::gIII/p53; vector; gp53 protein mutant;
KM bovine viral diarrhoea virus 2724; major glycoprotein;
KM pseudorabies virus gIII signal peptide; attenuation;
KM Plasmid pUC1564; Escherichia coli; recombinant vaccine; ds.
XX
OS Bovine viral diarrhoea virus (2724).
OS
XX
PN WO9512682-A2.
XX
PD 11-MAY-1995.
XX
PF 31-OCT-1994; 94WO-US12198.
XX
PR 05-NOV-1993; 93US-0147810.
XX
PA (UPJO) UPJOHN CO.
XX
PI Haanes EJ, Wardley RC;
XX
DR WPI: 1995-185781/24.
XX
PT A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
PS Claim 17; Page 30-34; 60pp; English.
XX
CC The sequence corresponds to plasmid PBHVKex-1::gIII/p53, which
CC contains a bovine viral diarrhoea virus (BVDV) major glycoprotein
CC gp53 mutant gene preceded by a pseudorabies virus gIII signal
CC peptide sequence in plasmid pHAS4-delta-Bxex-1. The plasmid
CC may be used to produce a replicating non-pathogenic virus, T11-3
CC (deposited as plasmid pUC1564 in Escherichia coli 15085, NRRL

CC B-21350), for use as a safe attenuated recombinant vaccine
CC against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8135 BP; 1778 A; 2325 C; 2180 G; 1852 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8135;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7319 GTGACGCCCTGCGGCCAG 7339
DB 904 GTGACGCCCTGCGGCCAG 884
|||||

RESULT 30
AAO90136/C
ID AAO90136 standard; DNA; 8135 BP.
XX
AC AAO90136;
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1995 (first entry)
XX
DE Plasmid PBHVKex-3::gIII/p53.
XX
KM Plasmid PBHVKex-3::gIII/p53; vector; gp53 protein mutant;
KM bovine viral diarrhoea virus 2724; major glycoprotein;
KM pseudorabies virus gIII signal peptide; attenuation;
KM Plasmid pUC1565; Escherichia coli; recombinant vaccine; ds.
XX
OS Bovine viral diarrhoea virus (2724).
OS
XX
PN WO9512682-A2.
XX
PD 11-MAY-1995.
XX
PF 31-OCT-1994; 94WO-US12198.
XX
PR 05-NOV-1993; 93US-0147810.
XX
PA (UPJO) UPJOHN CO.
XX
PI Haanes EJ, Wardley RC;
XX
DR WPI: 1995-185781/24.
XX
PT A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
PS Claim 17; Page 39-43; 60pp; English.
XX
CC The sequence corresponds to plasmid PBHVKex-3::gIII/p53, which
CC contains a bovine viral diarrhoea virus (BVDV) major glycoprotein
CC gp53 mutant gene preceded by a pseudorabies virus gIII signal
CC peptide sequence in plasmid pHAS4-delta-Bxex-3. The plasmid
CC may be used to produce replicating non-pathogenic virus T11-8
CC (deposited as plasmid pUC1565 in Escherichia coli UC 15086, NRRL
CC B-21351), for use as a safe attenuated recombinant vaccine
CC against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8135 BP; 1833 A; 2242 C; 2262 G; 1798 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8135;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7319 GTGACGCCCTGCGGCCAG 7339
DB 904 GTGACGCCCTGCGGCCAG 884
|||||

```
RESULT 31
AA090133/c
ID AA090133 standard; DNA: 8149 BP.
XX
XX
AC AA090133;
XX
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1995 (first entry)
XX
XX
DE Plasmid PBHVKex-1::gBGH/p53.
XX
XX
KW Plasmid PBHVKex-1::gBGH/p53; vector: gp53 protein mutant;
KW bovine viral diarrhoea virus 2724; major glycoprotein;
KW bovine somatotropin signal peptide; attenuation;
KW recombinant vaccine; ds.
XX
XX
OS Bovine viral diarrhoea virus (2724).
XX
XX
PN W09512682-A2.
XX
XX
PD 11-MAY-1995.
XX
XX
PF 31-OCT-1994; 94WO-US12198.
XX
XX
PR 05-NOV-1993; 93US-0147810.
XX
XX
PA (UPJO ) UPJOHN CO.
XX
XX
PI Haanes EJ, Wardley RC;
XX
XX
DR WPI: 1995-185781/24.
XX
XX
PT A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
XX
XX
PS Claim 17; Page 26-30; 60pp; English.
XX
XX
XX
CC The sequence corresponds to plasmid PBHVKex-1::gBGH/p53, which
CC contains a bovine viral diarrhoea virus (BVDV) major glycoprotein
CC gp53 mutant gene preceded by a bovine somatotropin signal peptide
CC sequence in plasmid pHAS4-delta-BKex-1. The plasmid may be used
CC to produce a replicating non-pathogenic virus, T11-6 (deposited
CC as ATCC VR 2436) for use as a safe attenuated recombinant vaccine
CC against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 8149 BP; 1784 A; 2324 C; 2185 G; 1856 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8149;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7319 GTGACGCGCCTGCGGCCGAC 7339
DB 904 GTGACGCGCCTGCGGCCGAC 884

RESULT 32
AA090135/c
ID AA090135 standard; DNA: 8149 BP.
XX
XX
AC AA090135;
XX
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1995 (first entry)
XX
XX
DE Plasmid PBHVKex-3::BGH/p53.
XX
XX
KW Plasmid PBHVKex-3::BGH/p53; vector: gp53 protein mutant;
KW bovine viral diarrhoea virus 2724; major glycoprotein;
KW bovine somatotropin signal peptide; attenuation;
KW recombinant vaccine; ds.
XX
XX
```

```
OS Bovine viral diarrhoea virus (2724).
XX
XX
PN W09512682-A2.
XX
XX
ED 11-MAY-1995.
XX
XX
PF 31-OCT-1994; 94WO-US12198.
XX
XX
PR 05-NOV-1993; 93US-0147810.
XX
XX
PA (UPJO ) UPJOHN CO.
XX
XX
PI Haanes EJ, Wardley RC;
XX
XX
DR WPI: 1995-185781/24.
XX
XX
PT A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
XX
XX
PS Claim 17; Page 35-38; 60pp; English.
XX
XX
XX
CC The sequence corresponds to plasmid PBHVKex-3::BGH/p53, which
CC contains a bovine viral diarrhoea virus (BVDV) major glycoprotein
CC gp53 mutant gene preceded by a bovine somatotropin signal
CC peptide sequence in plasmid pHAS4-delta-BKex-3. The plasmid
CC may be used to produce a replicating non-pathogenic virus for use
CC as a safe attenuated recombinant vaccine against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 8149 BP; 1836 A; 2246 C; 2263 G; 1804 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8149;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7319 GTGACGCGCCTGCGGCCGAC 7339
DB 904 GTGACGCGCCTGCGGCCGAC 884

RESULT 33
AAS45354
ID AAS45354 standard; DNA: 8513 BP.
XX
XX
AC AAS45354;
XX
XX
DT 18-DEC-2001 (first entry)
XX
XX
XX
DE Chemically pretreated genomic DNA associated with cell cycle #30.
XX
XX
KW Cell cycle; human; CPG dinucleotide; cytosine methylation; HIV; aging;
KW human immunodeficiency virus; neurodegenerative disorder; solid tumour;
KW graft-versus-host disease; glomerular disease; Levy body disease; cancer;
KW arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritis;
KW immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
KW PCR primer.
XX
XX
OS Homo sapiens.
XX
XX
PN W0200168911-A2.
XX
XX
PD 20-SEP-2001.
XX
XX
PE 15-MAR-2001; 2001WO-EP02945.
XX
XX
PF 15-MAR-2000; 2000DE-1013847.
XX
XX
PR 06-APR-2000; 2000DE-1019058.
XX
XX
PR 07-APR-2000; 2000DE-1019173.
XX
XX
PR 30-JUN-2000; 2000DE-1032529.
XX
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
XX
PA (EPIG-) EPIGENOMICS AG.
XX
XX
```

PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-602751/68.
 DR
 XX
 PS Designing primers and probes for analysing diseases associated with
 PT cytosine methylation state e.g. arthritis, cancer, aging,
 PT arteriosclerosis comprising fragments of chemically modified genes
 PT associated with cell cycle -
 XX
 PS Claim 1; SEQ ID No 59; 28bp; English.
 XX
 CC Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA
 CC molecules associated with the cell cycle and specific PCR primers of the
 CC invention. The sequences are useful for detecting the methylation state
 CC of all CpG dinucleotides in a sequence and therefore for analysing
 CC associated diseases. By analysing cytosine methylations in the pretreated
 CC DNA, genetic and/or epigenetic parameters for the diagnosis and therapy
 CC of existing diseases or the predisposition to specific diseases can be
 CC ascertained. The parameters may be compared to another set of genetic
 CC and/or epigenetic parameters, the differences serving as basis for
 CC diagnosis and/or prognosis events which are disadvantageous to patients.
 CC The sequences of the invention are useful for the diagnosis and therapy
 CC of HIV infection, neurodegenerative disorders, graft-versus-host disease,
 CC aging, glomerular disease, Lewy body disease, arthritis,
 CC arteriosclerosis, solid tumours and cancers.
 CC
 SQ Sequence 8513 BP; 1821 A; 233 C; 2456 G; 4003 T; 0 other;
 XX
 Query Match 0.1%; Score 21; DB 22; Length 8513;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 16956 GAGTCGGGAGATTGTTT 16976
 DB 5725 GAGTCGGGAGATTGTTT 5745
 RESULT 34
 AAS46367
 ID AAS46367 standard; DNA; 8513 BP.
 XX
 AC AAS46367;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Tumour suppressor gene derived chemically modified sequence #89.
 XX
 KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
 KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
 KW cytosine methylation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200168912-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-EP02955.
 XX
 PR 15-MAR-2000; 2000DE-1013847.
 PR 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-602752/68.
 XX
 PT Fragments of chemically modified genes associated with tumour suppressor
 PT genes and oncogenes, useful in designing primers and probes for

PT analysing diseases associated with cytosine methylation state e.g.
 PT cancer -
 XX
 XX Claim 1; SEQ ID No 89; 27bp; English.
 XX
 CC The invention relates to a nucleic acid comprising a sequence of 18
 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and
 CC oncogenes having a sequence taken from 536 (actually 533 since
 CC numbers 408; 458 and 500 are missing from the sequence listing) sequences
 CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a
 CC peptide nucleic acid-oligonucleotide (PNA) of at least 9 nucleotides and may
 CC form part of a set of probes for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms and also to be used in an
 CC array for analysing diseases associated with CpG dinucleotides e.g.
 CC cancers and tumours. The probes can also be used in a method for
 CC ascertaining genetic and/or epigenetic parameters for the diagnosis
 CC and/or therapy of existing diseases or the predisposition to specific
 CC diseases, by analysing cytosine methylations. The parameters may be
 CC compared to another set of genetic and/or epigenetic parameters, the
 CC differences serving as basis for diagnosis and/or prognosis events which
 CC are disadvantageous to patients. The present sequence is one of the
 CC 533 genomic sequences derived from tumour suppressor genes and
 CC oncogenes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 8513 BP; 1821 A; 233 C; 2456 G; 4003 T; 0 other;
 XX
 Query Match 0.1%; Score 21; DB 22; Length 8513;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 16956 GAGTCGGGAGATTGTTT 16976
 DB 5725 GAGTCGGGAGATTGTTT 5745
 RESULT 35
 ABN80094
 ID ABN80094 standard; DNA; 8513 BP.
 XX
 AC ABN80094;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human chemically modified disease associated gene SEQ ID NO 111.
 XX
 KW Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;
 KW heart disease; epilepsy; histone deacetylation; muscular dystrophy;
 KW dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
 KW antidiabetic; cytostatic; anticonvulsant; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200200927-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-EP07536.
 XX
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-130908/17.
 XX

PT Novel nucleic acid useful for diagnosis and therapy of diseases
 PT associated with development genes such as diabetes, comprises a
 PT sequence of a segment of chemically pretreated DNA of genes associated
 PT with development
 PS Claim 1; SEQ ID NO 111; 27pp; English.
 XX
 CC The invention relates to a nucleic acid (I) comprising a sequence at
 CC least 18 bases in length of a segment of chemically pretreated DNA (II)
 CC of genes associated with development selected from 87 genes listed in
 CC the specification such as ACCPN, ADPN, or AFD and comprising one of 350
 CC sequences (ABN79984-ABN80333) or their complements. The invention is
 CC useful for the diagnosis or therapy of diseases associated with
 CC development genes, in particular disease related to homeobox containing
 CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes
 CC associated with congenital heart disease, epilepsy, diseases related to
 CC histone deacetylation, Currarino syndrome, diseases related with the
 CC development of the brain and limb girdle muscular dystrophy and dwarfism.
 CC Oligomers specific to each of the genes are useful for detecting the
 CC methylation state of all CpG dinucleotides within the 350 sequences or
 CC (II) and their complementary sequences, as primer oligonucleotides for
 CC the amplification of the 350 sequences, (II) and/or their complements and
 CC as oligomer probes for detecting the cytosine methylation state and/or
 CC single nucleotide polymorphisms (SNPs).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX
 SQ Sequence 8513 BP; 1821 A; 233 C; 2456 G; 4003 T; 0 other;
 Query Match 0.1%; Score 21; DB 24; Length 8513;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 16956 GAGTCGGGAGATTGTTT 16976
 Db 5725 GAGTCGGGAGATTGTTT 5745
 RESULT 36
 ABR28187
 ID ABR28187 standard; DNA; 8513 BP.
 XX
 AC ABR28187;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE DNA transcription associated genomic DNA #31.
 XX
 XX PNA transcription associated gene; peptide nucleic acid; PNA-oligomer;
 KW DNA: cytosine methylation state; SNP; retroviral infection; gene; ds;
 KW single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
 KW viral infection; Sezary syndrome; hematological disorder; tuberculosis;
 KW immunological disorder; Werner syndrome; developmental disorder;
 KW neuroblastis; Rieger's syndrome; neurological disorder; erythropoiesis;
 KW neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease;
 KW myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;
 KW angiodysgenesis; congenital heart disease; HDR syndrome; gene therapy;
 KW polyglutamine disorder; solid tumour.
 XX
 OS Unidentified.
 OS
 XX
 PN WO200192565-A2.
 XX
 PD 06-DEC-2001.
 XX
 PE 06-APR-2001; 2001WO-EP03973.
 XX
 PR 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX

PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI: 2002-090046/12.
 XX
 XX New nucleic acids or oligomers, useful for diagnosing or treating
 PT diseases associated with DNA transcription, e.g. immunological
 PT disorders, Werner syndrome, psoriasis, myocardial infarction, solid
 PT tumours or cancer
 PS Claim 1; SEQ ID NO 61; 32pp; English.
 XX
 CC The invention relates to a nucleic acid, which comprises a segment of the
 CC chemically pretreated DNA of genes associated with DNA transcription from
 CC one of 346 sequences, and an oligomer, in particular an oligonucleotide
 CC or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical
 CC to the chemically pretreated DNA of genes associated with DNA
 CC transcription. The set of oligomer probes are useful for detecting the
 CC cytosine methylation state and/or single nucleotide polymorphisms (SNPs)
 CC in a chemically pretreated genomic DNA. The nucleic acids are useful for
 CC diagnosing or treating diseases associated with DNA transcription
 CC (particularly with the methylation status), e.g. adenosine deaminase
 CC deficiency, viral infection, retroviral infection, Sezary syndrome,
 CC haematological disorders, immunological disorders, Werner syndrome,
 CC tuberculosis, developmental disorders, psoriasis, Rieger's syndrome,
 CC neurological disorders, neurodegenerative disorders, Waardenburg
 CC syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial
 CC infarction, hypertension, angiodysgenesis, erythropoiesis, congenital heart
 CC disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours
 CC or cancer. Sequences ABR28127-ABR28472 represent DNA transcription
 CC associated genomic DNA molecules of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from the
 CC European Patent Office.
 XX
 SQ Sequence 8513 BP; 1821 A; 233 C; 2456 G; 4003 T; 0 other;
 Query Match 0.1%; Score 21; DB 24; Length 8513;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 16956 GAGTCGGGAGATTGTTT 16976
 Db 5725 GAGTCGGGAGATTGTTT 5745
 RESULT 37
 ABL05364/C
 ID ABL05364 standard; cDNA; 36383 BP.
 XX
 AC ABL05364;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10574.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 KW
 KW Drosophila melanogaster.
 OS
 OS
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PE 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX

PI Venter JC, Adams M, Li PMD, Myers EW;
XX WPI; 2001-656860/75.
DR P-PSDB; ABB61261.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
XX Claim 1; SEQ ID NO 10574; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 36383 BP; 10996 A; 6940 C; 6697 G; 11550 T; 0 other;

Query Match 0.1%; Score 21; DB 23; Length 36383;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28437 TAAATTAATTAACACGCA 28457
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 11364 TAAATTAATTAACACGCA 11344

RESULT 38
AAH74201
ID AAH74201 standard; DNA; 124884 BP.
XX
XX AAH74201;
XX
XX 15-OCT-2001 (first entry)
XX
XX Nucleotide sequence of the Varicella virus Dumas strain.
XX
XX Dumas strain; pox vaccine; vaccine; poxvirus disease; chickenpox; ss.
XX
XX Varicella virus.
XX
XX WO200156600-A1.
XX
XX 09-AUG-2001.
XX
XX 31-JAN-2001; 2001WO-JP00678.
XX
XX 31-JAN-2000; 2000JP-0062734.
XX
XX (OSAU) UNITV OSAKA.
XX
XX Gomi Y, Sunamachi H, Takahashi M, Yamanishi K;
XX
XX WPI; 2001-488845/53.
XX
XX Method for checking absence of mutation at specific positions of
PT varicella virus genome for quality control of attenuated live varicella
PT vaccine -
XX
XX
XX Claim 1; Page 61-105; 158pp; Japanese.
XX
XX The present sequence represents the nucleotide sequence of Varicella
CC virus, Dumas strain. The specification describes a method for the
CC quality control of an attenuated pox vaccine, characterised in that
CC the DNA sequence of specific parts of the viral genome in a sample is
CC determined and proved to be conserved rather than mutated in comparison

CC with the same parts of a reference viral genome. The method is useful
CC for quality control of vaccines for use in the prevention of poxvirus
CC diseases such as chickenpox.
XX
XX
XX Sequence 124884 BP; 33789 A; 29295 C; 28177 G; 33623 T; 0 other;

Query Match 0.1%; Score 21; DB 22; Length 124884;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 26777 CATAGTATCGTCGTCGCC 26797
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 96832 CATAGTATCGTCGTCGCC 96852

RESULT 39
AAH74202
ID AAH74202 standard; DNA; 125157 BP.
XX
XX AAH74202;
XX
XX 15-OCT-2001 (first entry)
XX
XX Nucleotide sequence of the Varicella virus Oka strain.
XX
XX Oka strain; pox vaccine; vaccine; poxvirus disease; chickenpox; ss.
XX
XX Varicella virus.
XX
XX WO200156600-A1.
XX
XX 09-AUG-2001.
XX
XX 31-JAN-2001; 2001WO-JP00678.
XX
XX 31-JAN-2000; 2000JP-0062734.
XX
XX (OSAU) UNITV OSAKA.
XX
XX Gomi Y, Sunamachi H, Takahashi M, Yamanishi K;
XX
XX WPI; 2001-488845/53.
XX
XX Method for checking absence of mutation at specific positions of
PT varicella virus genome for quality control of attenuated live varicella
PT vaccine -
XX
XX
XX Disclosure; Page 106-150; 158pp; Japanese.
XX
XX The present sequence represents the nucleotide sequence of Varicella
CC virus, Oka strain. The specification describes a method for the
CC quality control of an attenuated pox vaccine, characterised in that
CC the DNA sequence of specific parts of the viral genome in a sample is
CC determined and proved to be conserved rather than mutated in comparison
CC with the same parts of a reference viral genome. The method is useful
CC for quality control of vaccines for use in the prevention of poxvirus
CC diseases such as chickenpox.
XX
XX
XX Sequence 125157 BP; 33776 A; 29439 C; 28285 G; 33624 T; 33 other;

Query Match 0.1%; Score 21; DB 22; Length 125157;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 26777 CATAGTATCGTCGTCGCC 26797
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 96778 CATAGTATCGTCGTCGCC 96798

RESULT 40
ABK80864/C
ID ABK80864 standard; DNA; 255 BP.
XX

AC ABK80864;
XX 13-AUG-2002 (first entry)
XX
XX
DE Bacillus clausii genomic sequence tag (GST) #3707.
XX
KM Differential gene expression; genomic sequenced tag; GST;
KW altered culture condition; environmental stress;
XX physiological provocation; ds.
XX
OS Bacillus clausii.
XX
PN WO200229113-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US31437.
XX
PR 06-OCT-2000; 2000US-0680598.
PR 27-MAR-2001; 2001US-279526P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
XX
PI Berka R, Clausen IG;
XX
XX WPI; 2002-416684/44.
DR
XX
XX
PT Monitoring differential expression of several genes in first Bacillus
PT cell relative to expression of same genes in one or more second
PT Bacillus cells, by using substrate containing Bacillus genomic
PT sequenced tag array -
XX
XX
PS Claim 11; SEQ ID NO 8155; 200bp; English.
XX
XX
CC The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC isolated from Bacillus cells to a substrate containing array of Bacillus
CC genomic sequenced tags (GST), examining the array, and determining
CC relative gene expression by an observed hybridisation reporter signal of
CC a spot in the array. The method is useful for measuring the expression of
CC genes in a first Bacillus cell relative to expression of the same genes
CC in one or more second Bacillus cells. The method is useful for monitoring
CC global expression of several genes from a Bacillus cell, discovering new
CC genes, identifying possible functions of unknown open reading frames and
CC monitoring gene copy number variation and stability. Monitoring changes
CC in expression of genes may be used to provide a representation of the way
CC in which Bacillus cells adapt to changes in culture conditions,
CC environmental stress or other physiological provocation. Extensive
CC follow-up characterisation is unnecessary, when one spot on an array
CC equals one gene or one open reading frame, since sequence information is
CC available. This sequence represents a genomic sequence tag (GST) used in
CC the method of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
SQ Sequence 255 BP; 71 A; 43 C; 68 G; 73 T; 0 other;
Query Match 0.1%; Score 20; DB 24; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 32834 CAACACAGAAAAATTTTGA 32853
DB 42 CAACACAGAAAAATTTTGA 23
RESULT 41
ABX74858/c
ID ABX74858 standard; cDNA; 282 BP.

```

XX ABX74858:
AC
XX
XX 21-MAR-2003 (first entry)
DT
XX
XX Human CDNA sequence #109 up-regulated in CC-RCC patients.
DE
XX
XX Human; microarray; solid surface; immobilised probe; CC-RCC;
KW differential expression profile; aggressive CC-RCC tumour type;
RW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
KW gene expression profiling; tumour tissue; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200279411-A2.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-US09576.
XX
XX 29-MAR-2001; 2001US-279411P.
XX
XX (VAND-) VAN ANDEL INST.
XX
XX Haab B, Rhodes D, Teh BT, Takashi M;
PI
XX WPI; 2003-040679/03.
XX
XX New microarray, comprising a matrix of CDNA probe from a set of probes
PT immobilised to a solid surface in predetermined order, useful in the
PR prognosis of patients with clear cell renal carcinoma
PT
XX
XX Claim 35; SEQ ID NO 219; 179pp; English.
XX
XX The present invention relates to a microarray comprising a matrix of
CC at least one CDNA probe from a set of probes immobilised to a solid
CC surface in a predetermined order, where a row of pixels corresponds
CC to replicates of one distinct probe from the set. The probes are
CC complementary to nucleic acid sequences that are expressed
CC differentially in aggressive as compared to non-aggressive types of
CC clear cell renal carcinoma (CC-RCC) and that hybridise to the probes
CC under high stringency conditions. The microarray is useful for the
CC prognosis of patients with CC-RCC, wherein aggressive and
CC non-aggressive CC-RCC tumour types are characterised by differential
CC expression profiles of genes that hybridise with one or more probes
CC immobilised on the microarray. The arrays are useful for gene
CC expression profiling of tumour and normal tissues. The present
CC sequence represents a human CDNA sequence up-regulated in CC-RCC
CC patients.
CC
XX
XX Sequence 282 BP; 109 A; 49 C; 39 G; 82 T; 3 other;
SQ
XX
XX Query Match 0.1%; Score 20; DB 25; Length 282;
XX Best Local Similarity 100.0%; Pred. No. 1e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX 3732 AAGTAAACCCCAAAATGTTA 3751
QY |||||||
DB 207 AAGTAAACCCCAAAATGTTA 188
XX
XX RESULT 42
XX ABV62066/C
XX ID ABV62066 standard; CDNA; 310 BP.
XX
XX ABV62066;
XX
XX 13-SEP-2002 (first entry)
DT
XX
XX Human prostate expression marker CDNA 62057.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

```

xx	Homo sapiens.
os	
xx	WO200160860-A2.
xx	
xx	23-AUG-2001.
xx	
xx	20-FEB-2001; 2001WO-US05171.
xx	
xx	17-FEB-2000; 2000US-183319P.
xx	16-MAR-2000; 2000US-189862P.
xx	25-MAY-2000; 2000US-207454P.
xx	09-JUN-2000; 2000US-211314P.
xx	18-JUL-2000; 2000US-219007P.
xx	13-DEC-2000; 2000US-255281P.
xx	
xx	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
xx	
xx	Schlegel R, Endege WO, Monahan JE;
xx	
xx	WPI; 2001-662795/76.
xx	
xx	Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
xx	
xx	Claim 1; Page 11728; 11750pp; English.
xx	
xx	The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
xx	(a) assessing whether a patient is afflicted with prostate cancer;
xx	(b) monitoring the progression of prostate cancer in a patient;
xx	(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
xx	(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
xx	(e) selecting a composition for inhibiting prostate cancer in a patient;
xx	(f) assessing the prostate cell carcinogenic potential of a compound;
xx	(g) determining whether prostate cancer has metastasized in a patient;
xx	(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
xx	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.
xx	
xx	Sequence 310 BP; 94 A; 42 C; 59 G; 115 T; 0 other;
xx	
xx	Query Match 0.1%; Score 20; DB 23; Length 310;
xx	Best Local Similarity 100.0%; Pred. No. 1e+03;
xx	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
xx	
xx	30927 GCAACATCAATATATATATA 30946
xx	
xx	37 GCAACATCAATATATATATA 18
xx	
xx	RESULT 43
xx	ABK79195
xx	ID ABK79195 standard; DNA; 356 BP.
xx	
xx	ABK79195;
xx	
xx	13-AUG-2002 (first entry)
xx	
xx	Bacillus clausii genomic sequence tag (GST) #2038.
xx	
xx	Differential gene expression; genomic sequenced tag; GST;
xx	altered culture condition; environmental stress;
xx	physiological provocation; ds.
xx	
xx	Bacillus clausii.
xx	
xx	WO200229113-A2.
xx	

XX	11-APR-2002.
PD	
PF	05-OCT-2001; 2001WO-US31437.
PR	
XX	06-OCT-2000; 2000US-0680598.
PR	27-MAR-2001; 2001US-279526P.
XX	
PA	(NOVO) NOVOZYMES BIOTECH INC.
PA	(NOVO) NOVOZYMES AS.
PI	Berka R, Clausen IG;
PT	WPI; 2002-416684/44.
DR	
XX	
PT	Monitoring differential expression of several genes in first Bacillus
PT	cell relative to expression of same genes in one or more second
PT	Bacillus cells, by using substrate containing Bacillus genomic
PT	sequenced tag array -
XX	
PS	
XX	Claim 11; SEQ ID NO 6486; 200pp; English.
CC	
CC	The invention describes a method of monitoring differential expression of
CC	genes in a first Bacillus cell relative to expression of the genes in
CC	other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC	isolated from Bacillus cells to a substrate containing array of Bacillus
CC	genomic sequenced tags (GST), examining the array, and determining
CC	relative gene expression by an observed hybridisation reporter signal of
CC	a spot in the array. The method is useful for measuring the expression of
CC	genes in a first Bacillus cell relative to expression of the same genes
CC	in one or more second Bacillus cells. The method is useful for monitoring
CC	global expression of several genes from a Bacillus cell, discovering new
CC	genes, identifying possible functions of unknown open reading frames and
CC	monitoring gene copy number variation and stability. Monitoring changes
CC	in expression of genes may be used to provide a representation of the way
CC	in which Bacillus cells adapt to changes in culture conditions,
CC	environmental stress or other physiological provocation. Extensive
CC	follow-up characterisation is unnecessary, when one spot on an array
CC	equals one gene or one open reading frame, since sequence information is
CC	available. This sequence represents a genomic sequence tag (GST) used in
CC	the method of the invention.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
at	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 356 BP; 107 A; 62 C; 89 G; 97 T; 1 other:
	Query Match 0.1%; Score 20; DB 24; Length 356;
	Best Local Similarity 100.0%; Pred. No. 1e+03;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY	26291 TGTCGCTGGGAAAGTACCA 26310
	TTTTTTTTTTTTTTT
Dc	68 TGTGCTGGGAAAAGTACCA 87
RESULT 44	
ID	ABAI4638/C
XX	ABAI4638 standard; DNA; 456 BP.
XX	
XX	ABAI4638;
DT	
DE	23-JAN-2002 (first entry)
XX	
Human nervous system related polynucleotide SEQ ID NO 6969.	
KM	Human; nootropic; neuroprotective; cytosstatic; dermatological; virocidic;
KM	immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
KM	antiparkinsonian; antispasmodic; antianaemic; antiarthritic; cancer;
KM	antihaematic; hepatotropic; cerebroprotective; antiinflammatory;
KM	antiallergic; nephrodiabetic; anticancer; anticoagulant; antifungal;
KM	antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KM	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX Homo sapiens.
XX WO200159063-A2.
XX 16-AUG-2001.
XX 17-JAN-2001; 2001WO-US01334.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14-SEP-2000; 2000US-0232398.
XX 14-SEP-2000; 2000US-0232399.
XX 14-SEP-2000; 2000US-0232400.
XX 14-SEP-2000; 2000US-0232401.
XX 14-SEP-2000; 2000US-0233063.
XX 14-SEP-2000; 2000US-0233064.
XX 14-SEP-2000; 2000US-0233065.
XX 21-SEP-2000; 2000US-0234223.
XX 21-SEP-2000; 2000US-0234274.
XX 25-SEP-2000; 2000US-0234997.
XX 25-SEP-2000; 2000US-0234998.

PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
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PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 DR
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 PS
 PS Disclosure; SEQ ID NO 6969; 1701pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABAI1004-ABA21534) and proteins
 CC (ABAI4678-ABAI8001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer; e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 456 BP; 143 A; 63 C; 83 G; 167 T; 0 other;
 QY
 DB 30927 GCAACATCAATTAATATA 30946
 DB 78 GCAACATCAATTAATATA 59
 RESULT 45
 ABN94325
 ID ABN94325 standard; DNA; 461 BP.
 XX
 AC ABN94325;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Gene #823 used to diagnose liver cancer.
 XX
 KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX
 OS Homo sapiens.
 XX
 PN WO200229103-A2.
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US30589.
 XX
 PR 02-OCT-2000; 2000US-237054P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 DR WPI; 2002-426119/45.
 XX
 PT Diagnosing and detecting the progression of liver cancer,

PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample -
 PS
 PS Claim 1; SEQ ID NO 823; 298pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumour in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 461 BP; 162 A; 85 C; 62 G; 152 T; 0 other;
 QY
 DB 30927 GCAACATCAATTAATATA 30946
 DB 360 GCAACATCAATTAATATA 379

Search completed: September 29, 2003; 20:40:34
 Job time : 28489 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2003, 10:19:43 ; Search time 7608 Seconds
(without alignments)
12454.387 Million cell updates/sec

Title: US-09-831-000-1_COPY_69900_105000
Perfect score: 35101
Sequence: 1 cgacatgcctagcgcctatcc.....ttatgtccacacgcgtacac 35101

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

N_Geneseq_19Jun03:*

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- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35101	100.0	128139	24	AA164291	RRV genome nucleot
2	35101	100.0	133719	21	AA64754	Macaca mulatta rha
3	23	0.1	370	22	AA135004	Human musculoskele
4	23	0.1	370	25	ABX57992	CDNA encoding nove
5	23	0.1	2004	22	AA137650	Human musculoskele
6	23	0.1	2004	22	AA137651	Human musculoskele
7	23	0.1	2004	25	ABX60638	CDNA encoding nove
8	23	0.1	2004	25	ABX60639	CDNA encoding nove

9	22	0.1	917	24	AB070267	Listeria monocytog
10	22	0.1	1393	24	ABK74889	Bacillus lichenifo
11	22	0.1	19233	24	ABL49345	Human polynucleoti
12	22	0.1	77536	21	AA114651	Nucleotide sequenc
13	22	0.1	77536	21	AA114651	Nucleotide sequenc
14	22	0.1	684707	24	AB067196	Listeria innocua c
15	22	0.1	910715	20	AA20248	Borrelia burgdorfe
16	22	0.1	2944528	24	ABA03041	Listeria monocytog
17	22	0.1	3011208	24	AB069245	Listeria innocua D
18	21	0.1	486	24	AB101517	Murine apoptotic r
19	21	0.1	597	23	ABV59094	Human prostate exp
20	21	0.1	626	25	ABZ53947	Aspergillus oryzae
21	21	0.1	713	22	AA522986	DNA encoding novel
22	21	0.1	1098	21	AAA76288	Maize glutathione-
23	21	0.1	4912	25	AB083863	Human MDR1-5 encod
24	21	0.1	5242	22	AA546706	Tumour suppressor
25	21	0.1	5728	24	ABL32101	Human immune syste
26	21	0.1	17674	24	ABL33344	Human immune syste
27	21	0.1	32192	22	AAK89452	Human digestive sy
28	21	0.1	1163020	24	AB067197	Listeria innocua c
29	21	0.1	3011208	24	AB069245	Listeria innocua D
30	20	0.1	114	24	ABN71329	Streptococcus poly
31	20	0.1	371	23	ABL15723	Drosophila melanog
32	20	0.1	406	22	AA193665	Human polynucleoti
33	20	0.1	443	22	AA191552	Human polynucleoti
34	20	0.1	492	24	ABK80077	Bacillus clausii g
35	20	0.1	628	21	AAK09895	Fusarium venenatum
36	20	0.1	676	24	ABN07203	Human CPG-island r
37	20	0.1	700	22	AAH92965	Human inflammatory
38	20	0.1	720	14	AA053372	Sequence encoding
39	20	0.1	852	20	AA24801	Vibrio cholerae th
40	20	0.1	913	24	AB040312	Oligonucleotide fo
41	20	0.1	913	24	AB040313	Oligonucleotide fo
42	20	0.1	1016	21	AA48637	Arabidopsis thalia
43	20	0.1	1285	23	AA581345	DNA encoding novel
44	20	0.1	1845	22	ABA19992	Human nervous syst
45	20	0.1	1983	23	AA572850	DNA encoding novel

ALIGNMENTS

RESULT 1
AA164291
ID AA164291 standard; DNA: 128139 BP.

XX AA164291;

XX 22-APR-2002 (first entry)

XX RRV genome nucleotide sequence.

XX RRV; Rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;

KW JMW; cytosolic; antiaesthetic; antiallergic; dermatological;

KW inflammatory; gene therapy; leucopenia; thrombocytopenia;

KW inflammatory disease; asthma; allergy; dermatitis; virus; ds.

XX Macaca mulatta rhadinovirus 17577.

XX Key Location/Qualifiers

XX CDS 1353..2674

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XX /*tag- c

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XX /*tag- e

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FT      /product= "thymidylate synthase"
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FT      /note="has similarity to KSHV ORF18"
FT CDS   complement (29905..31548)
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FT      /product= "tegument protein"
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QY 61 TTCCCTCCACGACACTCGACATGAGAGATATTTCCAGAGTTAGTCCGCATCTAG 120  
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QY 181 CCACGCAACCGCGGCGATGCTTAACCGTAAATAATATCACCGGTTGAAAGTCCCTGGTG 240  
DB 64500 CCACGCAACCGCGGCGATGCTTAACCGTAAATAATATCACCGGTTGAAAGTCCCTGGTG 64559  
  
QY 241 CGACAAATAATGAGCTTAAACTTACCAATTTTCTGTCTATTTGGGACACTAAATAAT 300  
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QY 301 GTGCGCAGTGGCGCAATTTTAAAGTCTGTAAATGATGACATCTTTTCAAGTTCTGTGTC 360  
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QY 361 CTAGAAATTTTCAATCCAGTTTCAATATATTAAGACACCTGTTTGTTCGTGAATC 420  
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QY 481 AGAGACCCCAAGTCTGAATTTATGCAATAGATCTCCACGAGTGAACACACCGGGA 540  
DB 64800 AGAGACCCCAAGTCTGAATTTATGCAATAGATCTCCACGAGTGAACACACCGGGA 64859  
  
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QY 601 AGAATTAAGGCGCGTTTTCCCAATTAATGCAATGACAGAGCAATACGGGACAGGTG 660  
DB 64920 AGAATTAAGGCGCGTTTTCCCAATTAATGCAATGACAGAGCAATACGGGACAGGTG 64979
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DB 65760 CTATTCACCCCTTCAATAAATAATTAATTAAGTGTGCGGTTGTCTATTCCTGTCT 65819  
  
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QY 1621 TGGCGTGAATTTGCAAGGAGAGTCTGCTGCTGCCAACCTGCGACCTGACAGATGGGAAT 1680  
DB 65940 TGGCGTGAATTTGCAAGGAGAGTCTGCTGCTGCCAACCTGCGACCTGACAGATGGGAAT 65999  
  
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DB 66000 ACGAGGCGGTATACAGGACACTACTCGAAGAGTGGCGCAACATGAAAGCTGCGGAGAGCC 66059
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1801 GCATAAGACCTAAGCGTGTACATCAGGTCAAAATTAAGAGCGCTGGAGACAGCCGA 1860
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66120 GCATAAGACCTAAGCGTGTACATCAGGTCAAAATTAAGAGCGCTGGAGACAGCCGA 66179
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66180 GGGCGGAATCATACACAGACCTGGCAAGCATCAAGAGGTTAAGCGTCTCCGATTATCAA 66239
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Db
1981 GTGGGACACCTTGGAAAGCGGCGCCCGACGCGTTCATTATGCACACAAAGCATGCTCA 2040
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66300 GTGGGACACCTTGGAAAGCGGCGCCCGACGCGTTCATTATGCACACAAAGCATGCTCA 66359
Db
2041 ACCCATCTGTGCTCTGTCTTTCAAGACCATCCGTGCGCGGTCCACACAGCATACCGAGC 2100
|||||
66360 ACCCATCTGTGCTCTGTCTTTCAAGACCATCCGTGCGCGGTCCACACAGCATACCGAGC 66419
Db
2101 AGTCGGTTCGATGGGAACAGGTCACAGCAGCATGCTACCCCTGGCGCCCTTCCC 2160
|||||
66420 AGTCGGTTCGATGGGAACAGGTCACAGCAGCATGCTACCCCTGGCGCCCTTCCC 66479
Db
2161 TCTTTCAAGCCAGACCTCTGTCTACAGGTCGCGGTCTACCCCTTCGCGCCCAAGCATG 2220
|||||
66480 TCTTTCAAGCCAGACCTCTGTCTACAGGTCGCGGTCTACCCCTTCGCGCCCAAGCATG 66539
Db
2221 CAAGATAGCGCGAGTCCGACAAATATGCGACCAAAATTTGACCGCAAGAAATACACGCG 2280
|||||
66540 CAAGATAGCGCGAGTCCGACAAATATGCGACCAAAATTTGACCGCAAGAAATACACGCG 66599
Db
2281 GTCCGTTGAGCAGAGCGCCGATGAGCGCTGACGGGACCTCAAGCGCTCCGCTGTCAGAC 2340
|||||
66600 GTCCGTTGAGCAGAGCGCCGATGAGCGCTGACGGGACCTCAAGCGCTCCGCTGTCAGAC 66659
Db
2341 CCATTCTCCCTTCGCGCGAGCGCTGTGACCTGTGTTCAACCCCTGTGGGCTATGGCGGA 2400
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66660 CCATTCTCCCTTCGCGCGAGCGCTGTGACCTGTGTTCAACCCCTGTGGGCTATGGCGGA 66719
Db
2401 AATTTGGGCTCAGCATGCGCTTGTACAGCATATATCAAAATATATGACATAGAAACTAC 2460
|||||
66720 AATTTGGGCTCAGCATGCGCTTGTACAGCATATATCAAAATATATGACATAGAAACTAC 66779
Db
2461 ACAGGCTTCACTGGGAATAAAGTTTATTTATTTGACACATAGTCCGCGCTATTT 2520
|||||
66780 ACAGGCTTCACTGGGAATAAAGTTTATTTATTTGACACATAGTCCGCGCTATTT 66839
Db
2521 CTGTGTCGTGACTGGGCGCGCTCTCTGAGCGCGCCCTCCGCGCTGGCAGCATTCGG 2580
|||||
66840 CTGTGTCGTGACTGGGCGCGCTCTCTGAGCGCGCCCTCCGCGCTGGCAGCATTCGG 66899
Db
2581 CCTGTGTGTCTCTCTCATTTACAGCTCAGCGGATATCTAATTCGCGAGGGCGTCT 2640
|||||
66900 CCTGTGTGTCTCTCTCATTTACAGCTCAGCGGATATCTAATTCGCGAGGGCGTCT 66959
Db
2641 TCCATCTGCGCGGGGTACAGGCGCTTGGCGGTGGCGCGCTCAGCTTACCTTACCTTAACTTA 2700
|||||
66960 TCCATCTGCGCGGGGTACAGGCGCTTGGCGGTGGCGCGCTCAGCTTACCTTAACTTAA 67019
Db
2701 CGGGTTGGCAGCTTACATTAAGCGCAAAAGCGAGCTGCGATTGGCCCTCTTTTCGATG 2760
|||||
67020 CGGGTTGGCAGCTTACATTAAGCGCAAAAGCGAGCTGCGATTGGCCCTCTTTTCGATG 67079
Db
2761 TTAGAGATGACGGGGTCCGAGCGGACCTGTGGGATCCCGAGAAATTTATCAGCTTTTGG 2820
|||||
67080 TTAGAGATGACGGGGTCCGAGCGGACCTGTGGGATCCCGAGAAATTTATCAGCTTTTGG 67139
Db
2821 AGCTCTTGTCTTTCAACGAGCAATTTTGGACCTAGAGGGGCTAAGTCTCCCATTTGTACAGC 2880

|||||
67140 AGCTCTTGTCTTTCAACGAGCAATTTTTCACCTGAGCGGCTAAGTCTCCATTTGTACAGC 67199
Db
2881 TCTTTTGGGGCGCGGCTCTTGGGACCGTGGAAAGACATGGACACTACATGCAATTAC 2940
|||||
67200 TCTTTTGGGGCGCGGCTCTTGGGACCGTGGAAAGACATGGACACTACATGCAATTAC 67259
Db
2941 AGAGTACAGCGGGAGCTTTAAATCTTTCAGGCGCGCCCTGAGGTACTGTGGCGCAGC 3000
|||||
67260 AGAGTACAGCGGGAGCTTTAAATCTTTCAGGCGCGCCCTGAGGTACTGTGGCGCAGC 67319
Db
3001 GTTTCAACAAATTTAAAAAGACATATATGTTAGTACAGAAATGTTCAACCGCGAGC 3060
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67320 GTTTCAACAAATTTAAAAAGACATATATGTTAGTACAGAAATGTTCAACCGCGAGC 67379
Db
3061 AGAAGAGTGTATATCAGCGCCCATATATACGAAAAAATCTGACAGCAGCGGCTGATAGT 3120
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67380 AGAAGAGTGTATATCAGCGCCCATATATACGAAAAAATCTGACAGCAGCGGCTGATAGT 67439
Db
3121 TCCGCGGAGCAATCATATGTCATAAAAAGAGGCGTTACGGAGGAGCCGCGAGGGGTTT 3180
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67440 TCCGCGGAGCAATCATATGTCATAAAAAGAGGCGTTACGGAGGAGCCGCGAGGGGTTT 67499
Db
3181 GTAGTACAGAGAGCGGTGCGCGTCTGATGTCAGAGAGTGTGACAGGTGGCGGACAC 3240
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67500 GTAGTACAGAGAGCGGTGCGCGTCTGATGTCAGAGAGTGTGACAGGTGGCGGACAC 67559
Db
3241 GGCAGACAGATATTAAGCAGCGCAACAGGGCTTAACGCGAGCAATTAAGCCGTGAT 3300
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67560 GGCAGACAGATATTAAGCAGCGCAACAGGGCTTAACGCGAGCAATTAAGCCGTGAT 67619
Db
3301 TTCAAGCGCGGCTTGGGACGGCAACCTTCACCTTTGGACGCGCGCTCTCTTATATACT 3360
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67620 TTCAAGCGCGGCTTGGGACGGCAACCTTCACCTTTGGACGCGCGCTCTCTTATATACT 67679
Db
3361 ACCAGTTAAACATTTATGAGAGTGAACCGCCCATACGTTTCGTAAGCGCTTGTACTCT 3420
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67680 ACCAGTTAAACATTTATGAGAGTGAACCGCCCATACGTTTCGTAAGCGCTTGTACTCT 67739
Db
3421 GTAGTTTGAATTAATTAACAAAAAACACTCATCTGTTAGACGTTACGCAAAATTTTC 3480
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67740 GTAGTTTGAATTAATTAACAAAAAACACTCATCTGTTAGACGTTACGCAAAATTTTC 67799
Db
3481 CCGTGTGTCAAACCGGAGAACTCTAGTGTGCGCCCTGGGACATAAAATATATCCGG 3540
|||||
67800 CCGTGTGTCAAACCGGAGAACTCTAGTGTGCGCCCTGGGACATAAAATATATCCGG 67859
Db
3541 GCGCCGAGTGGCATTTCTTCTCAGGCGAGCGCCGACGATAGGTTATACCAACCG 3600
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67860 GCGCCGAGTGGCATTTCTTCTCAGGCGAGCGCCGACGATAGGTTATACCAACCG 67919
Db
3601 GACTTATAGATCAAGGGTATCGTGAGAAATAAATCTCATCTCAATTAAGACTAAAC 3660
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67920 GACTTATAGATCAAGGGTATCGTGAGAAATAAATCTCATCTCAATTAAGACTAAAC 67979
Db
3661 AGTGTGTCACTTTACGGGGGAGAAATCAAGTCTCACTCATCCGTTTATGTACGCT 3720
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67980 AGTGTGTCACTTTACGGGGGAGAAATCAAGTCTCACTCATCCGTTTATGTACGCT 68039
Db
3721 GCGCCGAGGCGCTTAATAATCCCGATACTGAACCTTACCATTTACTCTGAGCGCTGAT 3780
|||||
68040 GCGCCGAGGCGCTTAATAATCCCGATACTGAACCTTACCATTTACTCTGAGCGCTGAT 68099
Db
3781 TTGATGTTACGTGCGCACATGACCATTAACCCCAACGAGCAAGAAACCCGTTTACGT 3840
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68100 TTGATGTTACGTGCGCACATGACCATTAACCCCAACGAGCAAGAAACCCGTTTACGT 68159
Db
3841 TGAGTTTGTATTAATTAAGAGTCCACAGCTAGACACCCCGACGCTCCCATTAATGTGGGCG 3900
|||||
68160 TGAGTTTGTATTAATTAAGAGTCCACAGCTAGACACCCCGACGCTCCCATTAATGTGGGCG 68219
Db
3901 GCTGTGAGACTGGCGCAAAAGGGGCTTACCGTGTGAGCGGCAAAATGAGCCCGTGTGGTGG 3960
|||||

Db 68220 GCTGTGAGTGGCGACAAAGGGGCTTACCGTCGACGGCACCATAATGAGACCACTGCTTGG 68279
Qy 3961 TACATCTGAGGTTTTTATACCTTTACAAAGAGCCAAATAGATATATACAGCAACAGCGCA 4020
Db 68280 TACATCTGAGGTTTTTATACCTTTACAAAGAGCCAAATAGATATATACAGCAACAGCGCA 68339
Qy 4021 TATGTCAAGTATGTTTTATCCAGAGACACAGTCCCAAGCGGGTGAACATTTCTATGAT 4080
Db 68340 TATGTCAAGTATGTTTTATCCAGAGACACAGTCCCAAGCGGGTGAACATTTCTATGAT 68399
Qy 4081 CCGGCGTACAACTCGGAGACACCTCCAGATATCTGTGGGCCAAATATAGGTTTACGACG 4140
Db 68400 CCGGCGTACAACTCGGAGACACCTCCAGATATCTGTGGGCCAAATATAGGTTTACGACG 68459
Qy 4141 TGGCAGAGCTCCGCCAAACCCACCGCTCAACTCCGCCACACTCAAGCCAAACCGGAC 4200
Db 68460 TGGCAGAGCTCCGCCAAACCCACCGCTCAACTCCGCCACACTCAAGCCAAACCGGAC 68519
Qy 4201 CGGAGACCGCCCGCGGCGCAAGGGGTTGGGGTCTAGGGGTTATTAATTTTAAACATGG 4260
Db 68520 CGGAGACCGCCCGCGGCGCAAGGGGTTGGGGTCTAGGGGTTATTAATTTTAAACATGG 68579
Qy 4261 CATTAATTTTAAAGTGTGTTATTTTATTAATAACAAATCCAAATTTACTTAACCATGAGT 4320
Db 68580 CATTAATTTTAAAGTGTGTTATTTTATTAATAACAAATCCAAATTTACTTAACCATGAGT 68639
Qy 4321 TGGCAGATCTGTATTTATTTTGTCTGCGACATATTTATCCGCCAACCGCAACTGGGGCTC 4380
Db 68640 TGGCAGATCTGTATTTATTTTGTCTGCGACATATTTATCCGCCAACCGCAACTGGGGCTC 68699
Qy 4381 GGTGTTCGAATCAACCGGATGGAGGGGTTGGAGAGCGTTGCTGTACCAACACATTA 4440
Db 68700 GGTGTTCGAATCAACCGGATGGAGGGGTTGGAGAGCGTTGCTGTACCAACACATTA 68759
Qy 4441 TTATATTTCCGACGCCGCGTACAGAAATCATTCGAGCGCATTCGTCGATGACAGTTTTC 4500
Db 68760 TTATATTTCCGACGCCGCGTACAGAAATCATTCGAGCGCATTCGTCGATGACAGTTTTC 68819
Qy 4501 ATTTCCAGAGTACACAGGTCGTCTGCGGCCGTTTATTAACAAAGCGCGTGAAGGCGCTC 4560
Db 68820 ATTTCCAGAGTACACAGGTCGTCTGCGGCCGTTTATTAACAAAGCGCGTGAAGGCGCTC 68879
Qy 4561 TCGTCCACGCTAATATCCCTATATGCCAGGACAAACATGCGCTTCCAGATTAACGTTCTGT 4620
Db 68880 TCGTCCACGCTAATATCCCTATATGCCAGGACAAACATGCGCTTCCAGATTAACGTTCTGT 68939
Qy 4621 ATAGACTTTAGCTTAGATATTTGATCTTAACGTCCTCCGCGACCCCGGGGTAACCTTA 4680
Db 68940 ATAGACTTTAGCTTAGATATTTGATCTTAACGTCCTCCGCGACCCCGGGGTAACCTTA 68999
Qy 4681 GCCGCGTCAAAAGACGAGATACTCGGTTATTTTATTTGATTTGAAGGCCAACAGATTAAC 4740
Db 6900 GCCGCGTCAAAAGACGAGATACTCGGTTATTTTATTTGATTTGAAGGCCAACAGATTAAC 69059
Qy 4741 GTCTGCCGAAGGGGCGGCGTGCACATCTGTGCTTCCATCTCCCATATTCACGTCCTC 4800
Db 69060 GTCTGCCGAAGGGGCGGCGTGCACATCTGTGCTTCCATCTCCCATATTCACGTCCTC 69119
Qy 4801 GGGGGCAGACCATGCTATTTTGGTCCGCGAGTGAATAGAGACCTGTTAAAGAGATCT 4860
Db 69120 GGGGGCAGACCATGCTATTTTGGTCCGCGAGTGAATAGAGACCTGTTAAAGAGATCT 69179
Qy 4861 GGGAGGGAGAGATATTTGACATCTCCACGCTCAAAAGGAGCTAAACCCGCAACAGTCCAA 4920
Db 69180 GGGAGGGAGAGATATTTGACATCTCCACGCTCAAAAGGAGCTAAACCCGCAACAGTCCAA 69239
Qy 4921 AAGGAACAGGCGCGGCTATTTGCCAAACAAATGATGATGAATTTAGGCAATTTTCTC 4980
Db 69240 AAGGAACAGGCGCGGCTATTTGCCAAACAAATGATGATGAATTTAGGCAATTTTCTC 69299
Qy 4981 TACTAGTGAATATGCGGACGAAGTAAATACGATATCTGACTGAACGCAAGCAAGCGG 5040
Db 69300 TACTAGTGAATATGCGGACGAAGTAAATACGATATCTGACTGAACGCAAGCAAGCGG 69359

Qy 5041 GTCCCTCTGTGCTGTCTCCAGCATCGGGGCGACGCGCTATTAATATCTCCACATGCGCT 5100
Db 69360 GTCCCTCTGTGCTGTCTCCAGCATCGGGGCGACGCGCTATTAATATCTCCACATGCGCT 69419
Qy 5101 AATTAACCTGCTGCTGCGGCAAGCGCCACAGCGCGGCGGCAAGGTTTACCGTTGAT 5160
Db 69420 AATTAACCTGCTGCTGCGGCAAGCGCCACAGCGCGGCGGCAAGGTTTACCGTTGAT 69479
Qy 5161 GGTGCTAACCTACCGGCGTGGCGAGTTCATTTCTTAACAGGTACGACCATGATGAC 5220
Db 69480 GGTGCTAACCTACCGGCGTGGCGAGTTCATTTCTTAACAGGTACGACCATGATGAC 69539
Qy 5221 CTCGGATTAACATTTAAACACCGCATTTGACTGCTCAACACGAGGAAATATCTGAACCAT 5280
Db 69540 CTCGGATTAACATTTAAACACCGCATTTGACTGCTCAACACGAGGAAATATCTGAACCAT 69599
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Db 69600 ATTAAGCGTACTGCGATGCAAAAGCGTCCGCGACAGACCAACATGACTGTTTAAATC 69659
Qy 5341 TAAAGTGGCGTGTGAGGCAAGTTCGTGCGCCCTAAGAAAGTACCAAAATGAC 5400
Db 69660 TAAAGTGGCGTGTGAGGCAAGTTCGTGCGCCCTAAGAAAGTACCAAAATGAC 69719
Qy 5401 CCCATCCCGCTATTTGATGATTAACGCTGTGGGCTGCTGAGGCAATCGTTTGTACTGGC 5460
Db 69720 CCCATCCCGCTATTTGATGATTAACGCTGTGGGCTGCTGAGGCAATCGTTTGTACTGGC 69779
Qy 5461 CGGCACTTTTATTTTCCAGTCTCATATATGACGCGGAGACGCTGTGATCTTAC 5520
Db 69780 CGGCACTTTTATTTTCCAGTCTCATATATGACGCGGAGACGCTGTGATCTTAC 69839
Qy 5521 GAGGTTATTCAGTCCAGTACAGGCGCAGAGCTTGTACCGTAAACACTTATGACGAT 5580
Db 69840 GAGGTTATTCAGTCCAGTACAGGCGCAGAGCTTGTACCGTAAACACTTATGACGAT 69899
Qy 5581 AGGGCGGCTATTCGGGCGTCAAGATTTCTTTGAAATTTTCCAAATTTTGGGCGTATCT 5640
Db 69900 AGGGCGGCTATTCGGGCGTCAAGATTTCTTTGAAATTTTCCAAATTTTGGGCGTATCT 69959
Qy 5641 AAAATACAAATGCAACAGACGACGCTGAGTCCAGGCGCATGATCAACATCAATC 5700
Db 69960 AAAATACAAATGCAACAGACGACGCTGAGTCCAGGCGCATGATCAACATCAATC 70019
Qy 5701 CATACGTGGGGGTTGATGCTGACCTCAAGGACCTGTCATCTTACCTGATCT 5760
Db 70020 CATACGTGGGGGTTGATGCTGACCTCAAGGACCTGTCATCTTACCTGATCT 70079
Qy 5761 TTACGAGTGCATGACGACACAGACGTTCTGTCTACTCTGTCACACGTCACGTTTACC 5820
Db 70080 TTACGAGTGCATGACGACACAGACGTTCTGTCTACTCTGTCACACGTCACGTTTACC 70139
Qy 5821 GACCCCGCAACGGTTAAACCTCCGCACTGTGTGCGCGCTTAAGAGGATTTTAAAGA 5880
Db 70140 GACCCCGCAACGGTTAAACCTCCGCACTGTGTGCGCGCTTAAGAGGATTTTAAAGA 70199
Qy 5881 GCACGTATGGCATTAATTAACAATAAGCAAGCTACTGATCTTACATTAACATTTTAAAC 5940
Db 70200 GCACGTATGGCATTAATTAACAATAAGCAAGCTACTGATCTTACATTAACATTTTAAAC 70259
Qy 5941 CGTACCGGCTCTCTCCCGGAGGATACGAATTTTCAGGAATAGCATGTCATTAATCTG 6000
Db 70260 CGTACCGGCTCTCTCCCGGAGGATACGAATTTTCAGGAATAGCATGTCATTAATCTG 70319
Qy 6001 GTGTGACATATCGAGACAGTGGGCGGAAATCATATCATAGATTAATGACGATTTCCACA 6060
Db 70320 GTGTGACATATCGAGACAGTGGGCGGAAATCATATCATAGATTAATGACGATTTCCACA 70379
Qy 6061 GCTGAATCTTAACAAAGATTTATCCGCTCTCTGACTGACGCGGCTAGATCTGATATTC 6120
Db 70380 GCTGAATCTTAACAAAGATTTATCCGCTCTCTGACTGACGCGGCTAGATCTGATATTC 70439

QY 6121 CGAGGCCCAAGAAACCTTTTACGGTGGCTTCGACATTTCCACATACAGTCCGA 6180
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Db 70440 CGAGGCCCAAGAAACCTTTTACGGTGGCTTCGACATTTCCACATACAGTCCGA 70499
QY 6181 GTTTTGAATTAACATATTTTGTCTAATGACGAGACTGATAGACGGCTAGAA 6240
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Db 70500 GTTTTGAATTAACATATTTTGTCTAATGACGAGACTGATAGACGGCTAGAA 70559
QY 6241 ACAAAACATTTATCGTCCCGAAGACGCCAATTGCAAGGCTGACGATCAAGATCTCAC 6300
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Db 70560 ACAAAACATTTATCGTCCCGAAGACGCCAATTGCAAGGCTGACGATCAAGATCTCAC 70619
QY 6301 CTCACGATATTTTACTGGACCTCGGCTTATCTACCTACATTTTAAACAATTTCT 6360
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Db 70620 CTCACGATATTTTACTGGACCTCGGCTTATCTACCTACATTTTAAACAATTTCT 70679
QY 6361 AGTTTCACGCCACGATATTTTCAACCCAGACACTCCAGTTTATAGATGGTGTGATTT 6420
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Db 70680 AGTTTCACGCCACGATATTTTCAACCCAGACACTCCAGTTTATAGATGGTGTGATTT 70739
QY 6421 TGAATTAAGGTAAACGGAAGGTAGACGACTCTAAACGATATCTACACATATGCTAAC 6480
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Db 70740 TGAATTAAGGTAAACGGAAGGTAGACGACTCTAAACGATATCTACACATATGCTAAC 70799
QY 6481 GCTGGGCGAGTCAATTTAGAAACGTTGAGTTAATAGTCCACTTAAACCCGACACCC 6540
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Db 70800 GCTGGGCGAGTCAATTTAGAAACGTTGAGTTAATAGTCCACTTAAACCCGACACCC 70859
QY 6541 CGTGTATTTTAAAGTCCGCTGTCACGCCCTTAACCTGGCGGATATCTCAGACAC 6600
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Db 70860 CGTGTATTTTAAAGTCCGCTGTCACGCCCTTAACCTGGCGGATATCTCAGACAC 70919
QY 6601 CGCGTCTGTCACTGTGACGCAAAAATAGAGATGAGAAATGTAACCCGCTTCCGAGCGG 6660
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Db 70920 CGCGTCTGTCACTGTGACGCAAAAATAGAGATGAGAAATGTAACCCGCTTCCGAGCGG 70979
QY 6661 ATACTGTTTGGGGGTCGGCTCCACTCGTGTCCCGACGACATTTTAAACCGCTGCT 6720
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Db 70980 ATACTGTTTGGGGGTCGGCTCCACTCGTGTCCCGACGACATTTTAAACCGCTGCT 71039
QY 6721 TAACTGACACGCGGCTAGCTCAGAGATATCTGGGATCTTGAAGATTAAGACCAAT 6780
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Db 71040 TAACTGACACGCGGCTAGCTCAGAGATATCTGGGATCTTGAAGATTAAGACCAAT 71099
QY 6781 TGAATCTGCAATTTACGCCAAGGGGAGATGCTGGCGTACTCTGCTATTAAGTGTG 6840
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Db 71100 TGAATCTGCAATTTACGCCAAGGGGAGATGCTGGCGTACTCTGCTATTAAGTGTG 71159
QY 6841 CCCGGGGGCGAGCTGTACGGCTCCTTAAATTTATCTGTGCAACCCCGAAGAGTCAGA 6900
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Db 71160 CCCGGGGGCGAGCTGTACGGCTCCTTAAATTTATCTGTGCAACCCCGAAGAGTCAGA 71219
QY 6901 TAAATCGGGCTATTTGAAAAACGCGTTTAAAGTTTCTAATCTGTACATCACGCCCTTG 6960
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Db 71220 TAAATCGGGCTATTTGAAAAACGCGTTTAAAGTTTCTAATCTGTACATCACGCCCTTG 71279
QY 6961 AACTCTGTACCAAAAACGGCCACCTGTGTACGGGATCACTGACGAAAAAGAGGCTT 7020
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Db 71280 AACTCTGTACCAAAAACGGCCACCTGTGTACGGGATCACTGACGAAAAAGAGGCTT 71339
QY 7021 TCTAGAAAGCAAAACCAAGATTAATCTCCCAAAACAATCAGGACCTGGCCGAAAAAT 7080
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Db 71340 TCTAGAAAGCAAAACCAAGATTAATCTCCCAAAACAATCAGGACCTGGCCGAAAAAT 71399
QY 7081 TGAGCGAACACAGAAAAACCACTAATGATTTGGGCGAGCGACGAGTGTGCCAAAACT 7140
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Db 71400 TGAGCGAACACAGAAAAACCACTAATGATTTGGGCGAGCGACGAGTGTGCCAAAACT 71459
QY 7141 ACAGATTAACATACAGCGTTTCTTCCGAGATGCGGATCGGCCAATTTGATCTGTGAG 7200
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Db 71460 ACAGATTAACATACAGCGTTTCTTCCGAGATGCGGATCGGCCAATTTGATCTGTGAG 72059
QY 7201 CTTCATGCACTCCGAGACACATTAATACAACTTAAACCAAAAAAGAAACAACTTTT 7260
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Db 71520 CTTCATGCACTCCGAGACACATTAATACAGTTAATACCAAAAAAGAAACAACTTTT 71579
QY 7261 CTGTATTAATCAATTAACACGAAACCAACACTGACAGCTCCGCTATTTTAAACCTTACA 7320
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Db 71580 CTGTATTAATCAATTAACACGAAACCAACACTGACAGCTCCGCTATTTTAAACCTTACA 71639
QY 7321 TTCCACAAAAAAGAGGCTCAGCTGACCTTTATAGATCAGTCTTTGCTGCAAAATG 7380
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Db 71640 TTCCACAAAAAAGAGGCTCAGCTGACCTTTATAGATCAGTCTTTGCTGCAAAATG 71699
QY 7381 TATCATTAATGAGCCCACTGACATTTTCAATTAATGATTAATGATTAACCGGACGTAAGA 7440
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Db 71700 TATCATTAATGAGCCCACTGACATTTTCAATTAATGATTAATGATTAACCGGACGTAAGA 71759
QY 7441 GACACGATTAATCAATCCGTGTATGAGCCAGCTCTCCGCTACTTTGTTAATTTTAAAC 7500
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Db 71760 GACACGATTAATCAATCCGTGTATGAGCCAGCTCTCCGCTACTTTGTTAATTTTAAAC 71819
QY 7501 CGGTAACCCCAAAAAACAATCTGGACGATTTTGTGCGAAGCTGAACATGCGACAG 7560
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Db 71820 CGGTAACCCCAAAAAACAATCTGGACGATTTTGTGCGAAGCTGAACATGCGACAG 71879
QY 7561 GCAATGAGAGCTGGAATACATGAAGATATTTTGAAGGTAAGAACCCCTGTGGC 7620
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Db 71880 GCAATGAGAGCTGGAATACATGAAGATATTTTGAAGGTAAGAACCCCTGTGGC 71939
QY 7621 TCTTACGATCCCATTTTAAACCGCAACTTATCAAAAGGCTCTTTTATACGATTTTACAT 7680
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Db 71940 TCTTACGATCCCATTTTAAACCGCAACTTATCAAAAGGCTCTTTTATACGATTTTACAT 71999
QY 7681 GCGGTATGTGTTTACGCACTAATTTTGTATTAAGGGGCAATATCATCTGCGACTTCCA 7740
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Db 72000 GCGGTATGTGTTTACGCACTAATTTTGTATTAAGGGGCAATATCATCTGCGACTTCCA 72059
QY 7741 CGACTGCTCCTGGAGCAATGGAAGAGCACTGTCCCAAGCCGAGACCAAGAACCCGTCAC 7800
|||||
Db 72060 CGACTGCTCCTGGAGCAATGGAAGAGCACTGTCCCAAGCCGAGACCAAGAACCCGTCAC 72119
QY 7801 AACGCCGAACAGCTTCCGAGAGGGGCCAAATCACAAGTGTGAGCTTACCTTAAATCCG 7860
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Db 72120 AACGCCGAACAGCTTCCGAGAGGGGCCAAATCACAAGTGTGAGCTTACCTTAAATCCG 72179
QY 7861 TAAAGATTCGATCTGAGAACCGCGGTAAATTTAGAGCAATATCTCCACTTAACCGCTC 7920
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Db 72180 TAAAGATTCGATCTGAGAACCGCGGTAAATTTAGAGCAATATCTCCACTTAACCGCTC 72239
QY 7921 GCGATCTGATCAGAACCGGTCGCGGTCGCGTCAACGATCAACCACTCAGGACGATA 7980
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Db 72240 GCGATCTGATCAGAACCGGTCGCGGTCGCGTCAACGATCAACCACTCAGGACGATA 72299
QY 7981 CGTCAAGAGATTCAAACCAAGGTTGATGACCCGCTCATGAGAAACCGTGGCAGAGGG 8040
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Db 72300 CGTCAAGAGATTCAAACCAAGGTTGATGACCCGCTCATGAGAAACCGTGGCAGAGGG 72359
QY 8041 CGGTAAAGGAAAGGCCCTTTATCTCGCAGAGAACGCAATAGCTGGCGGCTGACGAC 8100
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Db 72360 CGGTAAAGGAAAGGCCCTTTATCTCGCAGAGAACGCAATAGCTGGCGGCTGACGAC 72419
QY 8101 ATAGGCGCACGACTATCGGGAAGAACCGCTTTAAGCGGACATTTAAAGAGTCTATTAA 8160
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Db 72420 ATAGGCGCACGACTATCGGGAAGAACCGCTTTAAGCGGACATTTAAAGAGTCTATTAA 72479
QY 8161 AAAGATGACCTTCCATCCACATCTCTCTGTCGCGACGATTAAGAAAGTATTCGAGGG 8220
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Db 72480 AAAGATGACCTTCCATCCACATCTCTCTGTCGCGACGATTAAGAAAGTATTCGAGGG 72539
QY 8221 ACTGTTGCGACAGACACTGAGCACTGTTTAAAGTGTGCTGCGCGCGCGCACCGCT 8280
|||||
Db 72540 ACTGTTGCGACAGACACTGAGCACTGTTTAAAGTGTGCTGCGCGCGCGCACCGCT 72599
QY 8281 GCAACCCGAGGTTCCAGGATCGACAGCTTACCGCTATGACAGTCTGGCGGCGGAG 8340
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Dd 72600 GCAACCGAGGTGTCACGGATGACAGCTTACCGCTATAGTCAGTCTGCGGGCCGAG 72659
Qy 8341 AGACGGCTGTGGCCAAAAAAGTTAGCTGGCTAACTAACAGCCTATACAAACCCCT 8400
Dd 72660 AGACGGCTGTGGCCAAAAAAGTTAGCTGGCTAACTAACAGCCTATACAAACCCCT 72719
Qy 8401 GCTACAGTTTGTGACGGGGGAAAAACAACAGGCCCACTGGTTGGCGACGGCCAAAAACAC 8460
Dd 72720 GCTACAGTTTGTGACGGGGGAAAAACAACAGGCCCACTGGTTGGCGACGGCCAAAAACAC 72779
Qy 8461 GCTAGCCTCTGCGGGGACTCCAGGCTCTGCGGGCCCTTTATGAGGAAAGTGTGGGTGGC 8520
Dd 72780 GCTAGCCTCTGCGGGGACTCCAGGCTCTGCGGGCCCTTTATGAGGAAAGTGTGGGTGGC 72839
Qy 8521 CCAAGTGTGGCTATCTCAAAAACAGATGTTGAACGACAGCACTAGATATCATCTAGAG 8580
Dd 72840 CCAAGTGTGGCTATCTCAAAAACAGATGTTGAACGACAGCACTAGATATCATCTAGAG 72899
Qy 8581 CAGTAGTCAGAGCGTGTGACACCTGGTTCATCTCCAAAATCAGGCACTTTCACATACAGTG 8640
Dd 72900 CAGTAGTCAGAGCGTGTGACACCTGGTTCATCTCCAAAATCAGGCACTTTCACATACAGTG 72959
Qy 8641 CTCTTGGAGAAATCAGGCTGAGGTTAGCTGGTGAAGCAGCTACTTACCTGCTGCTAT 8700
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QY 15721 CACGCCATAGTCTGGCGGCGACAGAAGCCGGAAGATAGCGTCACTGCTGTCCGCG 15780
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Db 80040 CACGCCATAGTCTGGCGGCGGACAGAAGCCGGAAGATAGCGTCACTGCTGTCCGCG 80099
QY 15781 TCGTGTCAATCTTGATGACCTTCCGATACCGTCTCTGTGATCACTTAAGCAGGCTCC 15840
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Db 80100 TCGTGTCAATCTTGATGACCTTCCGATACCGTCTCTGTGATCACTTAAGCAGGCTCC 80159
QY 15841 GAAAGGCGGTGAAGCATTCGCGCGCCGAGCATGTGCAACCGCATATTGGCAACTCAAG 15900
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Db 80160 GAAAGGCGGTGAAGCATTCGCGCGCCGAGCATGTGCAACCGCATATTGGCAACTCAAG 80219
QY 15901 CGGAGCGGCACACGCGGCGGACACACCGGACAAAGACATCTTTGATGATAGCAACCTTA 15960
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Db 80220 CGGAGCGGCACACGCGGCGGACACACCGGACAAAGACATCTTTGATGATAGCAACCTTA 80279
QY 15961 AAGACCAGCGCGTGAAGCAAAATGTATGAGGATTCCTTATCTTCCTCAAGATGAC 16020
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Db 80280 AAGACCAGCGCGTGAAGCAAAATGTATGAGGATTCCTTATCTTCCTCAAGATGAC 80339
QY 16021 TTTGCTTTCTTACGGCTCCAGCAGCGCGCCCTGTGCTTGACACAGCTGTCTTCCA 16080
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Db 80340 TTTGCTTTCTTACGGCTCCAGCAGCGCGCCCTGTGCTTGACACAGCTGTCTTCCA 80399
QY 16081 GACGGCAGTGGGATGTCTTAACTCAACAGTAGGACATCATATGTGTGACCGTGCCTTGA 16140
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Db 80400 GACGGCAGTGGGATGTCTTAACTCAACAGTAGGACATCATATGTGTGACCGTGCCTTGA 80459
QY 16141 TAATCATTAATTTGGAAACGAGCGGTGTAGCTGCCAACAACGCGCTGTGCTTGTGCTG 16200
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Db 80460 TAATCATTAATTTGGAAACGAGCGGTGTAGCTGCCAACAACGCGCTGTGCTTGTGCTG 80519
QY 16201 TCTGCCAAAAACAGCGCCGGGTACAGACACTATCGGCTTTGAAACGTCAACCATTCCTTG 16260
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Db 80520 TCTGCCAAAAACAGCGCCGGGTACAGACACTATCGGCTTTGAAACGTCAACCATTCCTTG 80579
QY 16261 AGGGCCATGCCATTAACAGATGGGCGCCCTGTGTGATTCGCCAGCGCCATGATTCAGTCG 16320
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Db 80580 AGGGCCATGCCATTAACAGATGGGCGCCCTGTGTGATTCGCCAGCGCCATGATTCAGTCG 80639
QY 16321 GCAACGTTTAAACCCCATGTAAAGTTTCAGTTCATTTAAATGACACACACTCGGCCAT 16380
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Db 80640 GCAACGTTTAAACCCCATGTAAAGTTTCAGTTCATTTAAATGACACACACTCGGCCAT 80699
QY 16381 GCTGTGCAAAACATTAAGAAAGTGGCACACGTGTGCGCTTTGGCCGCTGTGATGAA 16440
    |||||
Db 80700 GCTGTGCAAAACATTAAGAAAGTGGCACACGTGTGCGCTTTGGCCGCTGTGATGAA 80759
QY 16441 CCGCGCGGTAAACATTACTTCCCTCCATACGGGTGGAAGGTTAGATACATATGCTTCC 16500
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Db 80760 CCGCGCGGTAAACATTACTTCCCTCCATACGGGTGGAAGGTTAGATACATATGCTTCC 80819
QY 16501 CGTTGTTCCCGAAGACACCGACCGGCTCCAGAGGTCCTCGTCCCGGCTCATCTCC 16560
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Db 80820 CGTTGTTCCCGAAGACACCGACCGGCTCCAGAGGTCCTCGTCCCGGCTCATCTCC 80879
QY 16561 CCGGCGACGCTTCTGTGACATCATCTGACACATCATCATTTGACACAGTAGGAAATTCAG 16620
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Db 80880 CCGGCGACGCTTCTGTGACATCATCTGACACATCATCATTTGACACAGTAGGAAATTCAG 80939
QY 16621 GGCATATGGAGCATCCCATATTTTTCGAGTGTAGTACGCGGACATGAAATTCACAGC 16680
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Db 80940 GGCATATGGAGCATCCCATATTTTTCGAGTGTAGTACGCGGACATGAAATTCACAGC 80999
QY 16681 ACATGACGCGGCGGAGACATCTCTGAGTGTGCGATCTGCGCAGCTCCCTCAAAATATG 16740
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Db 81000 ACATGACGCGGCGGAGACATCTCTGAGTGTGCGATCTGCGCAGCTCCCTCAAAATATG 81059
QY 16741 CAAGAGATGACGCTGGAGCGGCTGCGAAGCGCGCAGCTCATAGTAAATTTCAAGATA 16800
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Db 81060 CAAGAGATGACGCTGGAGCGGCTGCGAAGCGCGCAGCTCATAGTAAATTTCAAGATA 81119
QY 16801 GTTGTGCAATGCCGTATGTGTGCTTCCAGGTTTTCACACAGATTCGAACTCCG 16860
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Db 81120 GTTGTGCAATGCCGTATGTGTGCTTCCAGGTTTTCACACAGATTCGAACTCCG 81179
QY 16861 CATTAACAGATCAAACTCTCTCGCATGTTTCTGACAGGCGCTGCAAAATCTGCGCTGCG 16920
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Db 81180 CATTAACAGATCAAACTCTCTCGCATGTTTCTGACAGGCGCTGCAAAATCTGCGCTGCG 81239
QY 16921 AAACCTGCAAGGAATCACTGGGACGAGGCAAGAAACAGTCAATGATTTATCGGCACA 16980
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Db 81240 AAACCTGCAAGGAATCACTGGGACGAGGCAAGAAACAGTCAATGATTTATCGGCACA 81299
QY 16981 ACACAGGTGTCGGGAGCTTTTGGGATCAGAGAGGCGCACATATACGACACCGGAGCGCG 17040
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Db 81300 ACACAGGTGTCGGGAGCTTTTGGGATCAGAGAGGCGCACATATACGACACCGGAGCGCG 81359
QY 17041 TCGCAAAATTTGAACTCGAGCTGTCTCCAAAGTAAAAAAGATACCTCAAGCGCCG 17100
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Db	18360	TCGCAAAATTTGAACTCCGAGCTTCTCTCAAAAGTAAAAAGATACCTCAACAGCCCC	81419
Qy	17101	TAGCAGAGTTGGCAGAGAAGATCCTGGAGTCGTTGGATTTCCTTTATAAACGGAGAC	17160
Db	81420	TAGCAGAGTTGGCAGAGAAGATCCTGGAGTCGTTGGATTTCCTTTATAAACGGAGAC	81479
Qy	17161	TCCTAGTGGCGCTTACGCTTCGCGCCGCTGCTCTCGAAACATCCTCTCGAAGCA	17220
Db	81480	TCTCAGTGGCGCTTACGCTTCGCGCCGCTGCTCTCGAAACATCCTCTCGAAGCA	81539
Qy	17221	ACTGCCATGGAACAGCTATGCAACGATGGTCCGCGATGAGTTACACAGATCCGAGCC	17280
Db	81540	ACTGCCATGGAACAGCTATGCAACGATGGTCCGCGATGAGTTACACAGATCCGAGCC	81599
Qy	17281	CACCGTAACCTCAGAGCAATTTGAAAGAGTCTGATCTTCCCGAGAGAGCCGCCGCC	17340
Db	81600	CACCGTAACCTCAGAGCAATTTGAAAGAGTCTGATCTTCCCGAGAGAGCCGCCGCC	81659
Qy	17341	CTTGGTCGCGGTGTACAGCTCCCTCAAAATACCTGTGAGATCTACCTGATATATACATCT	17400
Db	81660	CTTGGTCGCGGTGTACAGCTCCCTCAAAATACCTGTGAGATCTACCTGATATATACATCT	81719
Qy	17401	AATTTCTTAAATTTCTGGGCACTGTGAACCGGTTTGAACACAGCCGCGTACAGCAAAA	17460
Db	81720	AATTTCTTAAATTTCTGGGCACTGTGAACCGGTTTGAACACAGCCGCGTACAGCAAAA	81779
Qy	17461	ATCGCAATATCTGTTATATCTTCATTCAGCGGAGCTGTGGGTGACCGGTTGACAGG	17520
Db	81780	ATCGCAATATCTGTTATATCTTCATTCAGCGGAGCTGTGGGTGACCGGTTGACAGG	81839
Qy	17521	GACAGGTAAATGTCTTGTCTGCTCATCCCATTCACACTCCGGGGTATCGCTTAGACTC	17580
Db	81840	GACAGGTAAATGTCTTGTCTGCTCATCCCATTCACACTCCGGGGTATCGCTTAGACTC	81899
Qy	17581	CACGGCCTCGATGAACCAAGCTTTAAATTCATTCGCGGTTCCGCACTCTCGCGATTC	17640
Db	81900	CACGGCCTCGATGAACCAAGCTTTAAATTCATTCGCGGTTCCGCACTCTCGCGATTC	81959
Qy	17641	ATACCTGTACCGAGCGGCTCAGTTAAATACCGAGCCCGAGAACCCGAGGCTCCGTA	17700
Db	81960	ATACCTGTACCGAGCGGCTCAGTTAAATACCGAGCCCGAGAACCCGAGGCTCCGTA	82019
Qy	17701	ACAAAAGATCTAGATCTGAAGAAGCTTAACTATATACGCCCAAGGGAAAACTCTGTA	17760
Db	82020	ACAAAAGATCTAGATCTGAAGAAGCTTAACTATATACGCCCAAGGGAAAACTCTGTA	82079
Qy	17761	ACAAATGAAAAAATGTCTCTAGAAACGAAGAGAGAAAACTGACGACAGCCATCTAG	17820
Db	82080	ACAAATGAAAAAATGTCTCTAGAAACGAAGAGAGAAAACTGACGACAGCCATCTAG	82139
Qy	17821	TCAAACCAAGACCTTAAAGCGCTCACTGACCATATCTTCCCTCCGAGAGAGTGGC	17880
Db	82140	TCAAACCAAGACCTTAAAGCGCTCACTGACCATATCTTCCCTCCGAGAGAGTGGC	82199
Qy	17881	GTTTCTCAATGCGGTGAGCAAAACGAAACGCTACACATATTAACACAGTGTGAGAGA	17940
Db	82200	GTTTCTCAATGCGGTGAGCAAAACGAAACGCTACACATATTAACACAGTGTGAGAGA	82259
Qy	17941	AAACTTATTTGAGGAGAGGCAAAAGCAAGCTGTGACGCTTACAGATATGTGCACCTG	18000
Db	82260	AAACTTATTTGAGGAGAGGCAAAAGCAAGCTGTGACGCTTACAGATATGTGCACCTG	82319
Qy	18001	GCGCGCATCCCGCAGCGCCGCGCAGACACTCTGTCAAAATTTGAATGAGAGGGGAT	18060
Db	82320	GCGCGCATCCCGCAGCGCCGCGCAGACACTCTGTGTGAAATTTGAATGAGAGGGGAT	82379
Qy	18061	TGTGGGACAGGCTGCGCTTCCGAGGTGGAAAGCGCTCTTAGTGGAGAGAGCATAGGC	18120
Db	82380	TGTGGGACAGGCTGCGCTTCCGAGGTGGAAAGCGCTCTTAGTGGAGAGAGCATAGGC	82439
Qy	18121	GGCTGGAATGCGGTTCCGTGTGGGGGGGTGGCTACACCCGACATCATATTTGGCGAG	18180
Db	82440	GGCTGGAATGCGGTTCCGTGTGGGGGGGTGGCTACACCCGACATCATATTTGGCGAG	82499

Qy	18181	CGAAAAACAGCGCAGAACTCGCGCTTGTATTAATATCAACCGGCTCCAGCAACTCC	18240
Db	82500	CGAAAAACAGCGCAGAACTCGCGGCTTGTATTAATATCAACCGGCTCCAGCAACTCC	82559
Qy	18241	GTTACCCAGCAGGAAGGCTGGAAGCTGACCCATATACCGAATGTAATCCAGACCCGTC	18300
Db	82560	GTTACCCAGCAGGAAGGCTGGAAGCTGACCCATATACCGAATGTAATCCAGACCCGTC	82619
Qy	18301	TGGCTAATTCATCAACCCCGCTATGATCTCTTCCCGACGCCCTTTAGCATTCGTGTCTG	18360
Db	82620	TGGCTAATTCATCAACCCCGCTATGATCTCTTCCCGACGCCCTTTAGCATTCGTGTCTG	82679
Qy	18361	GTGAGAAACATATCTCTGTGGGATATGCGGCAACAGGCGCTTTCGCGCGAATCCGCC	18420
Db	82680	GTGAGAAACATATCTCTGTGGGATATGCGGCAACAGGCGCTTTCGCGCGAATCCGCC	82739
Qy	18421	ACAAAGTGTCTTCAAGTGTGCTGTGGCGCGGCAACAGCGAAGCGCTTGGGCGA	18480
Db	82740	ACAAAGTGTCTTCAAGTGTGCTGTGGCGCGGCAACAGCGAAGCGCTTGGGCGA	82799
Qy	18481	CCCGACCTCCATGTTCCCAACCAAGCCCATATGTAATTAACCAAGCCGTAAGATCCA	18540
Db	82800	CCCGACCTCCATGTTCCCAACCAAGCCCATATGTAATTAACCAAGCCGTAAGATCCA	82859
Qy	18541	ACACTGTCCCGCTGCGCTCCCAAGCGGCTTCTGACTCATCCCGGACCGAGATACCG	18600
Db	82860	ACACTGTCCCGCTGCGCTCCCAAGCGGCTTCTGACTCATCCCGGACCGAGATACCG	82919
Qy	18601	GAATCTGGGGTTTACCTCGTTGCGTACGTCAAGAGATGCGCGGTTGGATCCGCTTC	18660
Db	82920	GAATCTGGGGTTTACCTCGTTGCGTACGTCAAGAGATGCGCGGTTGGATCCGCTTC	82979
Qy	18661	GTTACAGAGCGGGCAAGATCGTAACAAGATCGGCAACAGCGCAATACGGGCACTGTT	18720
Db	82980	GTTACAGAGCGGGCAAGATCGTAACAAGATCGGCAACAGCGCAATACGGGCACTGTT	83039
Qy	18721	AGGCGCGGCGCGCAGAGGTTCTCCTAGTGAATACATCTTGTGAGCGTGTGACTGTGGC	18780
Db	83040	AGGCGCGGCGCGCAGAGGTTCTCCTAGTGAATACATCTTGTGAGCGTGTGACTGTGGC	83099
Qy	18781	TATACGCTGGCCAACCACTTCTTACATTCCTGACGCTCAATTCGTCTGTACCGGCTCG	18840
Db	83100	TATACGCTGGCCAACCACTTCTTACATTCCTGACGCTCAATTCGTCTGTGTACCGGCTCG	83159
Qy	18841	CCGTATGCTTAAATTTGACATATGCAAGATACATATGTTCTCATGCTGAGAGCGCC	18900
Db	83160	CCGTATGCTTAAATTTGACATATGCAAGATACATATGTTCTCATGCTGAGAGCGCC	83219
Qy	18901	ACCGCGCGCTTAAATGATTCACAGGTAAACGAACCAAGAGTCTTCTCATCCAGGCCA	18960
Db	83220	ACCGCGCGCTTAAATGATTCACAGGTAAACGAACCAAGAGTCTTCTCATCCAGGCCA	83279
Qy	18961	ATGCAATTCAGAGATCTTATCATTTATCGCAACATCGAGCAACATGCCCTGAGGCCAGA	19020
Db	83280	ATGCAATTCAGAGATCTTATCATTTATCGCAACATCGAGCAACATGCCCTGAGGCCAGA	83339
Qy	19021	GCGCGGTTTACGCGGATCGACCGTGGCGGCTTCCGCGCATCTCGAGGGGTCCGCTGCG	19080
Db	83340	GCGCGGTTTACGCGGATCGACCGTGGCGGCTTCCGCGCATCTCGAGGGGTCCGCTGCG	83399
Qy	19081	ATTAACCTGGCTTAAATATCTATCCCGCCCGGTGACCTGTACTTTTACATCACTACCTTCC	19140
Db	83400	ATTAACCTGGCTTAAATATCTATCCCGCCCGGTGACCTGTACTTTTACATCACTACCTTCC	83459
Qy	19141	GCGCACAGCGCTGAGGCTGTGAGGAGCGGACCCAGCAAGCTATTTTTCATCTGTACGCCG	19200
Db	83460	GCGCACAGCGCTGAGGCTGTGAGGAGCGGACCCAGCAAGCTATTTTTCATCTGTACGCCG	83519
Qy	19201	CCTACTAGGGGAATCTGGGGCTTACAAATCTACCGAGCGCGCGAATGTACCATGAG	19260
Db	83520	CCTACTAGGGGAATCTGGGGCTTACAAATCTACCGAGCGCGCGCGAATGTACCATGAG	83579

OY	19261	TCATTTCACTCTGCACATACATCCAAAGTGCAGGACCTG6GGTCTTTTACTGAGCCAG	19320
Db	83560	TCATTTCACTCTGCACATACATCCAAAGTGCAGGACCTG6GGTCTTTTACTGAGCCAG	83639
OY	19321	GGCAGCCCCCAAGGTAAAGAGTGCATCTGTTGGGAACAGTGC6GGGAA6GGGAG	19380
Db	83640	GGCAGCCCCCAAGGTAAAGAGTGCATCTGTTGGGAACAGTGC6GGGAA6GGGAG	83699
OY	19381	ACCGGGGAGTCTGCGCAGTAGAACCCATAACATAGAAGATTTGAGATTTGACAGAGATC	19440
Db	83700	ACCGGGGAGTCTGCGCAGTAGAACCCATAACATAGAAGATTTGAGATTTGACAGAGATC	83759
OY	19441	GCACAGCCCGTGTGCGTGGTCCCTCTCGCTGCTTCCCTGGCGACGACCGTGTGCC	19500
Db	83760	GCACAGCCCGTGTGCGTGGTCCCTCTCGCTGCTTCCCTGGCGACGACCGTGTGCC	83819
OY	19501	TGTTTTGTTTATTCACATATACATCCCGAGCTGCATTTGGCATGCAAAAAGAGCCCTCTCAC	19560
Db	83820	TGTTTTGTTTATTCACATATACATCCCGAGCTGCATTTGGCATGCAAAAAGAGCCCTCTCAC	83879
OY	19561	ACCGTTTTATATCTACACACAGGGTTCTCTGCTCCGCGCTTACGGGCCATCCAACT	19620
Db	83880	ACCGTTTTATATCTACACACAGGGTTCTCTGCTCCGCGCTTACGGGCCATCCAACT	83939
OY	19621	GAGTTTTTTGGAGGCCACATCTTATACGCTGTCCCATAGAAACACTGTAACCCGGTTTGG	19680
Db	83940	GAGTTTTTTGGAGGCCACATCTTATACGCTGTCCCATAGAAACACTGTAACCCGGTTTGG	83999
OY	19681	GGTTTTGGCGTTTATGCAATCGTACCCCTTACGGTCTGGGACGCGTGTCCGCGTACCA	19740
Db	84000	GGTTTTGGCGTTTATGCAATCGTACCCCTTACGGTCTGGGACGCGTGTGTCCGCTACCA	84059
OY	19741	GCGACCCCAATATATATATATCTGTATACGTAGCCGCCAAATGGAGTGAATCTGCTGAT	19800
Db	84060	GCGACCCCAATATATATATATCTGTATACGTAGCCGCCAAATGGAGTGAATCTGCTGAT	84119
OY	19801	GC6GTG6TGCACACGCTGCCAACCTGGCGCCCTGGCATATACGACCGCGCCACGCT	19860
Db	84120	GC6GTG6TGCACACGCTGCCAACCTGGCGCCCTGGCATATACGACCGCGCCACGCT	84179
OY	19861	CAGCCTCCGCGGAGCGGAGGAGGACGAGGGGCGTCCCTGGCTCAACCCATGAGACGAGG	19920
Db	84180	CAGCCTCCGCGGAGCGGAGGAGGACGAGGGGCGTCCCTGGCTCAACCCATGAGACGAGG	84239
OY	19921	CCGCTCTTAAGTATTTAGAGCGGTCTCCGAATGACTATCTAAGATGACGAGCATAAACA	19980
Db	84240	CCGCTCTTAAGTATTTAGAGCGGTCTCCGAATGACTATCTAAGATGACGAGCATAAACA	84299
OY	19981	GC6GATGCACGGGGGCTCTCAAGTAAATAATTTTCTCGCCGCAAAAGCGTGTGTGG	20040
Db	84300	GC6GATGCACGGGGGCTCTCAAGTAAATAATTTTCTCGCCGCAAAAGCGTGTGTGG	84359
OY	20041	CCCGGGCATGTCCTCTGTTTAAACCCAGCGTTTTCCGAGACACCCCTTACACTCTTTCC	20100
Db	84360	CCCGGGCATGTCCTCTGTTTAAACCCAGCGTTTTCCGAGAGCACCCCTTACACTCTTTCC	84419
OY	20101	GGCAGTCGCAAGTGTGCTGCGCTCCACATTCAGATCCGATCCCTATCCAGGAGTACGCA	20160
Db	84420	GGCAGTCGCAAGTGTGCTGCGCTCCACATTCAGATCCGATCCGATCCAGGAGTACGCA	84479
OY	20161	CCACAGGTTGCAATGCACATCTATACCTGCGGCGCATATATCCTAAAGCTCTCTTTCT	20220
Db	84480	CCACAGGTTGCAATGCACATCTATACCTGCGGCGCATATATCCTAAAGCTCTCTTTCT	84539
OY	20221	CGTGGCAACCAACAGTGTGGGGGAAGGTGTGCTTCCCAATTTGGAATAATACCATC	20280
Db	84540	CGTGGCAACCAACAGTGTGGGGGAAGGTGTGCTTCCCAATTTGGAATAATACCATC	84599
OY	20281	TTGCGAGGTATTTGAGTATTTCTATCTCGGCTCATTTGAACTTTGGTCCACGAAACT	20340
Db	84600	TTGCGAGGTATTTGAGTATTTCTATCTCGGCTCATTTGAACTTTGGTCCACGAAACT	84659
OY	20341	AACTCAAAAGCCTCAACACTCCCTCAACTGAGTGAATTTTATGTCCACTTATAGG	20400

Db	84660	AACTCAAAAGCCCTCACCACTCCCTAAACGTAGCGAAATTTATGTCCACTTATAG	84719
OY	20401	GTGCACGTTACGTATATGCCCCGTGAAAACCTGCACTTCCTCAATAATTTATCCCCAA	20460
Db	84720	GTGCACGTTACGTATATGCCCCGTGAAAACCTGCACTTCCTCAATAATTTATCCCCAA	84779
OY	20461	GGTTTGGGGTGGCTCACTTAACCTAATCGAGCATTACAGGTTCATAGTGTCCGGGT	20520
Db	84780	GGTTTGGGGTGGCTCACTTAACCTAATCGAGCATTACAGGTTCATAGTGTCCGGGT	84839
OY	20521	TTTCGCACATCCCCCAACGGCGACAGAAAGAAACCTTCAAATTTAAAGGCCACCAAGCTC	20580
Db	84840	TTTCGCACATCCCCCAACGGCGACAGAAAGAAACCTTCAAATTTAAAGGGCACCAAGCTC	84899
OY	20581	AACTTATTTTAAAGAGAAAAAAACACACGGCATAGAGGTTTCCGAGGACACACCCC	20640
Db	84900	AACTTATTTTAAAGAGAAAAAAACACACGGCATAGAGGTTTCCGAGGACACACCCC	84955
OY	20641	CAAGACTATTCGTGGCGATTGCGGCGACGCTGATTTTTCGTATTTTGTAAATTC	20700
Db	84960	CAAGACTATTCGTGGCGATTGCGGCGACGCTGATTTTTCGTATTTTGTAAATTC	85019
OY	20701	GCATCCATTCGCCCCCAAAATAGTCATTAATAAAAAACCGTAAACACACACTCTGGTGA	20760
Db	85020	GCATCCATTCGCCCCCAAAATAGTCATTAATAAAAAACCGTAAACACACACTCTGGTGA	85079
OY	20761	CAAAATTAATGCTTCTGTGGCCCCCAAGAGCTGCGTAGCGTACAGACACACGCGCTCTAA	20820
Db	85080	CAAAATTAATGCTTCTGTGGCCCCCAAGAGCTGCGTAGCGTACAGACACACGCGCTCTAA	85139
OY	20821	AACATTAACACAGGGCTTAACACGTTTGAACGGAACACAGTCCGAGGCAACAAAAAGCCC	20880
Db	85140	AACATTAACACAGGGCTTAACACGTTTGAACGGAACACAGTCCGAGGCAACAAAAAGCCC	85199
OY	20881	AACGTGGGAAGCAAAAAAATATGTGTACAAATGTCGAGAGAGAGAGGGGTGTCAAGGCAC	20940
Db	85200	AACGTGGGAAGCAAAAAAATATGTGTACAAATGTCGAGAGAGAGAGGGGTGTCAAGGCAC	85255
OY	20941	AGACAGCTACCCGCGCGCGCCCTCCCAATCAAAAACAGTACAGATTAATAAGTCCCATCC	21000
Db	85260	AGACAGCTACCCGCGCGCGCCCTCCCAATCAAAAACAGTACAGATTAATAAGTCCCATCC	85319
OY	21001	ACACACCTCAAGCGCTTGTCTTATAGAGTATGTATGTATACCGGCTAGAGGTGAGCGAAA	21060
Db	85320	ACACACCTCAAGCGCTTGTCTTATAGAGTATGTATGTATACCGGCTAGAGGTGAGCGAAA	85379
OY	21061	AATTGCAATGGGTGGCTGTGACAGCCCCGCTCATTAAGCGGATGTGACCGCAAGCGCTGTGAG	21120
Db	85380	AATTGCAATGGGTGGCTGTGACAGCCCCGCTCATTAAGCGGATGTGACCGCAAGCGCTGTGAG	85439
OY	21121	TGAACAAACGCGACCTACTATTAAGGGCACACAGGGGACAGCAAAAACACGGGGCTAAAAA	21180
Db	85440	TGAACAAACGCGACCTACTATTAAGGGCACACAGGGGACAGCAAAAACACGGGGCTAAAAA	85499
OY	21181	AAGGTTCTTAAGAACTAAAAAATATATACCGGAACGCTGTAAAAATCCAAATTCTGTA	21240
Db	85500	AAGGTTCTTAAGAACTAAAAAATATATACCGGAACGCTGTAAAAATCCAAATTCTGTA	85559
OY	21241	GTATCTGTGGGCATTCGTGGGGACAAATATACCAGTCAATTTGCCCGCAACAACACAGAG	21300
Db	85560	GTATCTGTGGGCATTCGTGGGGACAAATATACCAGTCAATTTGCCCGCAACAACACAGAG	85619
OY	21301	CAGACAGGACACGCGACGACCCACAAAAATGGAACGTTGAACCCATGGAAGGTCAACGCC	21360
Db	85620	CAGACAGGACACGCGACGACCCACAAAAATGGAACGTTGAACCCATGGAAGGTCAACGCC	85679
OY	21361	GAGGGTGGATGCCATAGAACCGGGCGTTATTAAGAAAACGCCGAGATGGTACACGGTACATC	21420
Db	85680	GAGGGTGGATGCCATAGAACCGGGCGTTATTAAGAAAACGCCGAGATGGTACACGGTACATC	85739
OY	21421	CACCTGCCGAGACGACGGCCGGTACCCCAATATACAGATATGCAAAAAGACGCCATG	21480

D	85740	CACCTGCCGCGAGACGAGCCGCTAGCCCAATATACAGAAATGCAAAAACGACCCCATG	85799
Q	21481	TAAACCAACGCGCCCGCAGAGAGATATATATGTTCTCAACGCTAATCAGGGGCTCTACAA	21540
D	85800	TAAAGCAACGCGCCCGCAGAGAGATATATATGTTCTCAACGCTAATCAGGGGCTCTACAA	85859
Q	21541	ATACAGGAGTGAATTAATAACACAGAAATTAACGGGGAAGCCGAGCCGCTCAT	21600
D	85860	ATACAGGAGTGAATTAATAACACAGAAATTAACGGGGAAGCCGAGCCGCTCAT	85919
Q	21601	AAAAGATAGCGAGGCGAGGAGCCGCTCCGAGCGTACGTGCCATGGCCGGGGTTTAA	21660
D	85920	AAAAGATAGCGAGGCGAGGAGCCGCTCCGAGCGTACGTGCCATGGCCGGGGTTTAA	85979
Q	21661	ACAACGGGTTGAACGTTGCGCGAGAGCGCTTGTGTTTTCTTTCGCCGAGCTGGGTAGC	21720
D	85980	ACAACGGGTTGAACGTTGCGCGAGAGCGCTTGTGTTTTCTTTCGCCGAGCTGGGTAGC	86039
Q	21721	TGCTGTGTTTTGCGTTGCGGTTGTTTTTTCGGTCCGAGAGCCGCTGTCGCAAGTATT	21780
D	86040	TGCTGTGTTTTGCGTTGCGGTTGTTTTTTCGGTCCGAGAGCCGCTGTCGCAAGTATT	86099
Q	21781	TGGGCGCCCGCTCTGTGGGCTCGGACCCGCTCTCGCAATTGGGAGCGACTGCTTTTA	21840
D	86100	TGGGCGCCCGCTCTGTGGGCTCGGACCCGCTCTCGCAATTGGGAGCGACTGCTTTTA	86159
Q	21841	AGTCAGAGTACAGGCGTTCTCGAGAGGAGGAGAGCTCAGAGACCCCTCGGAGTGGGAC	21900
D	86160	AGTCAGAGTACAGGCGTTCTCGAGAGGAGGAGAGCTCAGAGACCCCTCGGAGTGGGAC	86219
Q	21901	CTTCCGAGAGATTGCGCGGAGCGGCAATATTCGGCTCGGATCTCACTTTAATAGCA	21960
D	86220	CTTCCGAGAGATTGCGCGGAGCGGCAATATTCGGCTCGGATCTCACTTTAATAGCA	86279
Q	21961	TGACGCCCAACCTGACCTCAGCAAGGCTATCTGTACAGCGGAGCCCTCACTTCCAGAA	22020
D	86280	TGACGCCCAACCTGACCTCAGCAAGGCTATCTGTACAGCGGAGCCCTCACTTCCAGAA	86339
Q	22021	TCTCATTTGGGTGGCAGCAGGAAACAGCAGCAAAAAATCCCGGATCTTACATGCGTTCA	22080
D	86340	TCTCATTTGGGTGGCAGCAGGAAACAGCAGCAAAAAATCCCGGATCTTACATGCGTTCA	86399
Q	22081	ATGCGGCGACAGAGACTTAACTCAGATGAGTGTGTCAGGTGCTAGAAACACACACCA	22140
D	86400	ATGCGGCGACAGAGACTTAACTCAGATGAGTGTGTCAGGTGCTAGAAACACACACCA	86459
Q	22141	CGTCCAGACTTCTTCTCTAGCGCAAGTCCACTTGGGCTCCGGGTTTAAAT	22200
D	86460	CGTCCAGACTTCTTCTCTAGCGCAAGTCCACTTGGGCTCCGGGTTTAAAT	86519
Q	22201	CAATTAATTTTACTAACCCGCGCAGCGTAAACGTGGCACTGCGAGGTTTCGCTTAACG	22260
D	86520	CAATTAATTTTACTAACCCGCGCAGCGTAAACGTGGCACTGCGAGGTTTCGCTTAACG	86579
Q	22261	AGACGTTGACCACTGCTTGCCCTGTTTCTGCTCTTACGCACTTTAACAACAAG	22320
D	86580	AGACGTTGACCACTGCTTGCCCTGTTTCTGCTCTTACGCACTTTAACAACAAG	86639
Q	22321	TCACGCTCTTAACCGTAAGGAACAGCGGATCCCGCTCCCGGCTGCTTAAGCTGTGCT	22380
D	86640	TCACGCTCTTAACCGTAAGGAACAGCGGATCCCGCTCCCGGCTGCTTAAGCTGTGCT	86699
Q	22381	GGAAACGAGGATGTTGGGTTGCTGCAAGAGCTTGTGACAGGTCCTGCTGATGTTGT	22440
D	86700	GGAAACGAGGATGTTGGGTTGCTGCAAGAGCTTGTGACAGGTCCTGCTGATGTTGT	86759
Q	22441	CCCGGTAGGAGTGTGCTTAACAACAATGCGGCTTCTTCCGCTCCGAGCTGCGCC	22500
D	86760	CCCGGTAGGAGTGTGCTTAACAACAATGCGGCTTCTTCCGCTCCGAGCTGCGCC	86819
Q	22501	CGTGTGTGTAACGCGCACGTTCAATTTCCGCAATGTTAACTCAAAACATCTCAAGGTTGT	22560
D	86820	CGTGTGTGTAACGCGCACGTTCAATTTCCGCAATGTTAACTCAAAACATCTCAAGGTTGT	86879

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Q	y	25861	CTCAGCAGCTAGCATGCTAAACCTTAAGGGCAGACAGTAAAGCCAGTTAACGAATTT	25920
D	b	90180	CTACAGCAGTACGATACGTAACCTTAACGGCAGACAGTAAAGCCAGTTAACGAATTT	90239
Q	y	25921	GTTGATGCTTGGCTTGGCTTAAAGTCCCTGTAAGAACCCGTCAGAGGGCGCTGCTGTTT	25980
D	b	90240	GTTGATGCTTGGCTTGGCTTAAAGTCCCTGTAAGAACCCGTCAGAGGGCGCTGCTGTTT	90299
Q	y	25981	GACATAAACCGCGGAACCTGCTGCTTAAAGTCCCTGTAAGAACCCGTCAGAGGGCGCTGCTGTTT	26040
D	b	90300	GACATAAACCGCGGAACCTGCTGCTTAAAGTCCCTGTAAGAACCCGTCAGAGGGCGCTGCTGTTT	90359
Q	y	26041	ACGGTAACGAGGACCTGCTCATATTTCTGTCGAAGGAGACCGGGTATGAGTTG	26100
D	b	90360	ACGGTAACGAGGACCTGCTCATATTTCTGTCGAAGGAGACCGGGTATGAGTTG	90419
Q	y	26101	GCTCTATGCTCCATCCAAAGTGTGCTTTAAAGAAATTCACAGTGAATTCGGCGCATCGT	26160
D	b	90420	GCTCTATGCTCCATCCAAAGTGTGCTTTAAAGAAATTCACAGTGAATTCGGCGCATCGT	90479
Q	y	26161	TCAGGGTCAAGGCTTGAGCTACACCCCGCAGTTCCCGCGGTGCTACTAGGTTAAAGT	26220
D	b	90480	TCAGGGTCAAGGCTTGAGCTACACCCCGCAGTTCCCGCGGTGCTACTAGGTTAAAGT	90539
Q	y	26221	TTGGCAGATTTTGGCCGAGAGAAAGATTGGGTGCTTCAATTTGTAAGAAATGCTTCC	26280
D	b	90540	TTGGCAGATTTTGGCCGAGAGAAAGATTGGGTGCTTCAATTTGTAAGAAATGCTTCC	90599
Q	y	26281	AAGACCCCGGATTGGAACAAACTCCGTAATTTTAAACACCGGTAAGACAGCCGCTTTAA	26340
D	b	90600	AAGACCCCGGATTGGAACAAACTCCGTAATTTTAAACACCGGTAAGACAGCCGCTTTAA	90659
Q	y	26341	AGTGAAGCTTTGAAAGATGTTGTAACCGGAGACGCTTCCAAAGTCTGCAACTA	26400
D	b	90660	AGTGAAGCTTTGAAAGATGTTGTAACCGGAGACGCTTCCAAAGTCTGCAACTA	90719
Q	y	26401	CGCGAAGCAGGCTTATTAATATACAGTCAATCTCAGCTGAATATTTGGTGGCA	26460
D	b	90720	CGCGAAGCAGGCTTATTAATATACAGTCAATCTCAGCTGAATATTTGGTGGCA	90779
Q	y	26461	TCACGCGCTGTAAATAATCCCTCAATTTGGGACGCTATTTCAAAATCTTTTACAGACT	26520
D	b	90780	TCACGCGCTGTAAATAATCCCTCAATTTGGGACGCTATTTCAAAATCTTTTACAGACT	90839
Q	y	26521	TAAAAAACCCAAAGTCTTAAGGCGCGCTATTTATTTACCCTTAATAGTTAAGCAACT	26580
D	b	90840	TAAAAAACCCAAAGTCTTAAGGCGCGCTATTTATTTACCCTTAATAGTTAAGCAACT	90899
Q	y	26581	AAATAGCAGTGGGCGGGAAGAGGCTGTCGCGCAGCTGGAGCGGCGATGAGTCACTA	26640
D	b	90900	AAATAGCAGTGGGCGGGAAGAGGCTGTCGCGCAGCTGGAGCGGCGATGAGTCACTA	90959
Q	y	26641	AATCCAAACATGTCTACAGGAAGCTAAGGCCAATATGTATTAACAACGGGCTCTGG	26700
D	b	90960	AATCCAAACATGTCTACAGGAAGCTAAGGCCAATATGTATTAACAACGGGCTCTGG	91019
Q	y	26701	CGACTACGTTGCCCTTTAAGCAGAGCTCACTTTGGTGAACAAGTCTGAGCCGTTT	26760
D	b	91020	CGACTACGTTGCCCTTTAAGCAGAGCTCACTTTGGTGAACAAGTCTGAGCCGTTT	91079
Q	y	26761	GAACCAACGGCGGACCGGGGCAAGAAATGATGAACGAGCGGTTTCCAAACATCTT	26820
D	b	91080	GAACCAACGGCGGACCGGGGCAAGAAATGATGAACGAGCGGTTTCCAAACATCTT	91139
Q	y	26821	CAAAATTTGGGTATGCTCAAGTACAGCCGCTCTGTTGGCGTACCAAAACACGCTATTC	26880
D	b	91140	CAAAATTTGGGTATGCTCAAGTACAGCCGCTCTGTTGGCGTACCAAAACACGCTATTC	91199
Q	y	26881	TGTTGGTCTGGGGGAGAGTCCGCGTCACTCTAGACAGTCCGCCACGACGAGCTAGCG	26940
D	b	91200	TGTTGGTCTGGGGGAGAGTCCGCGTCACTCTAGACAGTCCGCCACGACGAGCTAGCG	91259

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D	b	91260	TGAATACATGTCAATGAGAGACCCAGTGTGCTGTTTAAAGAAACAGTAGGTGC	91319
Q	y	27001	CCGAGGTTCTGTGAACATAGTGTGAGAAATTAATCAAAAAATCTCATACGTTGAC	27060
D	b	91320	CCGAGGTTCTGTGAACATAGTGTGAGAAATTAATCAAAAAATCTCATACGTTGAC	91379
Q	y	27061	ATGAGGCGAGACGATTAATAATTCATCTTTGATGGGCTCCACCCAGTGGTGCACA	27120
D	b	91380	ATGAGGCGAGACGATTAATAATTCATCTTTGATGGGCTCCACCCAGTGGTGCACA	91439
Q	y	27121	CCACATTTTATAGAGAGATACAGAACCCCTTAGAAAGATGCGACCGGAGATTAAG	27180
D	b	91440	CCACATTTTATAGAGAGATACAGAACCCCTTAGAAAGATGCGACCGGAGATTAAG	91499
Q	y	27181	AAACCCGGTGAAGAGCGCGGCGAGTAGAGCATCAAACTATCATAGCTTGTTCAGCT	27240
D	b	91500	AAACCCGGTGAAGAGCGCGGCGAGTAGAGCATCAAACTATCATAGCTTGTTCAGCT	91559
Q	y	27241	TTGGTCCCTGCTGTGATGCGCTGCTCAATCTCTGCGGACGGGCTGATACGGTACG	27300
D	b	91560	TTGGTCCCTGCTGTGATGCGCTGCTCAATCTCTGCGGACGGGCTGATACGGTACG	91619
Q	y	27301	AGAACACGGGCGGCTTTACAAATTAACCTGACAACCTCTAACGTGACACGGATCGTAC	27360
D	b	91620	AGAACACGGGCGGCTTTACAAATTAACCTGACAACCTCTAACGTGACACGGATCGTAC	91679
Q	y	27361	AACAGCTTAAATCTCTGATGAGTTCACAACTAAACCACTAACACCGCACCTTTTAA	27420
D	b	91680	AACAGCTTAAATCTCTGATGAGTTCACAACTAAACCACTAACACCGCACCTTTTAA	91739
Q	y	27421	GCAATGCCACCGGTGACCGGTTTAAATCTGATTCAAATTAAGCAACCCCGTGGTT	27480
D	b	91740	GCAATGCCACCGGTGACCGGTTTAAATCTGATTCAAATTAAGCAACCCCGTGGTT	91799
Q	y	27481	CATTATTTCAAAAAACACCCCTGTGTTTAAATGAGAGTCCGAGGCTTCCGAGCCAG	27540
D	b	91800	CATTATTTCAAAAAACACCCCTGTGTTTAAATGAGAGTCCGAGGCTTCCGAGCCAG	91859
Q	y	27541	TCATTACAGACACCAAGGCGGACAAAGCTACAGGCTATCTTCGAGGTTGTAATG	27600
D	b	91860	TCATTACAGACACCAAGGCGGACAAAGCTACAGGCTATCTTCGAGGTTGTAATG	91919
Q	y	27601	TTCTTAATACAGATTCGAAACACACAGGCTCCGAGGGCTAAAGACAACTATTC	27660
D	b	91920	TTCTTAATACAGATTCGAAACACACAGGCTCCGAGGGCTAAAGACAACTATTC	91979
Q	y	27661	TCGACAAACCGTGCATATTTGGCATGATTAAGAAATACATCATACCTTAACCTA	27720
D	b	91980	TCGACAAACCGTGCATATTTGGCATGATTAAGAAATACATCATACCTTAACCTA	92039
Q	y	27721	CGCCCTGGGGATCCACCGACACACCAATGGGTATACGCAATCACTGCGTAGAGC	27780
D	b	92040	CGCCCTGGGGATCCACCGACACACCAATGGGTATACGCAATCACTGCGTAGAGC	92099
Q	y	27781	AAATTTTACAGAAACCCACCGGCAATATGGAACCTTAACCTCCGAGTGGCTATTTA	27840
D	b	92100	AAATTTTACAGAAACCCACCGGCAATATGGAACCTTAACCTCCGAGTGGCTATTTA	92159
Q	y	27841	TCGACATCGGGAGTGGCGCTCCGCTTACAGAGTGGGCTTAATCTATCGAATTTGAAA	27900
D	b	92160	TCGACATCGGGAGTGGCGCTCCGCTTACAGAGTGGGCTTAATCTATCGAATTTGAAA	92219
Q	y	27901	AACGTCAATGGGACCAACCGCCCTATTCACCTGTGACGAAGTGGCCGCTGTGG	27960
D	b	92220	AACGTCAATGGGACCAACCGCCCTATTCACCTGTGACGAAGTGGCCGCTGTGG	92279
Q	y	27961	TTACCGGCGACACAGATTTGTTTGTCCCTATGAGAGTCACTGGAACGTAATCAACA	28020
D	b	92280	TTACCGGCGACACAGATTTGTTTGTCCCTATGAGAGTCACTGGAACGTAATCAACA	92339

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Db 71280 AAAAGACGTCATGATTTAAAGCCACCTGGGTTACTAGTTTAAACTGCTAATTTGATT 71339
QY 1441 CTATTACCCCTCAATAAATTAATTAATACGTTTGCGGTTTGCATTTCCGCT 1500
Db 71340 CTATTACCCCTCAATAAATTAATTAATACGTTTGCGGTTTGCATTTCCGCT 71399
QY 1501 TAAAACTATTAACAATTCATTTGGGAATAGGATTTATGAGTTAAAGGATTTAAATTTT 1560
Db 71400 TAAAACTATTAACAATTCATTTGGGAATAGGATTTATGAGTTAAAGGATTTAAATTTT 71459
QY 1561 TTTGATCATGAGATTTGGGAACATACGCTGGGATGAGGTTATGCTCATGCTGGG 1620
Db 71460 TTTGATCATGAGATTTGGGAACATACGCTGGGATGAGGTTATGCTCATGCTGGG 71519
QY 1621 TGGCGGATGTCAGGGGAGGTGCTGCTGCAACCTGGCAGCGCAAGATGGGAAT 1680

Db 71520 TGGCTGATGTGCAGGGGAGCGGTGGGTGTGCCCAACCTGGGACCTGACAGATGGGAAT 71579
QY 1681 ACGAGCGGTATATACAGGCACTACTCTGAAGAGTGTCCGCAAAACATGAAGGCTCGGGAGCC 1740
Db 71580 ACGAGCGGTATATACAGGCACTACTCTGAAGAGTGTCCGCAAAACATGAAGGCTCGGGAGCC 71639
QY 1741 TGGAGGTTTCCGACAGACAAAGGGGTCTGGAAACCAAGCAACACCGAAGCTAATATAT 1800
Db 71640 TGGAGGTTTCCGACAGACAAAGGGGTCTGGAAACCAAGCAACACCGAAGCTAATATAT 71699
QY 1801 CGATTAAGACCTAAGTTTGTACATGACGTACAGTCAAAATTAAGAGCGGCTGGGACAGCCGA 1860
Db 71700 CGATTAAGACCTAAGTTTGTACATGACGTACAGTCAAAATTAAGAGCGGCTGGGACAGCCGA 71759
QY 1861 GGGCCGAATCATCACAGCACTTGCACAGCATCAAGCAGGTTAAAGCTCTCCGATTATCAA 1920
Db 71760 GGGCCGAATCATCACAGCACTTGCACAGCATCAAGCAGGTTAAAGCTCTCCGATTATCAA 71819
QY 1921 CCCCGAATTTGGCGCAACCACTCCGGTATGTAATATGACCTCCGGCGAGTCAAGTCAAG 1980
Db 71820 CCCCGAATTTGGCGCAACCACTCCGGTATGTAATATGACCTCCGGCGAGTCAAGTCAAG 71879
QY 1981 GTGGGACACCCGTGGAAGCGGGCGCCCGACGCGTTCAATTAAGCAACAAAGCATGCTCA 2040
Db 71880 GTGGGACACCCGTGGAAGCGGGCGCCCGACGCGTTCAATTAAGCAACAAAGCATGCTCA 71939
QY 2041 ACCCATCTGTGTCTGTCTTTCAGAGCCATCCGTGCGGGTCCACACGCGATACCGAGC 2100
Db 71940 ACCCATCTGTGTGTCTGTCTTTCAGAGCCATCCGTGCGGGTCCACACGCGATACCGAGC 71999
QY 2101 AGTCGTTGCGGATGCGGAACAGGTCACAGCAACGATATGTACCCCTGGCGCCCTTCCC 2160
Db 72000 AGTCGTTGCGGATGCGGAACAGGTCACAGCAACGATATGTACCCCTGGCGCCCTTCCC 72059
QY 2161 TCTTTCAAGCGAGACCTGTGTCTACAGGTGGGGGTACCCCTTGGCCCGCAAGCATG 2220
Db 72060 TCTTTCAAGCGAGACCTGTGTCTACAGGTGGGGGTACCCCTTGGCCCGCAAGCATG 72119
QY 2221 CAAGATACGCGAGTGGCAACAAATATGAGACCAAAATTAAGCCGCAAAAGATACAGCC 2280
Db 72120 CAAGATACGCGAGTGGCAACAAATATGAGACCAAAATTAAGCCGCAAAAGATACAGCC 72179
QY 2281 GTCCGTTTCAGCAGAGTGGCCGCTATGAGACCTGACAGGGACCTCAAGCTCCGCTGTAGAC 2340
Db 72180 GTCCGTTTCAGCAGAGTGGCCGCTATGAGACCTGACAGGGACCTCAAGCTCCGCTGTAGAC 72239
QY 2341 CCATTCCTCCCTTCCGCGAGCGCGTGGACCTGTGACCCCTGCGGCTATAGCGGGA 2400
Db 72240 CCATTCCTCCCTTCCGCGAGCGCGTGGACCTGTGACCCCTGCGGCTATAGCGGGA 72299
QY 2401 ATATTGGGCTCAGCATGCGCTTGTACAGATATATCAAAATATATGACATAGAAACTAC 2460
Db 72300 ATATTGGGCTCAGCATGCGCTTGTACAGATATATCAAAATATATGACATAGAAACTAC 72359
QY 2461 ACGAGCTTCATCGCAATTAAGGTTTATTTATTTGACACTAGTCCGCGCTTATTT 2520
Db 72360 ACGAGCTTCATCGCAATTAAGGTTTATTTATTTGACACTAGTCCGCGCTTATTT 72419
QY 2521 CTGCTGTCGAGCTGGGGCGGCGCTCCCTCGAGAGCGCCGTCGCGCTGACAGATTCGG 2580
Db 72420 CTGCTGTCGAGCTGGGGCGGCGCTCCCTCGAGAGCGCCGTCGCGCTGACAGATTCGG 72479
QY 2581 CCTGTGTGTGTCTGTCTATGACAGCTCACGCGGATATTAATTCGGCGAGGCGCT 2640
Db 72480 CCTGTGTGTGTCTGTCTATGACAGCTCACGCGGATATTAATTCGGCGAGGCGCT 72539
QY 2641 TCCATCTGCGCGCGGCTCACGCGCTTGGCGGCTGGCGCGCTTACCTTACCTTCAATCTTA 2700
Db 72540 TCCATCTGCGCGCGGCTCACGCGCTTGGCGGCTGGCGCGCTTACCTTACCTTCAATCTTA 72599
QY 2701 CGGGTTGACAGCTTAATTAAGCGGAAGCGAGCTGGGATTTGGCCCTCTTTCCGGG 2760
Db 72600 CGGGTTGACAGCTTAATTAAGCGGAAGCGAGCTGGGATTTGGCCCTCTTTCCGGG 72659

Qy	2761	TTAGAGATGACGGGGTCGAGCCGGACCTGGTGGGATGCCGACAAATTTATCAGCTTTTGG	2820
Db	72660	TTAAGATGACGGGGTCGAGCCGGACCTGGTGGGATGCCGACAAATTTATCAGCTTTTGG	72719
Qy	2821	AGCTGCTTGTTCACGCAATTTTTCACCTGACGGGCTAACCTCTCCATTTGTCACG	2880
Db	72720	AGCTGCTTGTTCACGCAATTTTTCACCTGACGGGCTAACCTCTCCATTTGTCACG	72779
Qy	2881	TCCTTTTGGGGGGGGCGCTCTTGGGGCGGTGGAAACATGGGCACTACTACGCAATTC	2940
Db	72780	TCCTTTTGGGGGGGGCGCTCTTGGGGCGGTGGAAACATGGGCACTACTACGCAATTC	72839
Qy	2941	AGAGTACAGCGGGACGTTTAAATACCTTCACGGCGGCCCTGAGGTCACCTGTCGGCCACG	3000
Db	72840	AGAGTACAGCGGGACGTTTAAATACCTTCACGGCGGCCCTGAGGTCACCTGTCGGCCACG	72899
Qy	3001	GTTTCACCAATTTAAAAAGCACATCTATGTAGTACAGAAATGTTGCACCGCGACC	3060
Db	72900	GTTTCACCAATTTAAAAAGCACATCTATGTAGTACAGAAATGTTGCACCGCGACC	72959
Qy	3061	AGAACACAGTTGATCACCAGCCCATATATCTCGAAACCTGACAGCACGGGGCTGTGCTCG	3120
Db	72960	AGAACACAGTTGATCACCAGCCCATATATCTCGAAACCTGACAGCACGGGGCTGTGCTCG	73019
Qy	3121	TCGCGCAGGACATCATGTATATAAAGAGGGGCTTACGGAGGAGCCCGGAGGGGTTT	3180
Db	73020	TCGCGCAGGACATCATGTATATAAAGAGGGGCTTACGGAGGAGCCCGGAGGGGTTT	73079
Qy	3181	GTAATTCACAGAGAGCGCTGCCGTTTCCCTGTAGTGGAGAGGTGGTACGGTGGCGCACAC	3240
Db	73080	GTAATTCACAGAGAGCGCTGCCGTTTCCCTGTAGTGGAGAGGTGGTACGGTGGCGCACAC	73139
Qy	3241	GGCAGACACAGATTTAAGCACGGCAACAGGGGCTAACGCGACACATTAACCTGTGATTT	3300
Db	73140	GGCAGACACAGATTTAAGCACGGCAACAGGGGCTAACGCGACACATTAACCTGTGATTT	73199
Qy	3301	TTCAAGCCGGCGTTTGGCAGGCAACCTCCACTTTTGGCACGGCGCTCTCTTATATACT	3360
Db	73200	TTCAAGCCGGCGTTTGGCAGGCAACCTCCACTTTTGGCACGGCGCTCTCTTATATACT	73259
Qy	3361	ACAGATTAAACATTATATGGCAGAAAGTGCACGGCCCATACGGTCCGTACGGCTTGGACTCCT	3420
Db	73260	ACAGATTAAACATTATATGGCAGAAAGTGCACGGCCCATACGGTCCGTACGGCTTGGACTCCT	73319
Qy	3421	GTAAGTTTGAATTAATACCAAAAAACAACACTCATCTGTATAGCGTTACGCAACAATTTTC	3480
Db	73320	GTAAGTTTGAATTAATACCAAAAAACAACACTCATCTGTATAGCGTTACGCAACAATTTTC	73379
Qy	3481	CCGTCGTGTGTCAACCGGGAGAAACCTCTAGTCTGCCCTGGGACTTAAAAATTTATCCGCG	3540
Db	73380	CCGTCGTGTGTCAACCGGGAGAAACCTCTAGTCTGCCCTGGGACTTAAAAATTTATCCGCG	73439
Qy	3541	CGCCCGAGTGGGCACTTCTTCTACGGGAGCGCGGAGGTGGGTGATTTACACACCGG	3600
Db	73440	CGCCCGAGTGGGCACTTCTTCTACGGGAGCGCGGAGGTGGGTGATTTACACACCGG	73499
Qy	3601	GACTTATATAGATCAAGGGTATCGTGGAGAAATTAACATCATCGTTCTCAATAAGACTAAAC	3660
Db	73500	GACTTATATAGATCAAGGGTATCGTGGAGAAATTAACATCATCGTTCTCAATAAGACTAAAC	73559
Qy	3661	AGGTCGTACACATTTACCGGGGAGAAAGTCAACGCTCTACATCAACGGGTTTATGTACGGCT	3720
Db	73560	AGGTCGTACACATTTACCGGGGAGAAAGTCAACGCTCTACATCAACGGGTTTATGTACGGCT	73619
Qy	3721	CGCCCGGGGCCCTTAAATGCGGCATTAAGTGAACCTACCACATTAACCTTGTGGAGCGCGGAT	3780
Db	73620	CGCCCGGGGCCCTTAAATGCGGCATTAAGTGAACCTACCACATTAACCTTGTGGAGCGCGGAT	73679
Qy	3781	TTGATGTTAGTGCCACATGCCATGACCATTTACCCCAACCGACAGAACCCCGTTTACGT	3840
Db	73680	TTGATGTTAGTGCCACATGCCATGACCATTTACCCCAACCGACAGAACCCCGTTTACGT	73739

QY	3841	TGAGTTGTTATTTAAGAGTCCACAGCTACGACCCCCACGTCCTCCACTAATCGTGGGC	3900
Db	73740	TGAGTTGTTATTTAAGAGTCCACAGCTACGACCCCCACGTCCTCCACTAATCGTGGGC	73799
QY	3901	GCCTGGACGCGGACAAAGGGGCTTACCGGTGACGCGACCAAAAGGACCCGTCGTTGG	3960
Db	73800	GCCTGGACGCGGACAAAGGGGCTTACCGGTGACGCGACCAAAAGGACCCGTCGTTGG	73859
QY	3961	TACATCTGAGGTTTATTAATCTTACCAAAAGGCAATTAATTTACAGCAAAACGCGCA	4020
Db	73860	TACATCTGAGGTTTATTAATCTTACCAAAAGGCAATTAATTTACAGCAAAACGCGCA	73919
QY	4021	TATGTCAAGTATGTTTTATTCACGAAGACCGTCCCAAGCGGTGAACATTTAGAT	4080
Db	73920	TATGTCAAGTATGTTTTATTCACGAAGACCGTCCCAAGCGGTGAACATTTAGAT	73979
QY	4081	CCGCGGTACAAACTCGGAGACCGCTCAGATTAATCGGGGCCAAATACGTTTTACCGAG	4140
Db	73980	CCGCGGTACAACTCGGAGACCGCTCAGATTAATCGGGGCCAAATACGTTTTACCGAG	74039
QY	4141	TGCGCAGCGTCCCAAAACCCACCGCTCAACTCCGCGCACACTCAAAAGCCAAACGAGC	4200
Db	74040	TGCGCAGCGTCCCAAAACCCACCGCTCAACTCCGCGCACACTCAAAAGCCAAACGAGC	74099
QY	4201	CGGAGACCGCCCGCGCGCAAGGGGTTGGGGTCTGACAGGTTATATTTTAAACATGG	4260
Db	74100	CGGAGACCGCCCGCGCGCAAGGGGTTGGGGTCTGACAGGTTATATTTTAAACATGG	74159
QY	4261	CATTATTTAAAGTGTGTTTATTTTAAATTAACCAATTTACGTTAACCATCACT	4320
Db	74160	CATTATTTAAAGTGTGTTTATTTTAAATTAACCAATTTACGTTAACCATCACT	74219
QY	4321	TGCGCATCTGTAATTTATTTGTGTGACAGATATTTCCGCGCACCGCAACTGGGGCGTC	4380
Db	74220	TGCGCATCTGTAATTTATTTGTGTGACAGATATTTCCGCGCACCGCAACTGGGGCGTC	74279
QY	4381	GGTTCGCAATCACCGGATGGAGGGGTTGAGAGACGTTCCGTGTCTACAGCATTA	4440
Db	74280	GGTTCGCAATCACCGGATGGAGGGGTTGAGAGACGTTCCGTGTCTACAGCATTA	74339
QY	4441	TTAATTTCCGACCGCACGATGAGAAATCATGAGCGGATGCTGTGACCGCTTTCC	4500
Db	74340	TTAATTTCCGACCGCACGATGAGAAATCATGAGCGGATGCTGTGACCGCTTTTC	74399
QY	4501	ATTTCCAGAGTGCACAGGTCCTGTGGGCCGCTTTATTAAGAAAGCGGTGAAGCGCTC	4560
Db	74400	ATTTCCAGAGTGCACAGGTCCTGTGGGCCGCTTTATTAAGAAAGCGGTGAAGCGCTC	74459
QY	4561	TCGTCCACGTAATATCCCTATAGCCAGGAGACAAATGGCTTCAGATAACGTTCTGT	4620
Db	74460	TCGTCCACGTAATATCCCTATAGCCAGGAGACAAATGGCTTCAGATAACGTTCTGT	74519
QY	4621	ATAACTTTAGCTTAGATATTTAAATCCTAACCGTCTCTGGCACCCCGGGGTACCTTA	4680
Db	74520	ATAACTTTAGCTTAGATATTTAAATCCTAACCGTCTCTGGCACCCCGGGGTACCTTA	74579
QY	4681	GC CGCGTCAAAAGCAGCAAGATCTCGGTATTTTATTTGATTTGAAGCGCCAAAGATAC	4740
Db	74580	GC CGCGTCAAAAGCAGCAAGATCTCGGTATTTTATTTGATTTGAAGCGCCAAAGATAC	74639
QY	4741	GTCGTCCGAAGGGCGGGGTGCACATCTGTGCTGCTTCATCTCCATATCACTCC	4800
Db	74640	GTCGTCCGAAGGGCGGGGTGCACATCTGTGCTGCTTCATCTCCATATCACTCC	74699
QY	4801	GGGGGCGAGACCATGGCTATTTGGTTCGCGCACTAGTACGACTCGTTAAGAGATCT	4860
Db	74700	GGGGGCGAGACCATGGCTATTTGGTTCGCGCACTAGTACGACTCGTTAAGAGATCT	74759
QY	4861	GGCGGGGAGAGATTAGACTCCCAAGCGGTCAAAAGGACTTAACCGCAACAGTCCAA	4920
Db	74760	GGCGGGGAGAGATTAGACTCCCAAGCGGTCAAAAGGACTTAACCGCAACAGTCCAA	74819
QY	4921	AACCAACAGCGCGGCGCATTTGCCAAACAAATGTAGATGGAATTTAGGCAATTTTCTC	4980

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Db 74820 AACGAACCGGCGGCCATTGCCAACAATAATGATGAAATTTAGGGCAATTTTCTC 74879
Oy 4981 TACTAGTGAAGATATGCGCGAAGTAATTACGATATCTAGCTGAAACGCAACGACG 5040
Db 74880 TACTAGTGAAGATATGCGCGAAGTAATTACGATATCTAGCTGAAACGCAACGACG 74939
Oy 5041 GTCTCTTCTCTCGCTGCTCCAGATCGGGGCGACCGGCTTAATACTCCACATGCGCT 5100
Db 74940 GTCTCTTCTCTCGCTGCTCCAGATCGGGGCGACCGGCTTAATACTCCACATGCGCT 74999
Oy 5101 AATTAACTCTGCGCGCGCAAGGCGCCAGGCGGGCGCAAGGTTTACCGTGTAT 5160
Db 75000 AATTAACTCTGCGCGCGCGCAAGGCGCCAGGCGGGCGCAAGGTTTACCGTGTAT 75039
Oy 5161 GGTGTGAACCTACCGGCGTGGCAGGTTAATCTATCTTCTACAGGTGACGACCAATTGAC 5220
Db 75060 GGTGTGAACCTACCGGCGTGGCAGGTTAATCTATCTTCTACAGGTGACGACCAATTGAC 75119
Oy 5221 CTCGGATTAACATTAAGACCGCATTTGACCTGGCTCAGACCGAGAAATCTGGAACCAT 5280
Db 75120 CTCGGATTAACATTAAGACCGCATTTGACCTGGCTCAGACCGAGAAATCTGGAACCAT 75179
Oy 5281 AATTAGCTACTGGCATGCAACGAGGTCGCGCAGGACGACCAACATGATCGTTTAAATC 5340
Db 75180 AATTAGCTACTGGCATGCAACGAGTCCGCGCAGACGACCAACATGATCGTTTAAATC 75239
Oy 5341 TAAAGTGCCCTGTTTCAGGCGCAAGTTCGTCTCGGCCCTAAGAAAAAGTGTACAAAATGAC 5400
Db 75240 TAAAGTGCCCTGTTTCAGGCGCAAGTTCGTCTCGGCCCTAAGAAAAAGTGTACAAAATGAC 75299
Oy 5401 CCCATCCCCCTATTTGGATGATATAACGCTGCTGGGCTCGTTGAGGACATCGTTTACTGCGC 5460
Db 75300 CCCATCCCCCTATTTGGATGATATAACGCTGCTGGGCTCGTTGAGGACATCGTTTACTGCGC 75359
Oy 5461 CGGACAGTTTATTTTTCCTCATATATATGCAAGGCGGAGAGCGCTGTGATCATTAAC 5520
Db 75360 CGGACAGTTTATTTTTCCTCATATATATGCAAGGCGGAGAGCGCTGTGATCATTAAC 75419
Oy 5521 GAGTTTATTCAGTCCAGTCAGGCGCAGAGCTTGGTCAACCGTAAACACCTATGACGAAT 5580
Db 75420 GAGTTTATTCAGTCCAGTCAGGCGCAGAGCTTGGTCAACCGTAAACACCTATGACGAAT 75479
Oy 5581 AGGGGCGCTATTCGGGCGCTGATTTCTTGGGAATTTTCCAAATTTTGGGCGTATCT 5640
Db 75480 AGGGGCGCTATTCGGGCGCTGATTTCTTGGGAATTTTCCAAATTTTGGGCGTATCT 75539
Oy 5641 AAAATACAAAATGCAACAGAGAGAGAGTGAATGCAAGGCGCATGATCAAAACAATCACTC 5700
Db 75540 AAAATACAAAATGCAACAGAGAGAGAGTGAATGCAAGGCGCATGATCAAAACAATCACTC 75599
Oy 5701 CATACGTGGGGGTTGATGCTGTCACTCAGGACCTCGTACACTTCATCTACCTGTATTT 5760
Db 75600 CATACGTGGGGGTTGATGCTGTCACTCAGGACCTCGTACACTTCATCTACCTGTATTT 75659
Oy 5761 TTACGAGTGCATGACGACAGAGAGTCTCTGTGCTGATCTGTGTACAGCTCCAGTTTACC 5820
Db 75660 TTACGAGTGCATGACGACAGAGAGTCTCTGTGCTGATCTGTGTACAGCTCCAGTTTACC 75719
Oy 5821 GACCCCGCAACGGTTAAACCTCCGACAGTGTGTGGGCGTTAGAACGGATTTTAAAGA 5880
Db 75720 GACCCCGCAACGGTTAAACCTCCGACAGTGTGTGGGCGTTAGAACGGATTTTAAAGA 75779
Oy 5881 GCACGTGATGGCATTTTACAAATTAAGCAAGCTACTGATCTACTTACATTAACATTTTAAAC 5940
Db 75780 GCACGTGATGGCATTTTACAAATTAAGCAAGCTACTGATCTACTTACATTAACATTTTAAAC 75839
Oy 5941 CGTACCGGCTCTCTCCCGGAGAGGATAGAAAACCTTTAGAGAACTAGATGTCAATCTG 6000
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Oy 6001 GTGTGCAATTCGAGAGAGCTGGCGGAATCATGATGAATTAATGACAGTATCCACA 6060
|||||
Db 75900 GTGTGCAATTCGAGAGAGCTGGCGGAATCATGATGAATTAATGACAGTATCCACA 75959
Oy 6061 GCTGAATCTAACAAAAAGATTTATCCGCTCTCCCTGACCTAGCGGCTTAGATCACTATTC 6120
Db 75960 GCTGAATCTAACAAAAAGATTTATCCGCTCTCCCTGACCTAGCGGCTTAGATCACTATTC 76019
Oy 6121 CGGAGGCGCCCAAGGAAACCTTTTACGCTGGCTTCGAGAAATTTCCACATTAAGTTCGGA 6180
Db 76020 CGGAGGCGCCCAAGGAAACCTTTTACGCTGGCTTCGAGAAATTTCCACATTAAGTTCGGA 76079
Oy 6181 GTTTTGAATTAACAGTATTTTGTCTTAATGACAGCAGCTGTATAGACGCTACTGGA 6240
Db 76080 GTTTTGAATTAACAGTATTTTGTCTTAATGACAGCAGCTGTATAGACGCTACTGGA 76139
Oy 6241 ACAAAACATTTATCGGCCGGAAGACGCCCAATTTGCAAGGCTGACGAGATCAAGATCTCAC 6300
Db 76140 ACAAAACATTTATCGGCCGGAAGACGCCCAATTTGCAAGGCTGACGAGATCAAGATCTCAC 76199
Oy 6301 CTCAGAGATTTTCTAGCGACCTGGGCTATCTCTACCTACATTTTAAACAATTCCT 6360
Db 76200 CTCAGAGATTTTCTAGCGACCTGGGCTATCTCTACCTACATTTTAAACAATTCCT 76259
Oy 6361 ACTTCACGCGCAGAGATTTTCAACCCAGACTCCAGTTTATAGATGGGTTGATTTT 6420
Db 76260 ACTTCACGCGCAGAGATTTTCAACCCAGACTCCAGTTTATAGATGGGTTGATTTT 76319
Oy 6421 TGATCTAAAGGTAAACGGAAGTAGACGAGCTCTAAACGATATCTAACATATGCGTAAAC 6480
Db 76320 TGATCTAAAGGTAAACGGAAGTAGACGAGCTCTAAACGATATCTAACATATGCGTAAAC 76379
Oy 6481 GCTGGGCGAGGCTAATTAAGAAAGCTGTCAGTTATAGTTCACATTAACCAACACACC 6540
Db 76380 GCTGGGCGAGGCTAATTAAGAAAGCTGTCAGTTATAGTTCACATTAACCAACACACC 76439
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Db 76440 CGTGTATTTTAAAGTGGGCTGTCCAGCCCTAACCTGACCGGAGTATCTCAGACAC 76499
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Db 76500 CGCGTTCTGTCTAGCTGACGCAAAAATAGGATGGAATTTGAAACCCGTTCCAGCGG 76559
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Db 76560 ATACTGTTTGGGGGTCGCGTCCACTGCTGCTGACCGGACATTTTAAACCGGCTGT 76619
Oy 6721 TAACTGGACACGCGGCTAGCCTCAGAGATTCCTGGGATCTTAAAGATTAAGACCAAT 6780
Db 76620 TAACTGGACACGCGGCTAGCCTCAGAGATTCCTGGGATCTTAAAGATTAAGACCAAT 76679
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Db 76680 TGACTCTGGCATTTACGCCAAGGGGCGATGCGTGGCGCTACTGCTATTAAGTTGG 76739
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Db 76800 TAAATCGCGATTTTGAATAACGCGTTTAAAGTTTCTAATCTGTATCATCAGCCCTGCG 76859
Oy 6961 AGACTCTGTACACAAAACGCGCACCTGTGTACGCGATCTGACGCAAAAAGAGGCTT 7020
Db 76860 AGACTCTGTGTACACAAAACGCGCACCTGTGTACGCGATCTGACGCAAAAAGAGGCTT 76919
Oy 7021 TCTGAAGAAGCAAAACCAAGATTAATCTTCCAAAACATTCAGGACCTGGCGAAAAAT 7080
Db 76920 TCTGAAGAAGCAAAACCAAGATTAATCTTCCAAAACATTCAGGACCTGGCGAAAAAT 76979
Oy 7081 TGAGGGAACCAAGAAAAACCACTAATTTGATTTGGGACGACGCGAGTGTGGCAAAACT 7140
Db 76980 TGAGGGAACCAAGAAAAACCACTAATTTGATTTGGGACGACGCGAGTGTGGCAAAACT 77039
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OY	7141	ACAGCATACCAATACAGCGTTTCTTTCGGATGACGCGATCGGCCAATTTGGACTGTGAG	7200
Db	77040	ACAGCATACCAATACAGCGTTTCTTTCGGATGACGCGATCGGCCAATTTGGACTGTGAG	77099
OY	7201	CTTCATCGCACTCCGGAGACACACTTATTACAGTTTAACCAAAAAAGAAACAACTTTT	7260
Db	77100	CTTCATCGCACTCCGGAGACACACTTATTACAGTTTAACCAAAAAAGAAACAACTTTT	77159
OY	7261	CTGTATTATATCATTAAGCAGCGAAGACACACTGACAGAGTCCGTATTATTTTAACCTTACA	7320
Db	77160	CTGTATTATATCATTAAGCAGCGAAGACACACTGACAGAGTCCGTATTATTTTAACCTTACA	77219
OY	7321	TTCCACAAAAGAAAGCAGGTACCGGTGACCTTTATGAGTCAGTCCCTTGTCTGCAAAATG	7380
Db	77220	TTCCACAAAAGAAAGCAGGTGACCGGTGACCTTTATGAGTCAGTCCCTTGTCTGCAAAATG	77279
OY	7381	TAAATCATTAATAGGCCAACTGCATATTTTCAATTTATGATGATACCATTAACCGGAGCTAAGA	7440
Db	77280	TAAATCATTAATAGGCCAACTGCATATTTTCAATTTATGATGATACCATTAACCGGAGCTAAGA	77339
OY	7441	GACACGAATAAATTCATCCGTGATGAGGCGCAGCTCTCCGGCTACTTGTATTAATTTAACAC	7500
Db	77340	GACACGAATAAATTCATCCGTGATGAGGCGCAGCTCTCCGGCTACTTGTATTAATTTAACAC	77399
OY	7501	CGCGTAAACCCCAAAACACATTTGGACGAGTTTCTTTCGCAAGCTGAACATGGCACAG	7560
Db	77400	CGCGTAAACCCCAAAACACATTTGGACGAGTTTCTTTCGCAAGCTGAACATGGCACAG	77459
OY	7561	GCAATGGTGAAGCCGTGAATTCATGAAGGATATTTTGGAGCGATAGAAAGACCCCTGTGGC	7620
Db	77460	GCAATGGTGAAGCCGTGAATTCATGAAGGATATTTTGGAGCGATAGAAAGACCCCTGTGGC	77519
OY	7621	TCTTACGAGCTCCATTTTAAACCAGCACTTATCAAAAGGCTCTTTTATATAGATTATACAT	7680
Db	77520	TCTTACGAGCTCCATTTTAAACCAGCACTTATCAAAAGGCTCTTTTATATAGATTATACAT	77579
OY	7681	GGCGTATGTTTTCACGCACTATATTTGTTTATAGGGGGCAATATCATGTCGCGACTTGA	7740
Db	77580	GGCGTATGTTTTCACGCACTATATTTGTTTATAGGGGGCAATATCATGTCGCGACTTGA	77639
OY	7741	CGACTCGTCTCGGAGCAATGAGACACGTGTCCCAAGCCGGAGCCAGAACCGTCCAC	7800
Db	77640	CGACTCGTCTCGGAGCAATGAGACACGTGTCCCAAGCCGGAGCCAGAACCGTCCAC	77699
OY	7801	AAGCCGCAACAGCTTTTCCGAGGGGCCCAATATCACAAATGTTGGCGTTACCTTAAATCCG	7860
Db	77700	AAGCCGCAACAGCTTTTCCGAGGGGCCCAATATCACAAATGTTGGCGTTACCTTAAATCCG	77759
OY	7861	TAAAGATCTTCGATCTTGAGACGCCGGGTAAAAATTTGAGACACATCTCCACTTAACCGTCC	7920
Db	77760	TAAAGATCTTCGATCTTGAGACGCCGGGTAAAAATTTGAGACACATCTCCACTTAACCGTCC	77819
OY	7921	GCGATCTTCGATCTTCAGAACGCGGTTCGCGGTCCGGTCAACATCAAAACACTCAGGAGATA	7980
Db	77820	GCGATCTTCGATCTTCAGAACGCGGTTCGCGGTCCGGTCAACATCAAAACACTCAGGAGATA	77879
OY	7981	CGTCAAGAGATTCAAACCAAGGTTGATGCAACCCGTCATCGAAGACCGTGGCACAGGGG	8040
Db	77880	CGTCAAGAGATTCAAACCAAGGTTGATGCAACCCGTCATCGAAGACCGTGGCACAGGGG	77939
OY	8041	CGGTAAGGAAAGGCCCCGTTTATCCGAGAGACGCAATGGCTGGCGCGGTTCGACGAC	8100
Db	77940	CGGTAAGGAAAGGCCCCGTTTATCCGAGAGACGCAATGGCTGGCGCGGTTCGACGAC	77999
OY	8101	ATTAGGCGCAGACTATGCGGAAACACCGCTTTAATGCGGAGCATTTAAAGATCTATTAA	8160
Db	78000	ATTAGGCGCAGACTATGCGGAAACACCGCTTTAATGCGGAGCATTTAAAGATCTATTAA	78059
OY	8161	AAAGATGACACTTTCATTCACCATGTCTCTCGTGGCACAGTAAAAAGTATTCGAGGG	8220
Db	78060	AAAGATGACACTTTCATTCACCATGTCTCTCGTGGCACAGTAAAAAGTATTCGAGGG	78119

QY	8221	ACTGTGGCAGACGACCTGGGACAGTCTTTCAAGTGTGCTCTGCCGGCCGCCACCGCT	8280
Db	78120	ACTGTGGCAGACGACCTGGGACAGTCTTTCAAGTGTGCTCTGCCGGCCGCCACCGCT	78173
QY	8281	GCAACCCGAGGTGTTCAACGGATGCACAGCAAGCTTATAGTCAAGTCTGGCGGGCGAC	8340
Db	78180	GCAACCCGAGGTGTTCAACGGATGCACAGCAAGCTTATAGTCAAGTCTGGCGGGCGAC	78233
QY	8341	AGACGCGCTGTGGCCAAAAAAGTTAGCTGGCTTAAACTAACAGCCTATACAAACCCCT	8400
Db	78240	AGACGCGCTGTGGCCAAAAAAGTTAGCTGGCTTAAACTAACAGCCTATACAAACCCCT	78299
QY	8401	GCTACACGTTTGTACGGGGAGAAACAACAGCCCACTGTTGGCCAGCGCAAAAAAC	8460
Db	78300	GCTACACGTTTGTACGGGGAGAAACAACAGCCCACTGTTGGCCAGCGCAAAAAAC	78353
QY	8461	GCTAGCGCTCTCGGGAGCTCGAGGCTCTCGGGCCCTTATGAGAGAACGTCGTGGCGGGC	8520
Db	78360	GCTAGCGCTCTCGGGAGCTCGAGGCTCTCGGGCCCTTATGAGAGAACGTCGTGGCGGGC	78411
QY	8521	CCAGGTGTGCATATCTCAAAAACAGATGTTGAAACGACAGCAACCTATGATTCATTGAGA	8580
Db	78420	CCAGGTGTGCATATCTCAAAAACAGATGTTGAAACGACAGCAACCTATGATTCATTGAGA	78477
QY	8581	CAGTAGTCAGAGCGGTGTGCACCTGTGTTCTCCAAAATCAGGCATTTGCACATPACAGTG	8640
Db	78480	CAGTAGTCAGAGCGGTGTGCACCTGTGTTCTCCAAAATCAGGCATTTGCACATPACAGTG	78533
QY	8641	CTTCTGTGAGAAATCAGGCTGAGGTGTAGCTGTGACGTGTGTAACAGCACTAACCTTACCTCGTGTAT	8700
Db	78540	CTTCTGTGAGAAATCAGGCTGAGGTGTAGCTGTGACGTGTGTAACAGCACTAACCTTACCTCGTGTAT	78599
QY	8701	AAATPACCCGCTGGCGGAGCGGCGGAACCTTGGCGGAGAGTGAACCTGAATTTTAAACT	8760
Db	78600	AAATPACCCGCTGGCGGAGCGGCGGAACCTTGGCGGAGAGTGAACCTGAATTTTAAACT	78655
QY	8761	CGGAATGCTGATTTGGGTTCCGCCCTTAACCTTGCGGCCTCTTGCAGACATAAGTTGTC	8820
Db	78660	CGGAATGCTGATTTGGGTTCCGCCCTTAACCTTGCGGCCTCTTGCAGACATAAGTTGTC	78711
QY	8821	TGGCAGAGCCGTGACGCTGTTAGTGTCTTTCCTGAGAAATATATPAGACCGGAGATGTGCAT	8880
Db	78720	TGGCAGAGCCGTGACGCTGTTAGTGTCTTTCCTGAGAAATATATPAGACCGGAGATGTGCAT	78777
QY	8881	GGGACTCTTAAATTCATATAGTGTGTGAGACATACACCAAATGTGCTAGCCGCGAGTGTGT	8940
Db	78780	GGGACTCTTAAATTCATATAGTGTGTGAGACATACACCAAATGTGCTAGCCGCGAGTGTGT	78833
QY	8941	CATTACAAACCCAGCCCATGTAGATCTGGCGAAACACAAAGGACTTTTTTCTTCTCC	9000
Db	78840	CATTACAAACCCAGCCCATGTAGATCTGGCGAAACACAAAGGACTTTTTTCTTCTCC	78899
QY	9001	AGTGAATATATTAACCCATGTGTAGTAACTTCCGCTATATATTTACAGGGCGCTTTAAA	9060
Db	78900	AGTGAATATATTAACCCATGTGTAGTAACTTCCGCTATATATTTACAGGGCGCTTTAAA	78955
QY	9061	TGCATTAACCCACATTAACAAATATAAATGTGTAAACCAAAACAGCGCTCAAGCTTTTTC	9120
Db	78960	TGCATTAACCCACATTAACAAATATAAATGTGTAAACCAAAACAGCGCTCAAGCTTTTTC	79011
QY	9121	TGCAGAGGTTCTGTGCTCGGAACAATAGCCAGAGTTCGCCACCTAGCGGACAGTTCCT	9180
Db	79020	TGCAGAGGTTCTGTGCTCGGAACAATAGCCAGAGTTCGCCACCTAGCGGACAGTTCCT	79077
QY	9181	ATAGCCTTGTGATACAGGGGATGTTATTTACGGAAGTGCACATGAAACCGTGGCCGGGT	9240
Db	79080	ATAGCCTTGTGATACAGGGGATGTTATTTACGGAAGTGCACATGAAACCGTGGCCGGGT	79133
QY	9241	GCGTACAGTAAACCGGGTCCAAATCGGCGCACTTACACAACATTAATAATPAGGAGACGT	9300
Db	79140	GCGTACAGTAAACCGGGTCCAAATCGGCGCACTTACACAACATTAATAATPAGGAGACGT	79199
QY	9301	TTATAGCGGTTATTTTGAACATACACACATTTTCAGAGAGTTCGGCTTTTATTAATAAT	9360

Db 79200 TTAATACGGTTATTTGAACATACACACATTGAGGTTTCGGCTTTTATAAAAT 79259
QY 9361 CTTCATTCAATCAAGATGCGATATATTTACAGCTGGTGGACAACAATACATATCGCGC 9420
Db 79260 CTTCATTCAATCAAGATGCGGATATATTTACAGCTGGTGGACAACAATACATATCGCGC 79319
QY 9421 CTGTGATGATCTCTCTCTCTGATAGGACACGAGACACCAATCTGTGCAAAACG 9480
Db 79320 CTGTGATGATCTCTCTCTCTGATAGGACACGAGACACCAATCTGTGCAAAACG 79379
QY 9481 ATCGGGTGGCCCGGGATCAGAGGCTGTGTGACTGGGCTAACTTTAACTGATTCATC 9540
Db 79380 ATCGGGTGGCCCGGGATCAGAGGCTGTGTGACTGGGCTAACTTTAACTGATTCATC 79439
QY 9541 GGTATCAAAAACGCGATGTCACCCAGATGGACGCGCTTGTTCAGAGGTGTTGA 9600
Db 79440 GGTATCAAAAACGCGATGTCACCCAGATGGACGCGCTTGTTCAGAGGTGTTGA 79499
QY 9601 GGTATGCGACGAGACCATTAATTAGAAATCCATAGCCATTCATATCCCATAC 9660
Db 79500 GGTATGCGACGAGACCATTAATTAGAAATCCATAGCCATTCATATCCCATAC 79559
QY 9661 ACAAGTGCACAAACAGATGCGCTCTCCAGAGGCTTAACGCGTTTACAACTGCTGCA 9720
Db 79560 ACAAGTGCACAAACAGATGCGCTCTCCAGAGGCTTAACGCGTTTACAACTGCTGCA 79619
QY 9721 CATAAATGCGTATCCATATAGGCGCCGCGGCGCAACCACTGAAGCGCCGCGAGC 9780
Db 79620 CATAAATGCGTATCCATATAGGCGCCGCGGCGCAACCACTGAAGCGCCGCGAGC 79679
QY 9781 CATGCAAGAGTGTGTTCAATTTTATCCGTTGTCTGCTGATTAACGAGCCCATCC 9840
Db 79680 CATGCAAGAGTGTGTTCAATTTTATCCGTTGTCTGCTGATTAACGAGCCCATCC 79739
QY 9841 AGAATGGTAAAGTGTGCTGAAGGACCCCATATATTAACCTGATATGATGATAA 9900
Db 79740 AGAATGGTAAAGTGTGCTGAAGGACCCCATATATTAACCTGATATGATGATAA 79799
QY 9901 TCCCAACGGGTGCTCAACAGATGCGCCAAACACGAGAAAGACCGCTGATGACATAG 9960
Db 79800 TCCCAACGGGTGCTCAACAGATGCGCCAAACACGAGAAAGACCGCTGATGACATAG 79859
QY 9961 CGGACAGGGGTGTCCCGCGGCGCAACGAGCGCCCTTGAATATGCTGCTGCTAC 10020
Db 79860 CGGACAGGGGTGTCCCGCGGCGCAACGAGCGCCCTTGAATATGCTGCTGCTAC 79919
QY 10021 GTCTTCACGAGAGCGGTGCGGTTGACAGCGCTGCTGCGGCGGCGTCAATGTA 10080
Db 79920 GTCTTCACGAGAGCGGTGCGGTTGACAGCGCTGCTGCGGCGGCGTCAATGTA 79979
QY 10081 GGTACCGGCGGAGCGGATAGCAAGATGCGCGAGCACTGCTTACCGTATTCAGATAC 10140
Db 79980 GGTACCGGCGGAGCGGATAGCAAGATGCGCGAGCACTGCTTACCGTATTCAGATAC 80039
QY 10141 CCGCGCCGCTGCTGCGGCGCCCTTGGGCTTAAACATCCGAAACCTTAACGCCGCGATT 10200
Db 80040 CCGCGCCGCTGCTGCGGCGCCCTTGGGCTTAAACATCCGAAACCTTAACGCCGCGATT 80099
QY 10201 TCGCGGTACCCAGAGAGCGCGAGGCAACCTGATACATCTTTCATCGAGGCGAA 10260
Db 80100 TCGCGGTACCCAGAGAGCGCGAGGCAACCTGATACATCTTTCATCGAGGCGAA 80159
QY 10261 CCGTGAAGACACGTTTGAATGAATAACTCCGCTCAAAAGCGTCTTTCCTATGA 10320
Db 80160 CCGTGAAGACACGTTTGAATGAATAACTCCGCTCAAAAGCGTCTTTCCTATGA 80219
QY 10321 AATAGGACTCTTCTTATGCAACCCATAGGCGCGCTTGGCTGGCCCAAGCTTACCT 10380
Db 80220 AATAGGACTCTTCTTATGCAACCCATAGGCGCGCTTGGCTGGCCCAAGCTTACCT 80279
QY 10381 CCGGACGAGAGGGGATGTTCTGATGAGTGTGCTGATATCTTCCATCCGCG 10440

Db 80280 CCGGACGAGAGGGGATGTTTCTGTGTTGAGATGTCCTGCTACATCTTCCATCCG 80339
QY 10441 AAGTATATCAAAATCCACAGACACGAGGCTGATGCGCCAGCAGCAACCTGCTTTTC 10500
Db 80340 AAGTATATCAAAATCCACAGACACGAGGCTGATGCGCCAGCAGCAACCTGCTTTTC 80399
QY 10501 GTGCTGTGCCCCAAACAGTCCCGAATACGTTGCAAGATTTTGGTGAATACATTC 10560
Db 80400 GTGCTGTGCCCCAAACAGTCCCGAATACGTTGCAAGATTTTGGTGAATACATTC 80459
QY 10561 TCGAATGCCATGCGCGAGACACCGCTGATGAGGCGCGCAGTGAAGCTGACTG 10620
Db 80460 TCGAATGCCATGCGCGAGACACCGCTGATGAGGCGCGCAGTGAAGCTGACTG 80519
QY 10621 ATATGCGAGGTTGATCTACCGCTTTCAGTTGCTTAAATTAACCAACTCCGCCAT 10680
Db 80520 ATATGCGAGGTTGATCTACCGCTTTCAGTTGCTTAAATTAACCAACTCCGCCAT 80579
QY 10681 GCGGCTACGCGCGTGGGCGCAGATGTTGTCAGCGCTACAAAAGAAATCCCACTGCGCA 10740
Db 80580 GCGGCTACGCGCGTGGGCGCAGATGTTGTCAGCGCTACAAAAGAAATCCCACTGCGCA 80639
QY 10741 ACTAATTCCTCAGCGCCCACTGACGCTGCTACGCTGCTATTTCACTCAAGACAGCA 10800
Db 80640 ACTAATTCCTCAGCGCCCACTGACGCTGCTACGCTGCTATTTCACTCAAGACAGCA 80699
QY 10801 CCCCATCATCTTCACCGCTGTTCCCGCGTCCGATGCTGATTAATGATCTGCTCGAGT 10860
Db 80700 CCCCATCATCTTCACCGCTGTTCCCGCGTCCGATGCTGATTAATGATCTGCTCGAGT 80759
QY 10861 CGCCCAAGCTTACTGCGCGGCTCATGCGATTTGGTCTGCTGCTGATCTTCATCT 10920
Db 80760 CGCCCAAGCTTACTGCGCGGCTCATGCGATTTGGTCTGCTGCTGATCTTCATCT 80819
QY 10921 GGAATGAACAGTGGTGGCGACCCCTGATGTTTCACTGCTCCGCGGTTAAACCAACCT 10980
Db 80820 GGAATGAACAGTGGTGGCGACCCCTGATGTTTCACTGCTCCGCGGTTAAACCAACCT 80879
QY 10981 CTGTACCGATACAGACGAGGTTTCGACACAGTAAACGAGTCTATGGCGGCAAT 11040
Db 80880 CTGTACCGATACAGACGAGGTTTCGACACAGTAAACGAGTCTATGGCGGCAAT 80939
QY 11041 CGACGGGATTTGGCGACTGGACCGACAGACAGGCGGATCTGTGATATCTCTAGG 11100
Db 80940 CGACGGGATTTGGCGACTGGACCGACAGACAGGCGGATCTGTGATATCTCTAGG 80999
QY 11101 GTTCGTCTCAGGTTTCGCGGACCTTGAAGAGCTTAAGATATCCACATATCAAAA 11160
Db 81000 GTTCGTCTCAGGTTTCGCGGACCTTGAAGAGCTTAAGATATCCACATATCAAAA 81059
QY 11161 CCGTGAAGGAGTCTGATGCGAGTCTTATCTGCTCTCATGTTAGTAAAGCACT 11220
Db 81060 CCGTGAAGGAGTCTGATGCGAGTCTTATCTGCTCTCATGTTAGTAAAGCACT 81119
QY 11221 TCATTTCCCGGTTCTCCAGGTTCTTACGCAAAATGCGATGCCGTAAGGTAATCA 11280
Db 81120 TCATTTCCCGGTTCTCCAGGTTCTTACGCAAAATGCGATGCCGTAAGGTAATCA 81179
QY 11281 CACCTTCTCAGACTTTTGTGATTAACCTTATGATCTTCTGCGCAACTGACATCA 11340
Db 81180 CACCTTCTCAGACTTTTGTGATTAACCTTATGATCTTCTGCGCAACTGACATCA 81239
QY 11341 CGACCCCGGAGGTAAGAAACAAAGTCTCTCATTTGGAACAAACAGCGTGGCGA 11400
Db 81240 CGACCCCGGAGGTAAGAAACAAAGTCTCTCATTTGGAACAAACAGCGTGGCGA 81299
QY 11401 CGAGGACGAGATGCTGACATGCGACACCGATTCACATGAACACGTTGAGGCGAA 11460
Db 81300 CGAGGACGAGATGCTGACATGCGACACCGATTCACATGAACACGTTGAGGCGAA 81359
QY 11461 CGGTCTCTCAAAATTAAGAAAGTTAATGATGCGCCCTGCGACGCAATCTCGCA 11520
Db 81360 CGGTCTCTCAAAATTAAGAAAGTTAATGATGCGCCCTGCGACGCAATCTCGCA 81419

QY	11521	CAGCCTGTTTGTTCATCCGACTCGAGCCATACCGTTGGGTAAAAACCCGCTTC	11580
Db	81420	CACCTGTGTTTGTTCATCCGACTCGAGCCATACCGTTGGGTAAAAACCCGCTTC	81479
QY	11581	TTTCAGTCCAGACCACCCCGCTGTCTATTGGAACTCAGTGTATTAACCAAGCACT	11640
Db	81480	TTTCAGTCCAGACCACCCCGCTGTGTCTATTGGAACTCAGTGTATTAACCAAGCACT	81539
QY	11641	GAGTTGCGTGGAGACATCAGATTACACATTGCACAACTTACCACCGGTTCCGGCACA	11700
Db	81540	GAGTTGCGTGGAGACATCAGATTACACAACTTACCACCGGTTCCGGCACA	81599
QY	11701	GGCGAAACGTCTATATCGACACCCGGTGGCCCATAGCCCTATTATTAATTAAGCT	11760
Db	81600	GGCGAAACGTCTATATCGACACCCGGTGGCCCATATTAAATTAATTAAGCT	81659
QY	11761	CTCGTATACCTTTTGGGTGTCATGTCTGATCAAGAAATCATTTTCTCTGAATGTGCAT	11820
Db	81660	CTCGTATACCTTTTGGGTGTCATGTCTGATCAAGAAATCATTTTCTCTGAATGTGCAT	81719
QY	11821	AGTGGAGCGGTTTTTGGCCCTGACATATGCTCGCATGTGTGCACTAGTCAAAAAACT	11880
Db	81720	AGTGGAGCGGTTTTTGGCCCTGACATATGCTCGCATGTGTGCACTAGTCAAAAAACT	81779
QY	11881	TCTGTGCTATTCATACGAGCAGATCTGCAGTTACTTTGTTCCACGGGACCCGGACAAG	11940
Db	81780	TCTGTGCTATTCATACGAGCAGATCTGCAGTTACTTTGTTCCACGGGACCCGGACAAG	81839
QY	11941	TCTTGTGCTCTATTCGCCAAACCAATCGGGGTACTGGCCGATTTGCACGGCGCAACGA	12000
Db	81840	TCTTGTGCTCTATTCGCCAAACCAATCGGGGTACTGGCCGATTTGCACGGCGCAACGA	81899
QY	12001	GCCAGGCGCTGATATCGACTCCACGGCCGCGCATTCGCGTATTGGAGGCTTGACGATC	12060
Db	81900	GCCAGGCGCTGATATCGACTCCACGGCCGCGCATTCGCGGATTTGGAGGCTTGACGATC	81959
QY	12061	AGCTCTCAAGCAAAATGAACCCCTTGCTGCTACGGCACAGTTATTAATGTATCTAAAT	12120
Db	81960	AGCTCTCAAGCAAAATGAACCCCTTGCTGCTACGGCACAGTTATTAATGTATCTAAAT	82019
QY	12121	GACGAGTCATGTGCTCCCTAAACATATGAGTAAAGTACTCAAACTGTGTAGGGGAAGA	12180
Db	82020	GACGAGTCATGTGCTCCCTAAACATATGAGTAAAGTACTCAAACTGTGTGTAGGGGAAGA	82079
QY	12181	GTGACAAACACCTGGCACTCAATAAATTTTGAAGTGGGGATTGACCCTGTCCCTC	12240
Db	82080	GTGACAAACACCTGGCACTCAATAAATTTTGAAGTGGGGATTGACCCTGTCCCTC	82139
QY	12241	TGTTAGTATTAACCCCATGTCCGCACATATTCAGAGAAACAAACACTCCAGATTCAAAAC	12300
Db	82140	TGTTAGTATTAACCCCATGTCCGCACATATTCAGAGAAACAAACACTCCAGATTCAAAAC	82199
QY	12301	ACTTATATACAGATAGAAAGGCGTCCAGCGGCTCACAAAAACGGTCCGGGCACAGGTAA	12360
Db	82200	ACTTATATACAGATAGAAAGGCGTCCAGCGGCTCACAAAAACGGTCCGGGCACAGGTAA	82259
QY	12361	CATTAAACATTAGCGGGGACAAACGCCCGCACAGACACTGTGCCACAGCTGATTAAT	12420
Db	82260	CATTAAACATTAGCGGGGACAAACGCCCGCACAGACACTGTGCCACAGCTGATTAAT	82319
QY	12421	AGCGGTACAGTCTTTCGACTCCGCGCTCGGGGTAGTACAGCCGCCAAAATATANGTAA	12480
Db	82320	AGCGGTACAGTCTTTCGACTCCGCGCTCGGGGTAGTACAGCCGCCAAAATATANGTAA	82379
QY	12481	ACACAAGCTTGTGAAGGCGGCTCGTCCGAGATGTTCTGGCCATGGGCTGTATATAG	12540
Db	82380	ACACAAGCTTGTGAAGGCGGCTCGTCCGAGATGTTCTGGGCAATGGGCTGTATATAG	82439
QY	12541	TCAACCAAGTTAAATGACGACGAGCGTTGGCGACAGACAGACCGAACCGCCCGCTA	12600
Db	82440	TCAACCAAGTTAAATGACGACGAGCGTTGGCGACAGACAGACCGAACCGCCCGCTA	82499
QY	12601	GATTCACAGTCTCCCTTGAACGAAAGCAGAGAAATGCCAACATCTATATGTAATGGCG	12660
Db	82500	GATTCACAGTCTCCCTTGAACGAAAGCAGAGAAATGCCAACATCTATATGTAATGGCG	82559
QY	12661	GAGGGGTGGGCCCAAAAGCCCAACCGCGCAAAAGCTTTTATCCAGGAAGGCGAACGCC	12720
Db	82560	GAGGGGTGGGCCCAAAAGCCCAACCGCGCAAAAGCTTTTATCCAGGAAGGCGAACGCC	82619
QY	12721	TGGGCTGAAACTCTGCTTAAGTGGCTGGAATCTCCGGAACCAAGTGCCTGTCCGCGATC	12780
Db	82620	TGGGCTGAAACTCTGCTTAAGTGGCTGGAATCTCCGGAACCAAGTGCCTGTCCGCGATC	82679
QY	12781	GTTGGCGGCGATATGTGCCCTTGAGGGGACAGTTGGACATGGGAGCACAGATGGCG	12840
Db	82680	GTTGGCGGCGATATGTGCCCTTGAGGGGACAGTTGGACAAAGGGGAGCACAGATGGCG	82739
QY	12841	TTGAGAGATTACAGTACCACTTACCAACTGTGTCCTCCCTTAATATAGAAAACTTATAGCT	12900
Db	82740	TTGAGAGATTACAGTACCACTTACCAACTGTGTCCTCCCTTAATATAGAAAACTTATAGCT	82799
QY	12901	AGCATCAACACTGTTCACCCCGGCTCCACCGCACAGTGTACCGAAACACCGGCGCA	12960
Db	82800	AGCATCAACACTGTTCACCCCGGCTCCACCGCACAGTGTACCGAAACACCGGCGCA	82859
QY	12961	ACCGGACAACTTATTCAGCGGCTCTGCGGCAACCCCGTAAACATACATCACTATGCGG	13020
Db	82860	ACCGGACAACTTATTCAGCGGCTCTGCGGCAACCCCGTAAACATACATCACTATGCGG	82919
QY	13021	GAGCGCTGATCGCAAGACACAGCACTCAGCGTAAATGGTAAAAAGGGAATGATTCGG	13080
Db	82920	GAGCGCTGATCGCAAGACACAGCACTCAGCGTAAATGGTAAAAAGGGAATGATTCGG	82979
QY	13081	CATCTGTCCGATATGAGTATCGAAAGTGTCTCTTATGATGACAGCTCCGACAGGTTTGA	13140
Db	82980	CATCTGTCCGATATGAGTATCGAAAGTGTCTCTTATGATGACAGCTCCGACAGGTTTGA	83039
QY	13141	CTATGGCGTATGGCGGTGATAGCCATTTTGTGCAATCCTTAGCGGTTAATTCCTGGCA	13200
Db	83040	CTATGGCGTATGGCGGTGATAGCCATTTTGTGCAATCCTTAGCGGTTAATTCCTGGCA	83099
QY	13201	GCGCGCTGCAAGATGCGCCCTGTGATCCACAGTAAATGATTTTTCGCGCTTC	13260
Db	83100	GCGCGCTGCAAGATGCGCCCTGTGATCCACAGTAAATGATTTTTCGCGCTTC	83159
QY	13261	TGCACTCTCTGTCTCCTCTGTCTGATTCACAGGTAATGCGGATTAATTAATCTTCTCG	13320
Db	83160	TGCACTCTCTGTCTCCTCTGTCTGATTCACAGGTAATGCGGATTAATTAATCTTCTCG	83219
QY	13321	TCAACCCACCGATTTCCGGGATGACAGCTGTCTGCAACATTTCCACCGCATCTCGA	13380
Db	83220	TCAACCCACCGATTTCCGGGATGACAGCTGTCTGCAACATTTCCACCGCATCTCGA	83279
QY	13381	AGGCTGGATGTGTGCTCACTGCGAGACGGGCGCTCCATATCTCGCGCGCTCACGGCA	13440
Db	83280	AGGCTGGATGTGTGCTCACTGCGAGACGGGCGCTCCATATCTCGCGCGCTCACGGCA	83339
QY	13441	TGCGAAACCTTGTCCAGTTACCTCTCTGAACAAACACTTCGACCCCTCACAGACTACGGC	13500
Db	83340	TGCGAAACCTTGTCTCAAGTTACTCTCTGAACAAACACTTCGACCCCTCACAGACTACGGC	83399
QY	13501	TGGCAAAAGGGAACTGTGGGTAGTCTGCTGGGACAGTAACTTATAGCGTTATTTATCT	13560
Db	83400	TGGCAAAAGGGAACTGTGGGTAGTCTGCTGGGACAGTAACTTATAGCGTTATTTATCT	83459
QY	13561	GTCTGTACACTCTTCGCGCGGAAGTTGTGTTTATGAGCACACCGGGAAGATTCATGT	13620
Db	83460	GTCTGTACACTCTTCGCGCGGAAGTTGTGTTTATGAGCACACCGGGAAGATTCATGT	83519
QY	13621	GTCTCTGACACACTGTCTCTGACAGACACACAGAAATATAGAACTTGTGGGCTCTCTT	13680
Db	83520	GTCTCTGACACACTGTCTCTGACAGACACACAGAAATATAGAACTTGTGGGCTCTCTT	83579
QY	13681	GGGCAACAGCTGTCTGAGAGTACAGTGTTCGCCCGTTTGGACGGGCGATGGCTCTCG	13740

Db	83580	GGGCGACCAAGGCTGCTGTGAGAAATACAGTTTCCCGGTTGCACGGCGCATGGCTCTCG	836359
Qy	13741	GTCCCGGAGAGCGGGCAGCTTTCTCATGAACCCATGAAGTTAAAAATTTCTGTTAG	138000
Db	83640	GTCCCGGAGAGCGGGCAGCTTTCTCATGAACCCATGAAGTTAAAAATTTCTGTTAG	836959
Qy	13801	AGAGGAACATGACCTCTCGTTGGATTAATATACATTACAGTCGTACCGCGCGGTAA	138660
Db	83700	AGAGGAACATGACCTCTCGTTGGATTAATATACATTACAGTCGTACCGCGCGGTAA	837959
Qy	13861	GCCTTTCCCTGTTCTTATATATACAGTACACTCCGGTTTCGTTGCCGTGTAGTAGATC	139200
Db	83760	GCCTTTCCCTGTTCTTATATATACAGTACACTCCGGTTTCGTTGCCGTGTAGTAGATC	838119
Qy	13921	CTCTGTTATACGGCAGCAGCATCGTTTTATTTGCGTTATCTGTTCTCGCGTACGTTTT	139800
Db	83820	CTCTGTTATACGGCAGCAGCATCGTTTTATTTGCGTTATCTGTTCTCGCGTACGTTTT	838790
Qy	13981	CACGATGTGGAGATGAGAAACCAACACAGTGAACCCGGTGCATAGAAACACATGACCG	140400
Db	83880	CACGATGTGGAGATGAGAAACCAACACAGTGAACCCGGTGCATAGAAACACATGACCG	839399
Qy	14041	GATGGGGAACCGGGCGCGAGTGCAGAAACACCTCTCGCATTTGGAGCTGTGATCA	141000
Db	83940	GATGGGGAACCGGGCGCGAGTGCAGAAACACCTCTCGCATTTGGAGCTGTGATCA	839999
Qy	14101	GTGCGCAGACGCCAAAATTAACACCTGAATTCTACACGCCCAAAACGGCACAATTTGAT	141600
Db	84000	GTGCGCAGACGCCAAAATTAACACCTGAATTCTACACGCCCAAAACGGCACAATTTGAT	840599
Qy	14161	GAGGCACCGCGCGCTTCGGGAGCCCGCAGAGATGCTCTGGGCGTACGCTGATCTCTCG	142200
Db	84060	GAGGCACCGCGCGCTTCGGGAGCCCGCAGAGATGCTCTGGGCGTACGCTGATCTCTCG	841119
Qy	14221	GAGGGAACAACGTTGGCAGAGGGGGCGGAGCGGCAATTCGCGCTTAAACCCGATGCCAC	142800
Db	84120	GAGGGAACAACGTTGGCAGAGGGGGCGGAGCGGCAATTCGCGCTTAAACCCGATGCCAC	841799
Qy	14281	ACACCTGCTCCAAATTAATTAATATCCCTTCAGAGTTCTCATCAGAGATACACGATAC	143400
Db	84180	ACACCTGCTCCAAATTAATTAATATCCCTTCAGAGTTCTCATCAGAGATACACGATAC	842399
Qy	14341	ATCCAGAAATCATCAAAAGTTTACCGCGGAAGCGGTCCAGCGCGCACCGTGGTCCGA	144000
Db	84240	ATCCAGAAATCATCAAAAGTTTACCGCGGAAGCGGTCCAGCGCGCACCGTGGTCCGA	842999
Qy	14401	CGAACCCCATCTCCACTTCTTGAATATCAGCATTTCTCCCTCAAAACCCCTCAAAAATCGTC	144600
Db	84300	CGAACCCCATCTCCACTTCTTGAATATCAGCATTTCTCCCTCAAAACCCCTCAAAAATCGTC	843599
Qy	14461	TCCTTACACTCTAGCAGGTTTCCATCTAGCCCAACCTGACAGACCTCTCTCACGCAGTAG	145200
Db	84360	TCCTTACACTCTAGCAGGTTTCCATCTAGCCCAACCTGACAGACCTCTCTCACGCAGTAG	844119
Qy	14521	CGACACAGCGTGGAGTTTCCAGCTGCCCTTCTTCCAAACAGCTTAAAGCTTTTTC	145800
Db	84420	CGACACAGCGTGGAGTTTCCAGCTGCCCTTCTTCCAAACAGCTTAAAGCTTTTTC	844799
Qy	14581	CTCATGCGACCAAGTTAGGTCGAATAGGTTTCTCGTGAAGTGAAGGTCCACGA	146400
Db	84480	CTCATGCGACCAAGTTAGGTCGAATAGGTTTCTCGTGAAGTGAAGGTCCACGA	845399
Qy	14641	TCGAGATAGGCTGTAGTTAGAAATCTCGATTCGGCATGACAGGGTACACCTATACAAATAG	147000
Db	84540	TCGAGATAGGCTGTAGTTAGAAATCTCGATTCGGCATGACAGGGTACACCTATACAAATAG	845999
Qy	14701	GGCGGATACGATGTACTTTTCCCTCGATGATATTTGCAAGGGCTCATCTCCTCAAAACG	147600
Db	84600	GGCGGATACGATGTACTTTTCCCTCGATGATATTTGCAAGGGCTCATCTCCTCAAAACG	846599
Qy	14761	TGCACCTGGCTAAGCAAGCAGCTCTATTTCTGCACTTCTCATTTATTAACCATATTG	148200

Db	84660	GGCACCTGGCTAAGCAAGAGAGCTCTATTTCCTGCACTTCCTCATTTATTAACCAATATG	84713
QY	14821	TTTCTGGTCTACAGCTTTTGACGCTACCTGCAACGACACGGTGAATGATCCCGAGTTTG	14880
Db	84740	TTTTCGGTCTACAGCTTTTGACGCTACCTGCAACGACACGGTGAATGATCCCGAGTTTG	84779
QY	14881	CTCCGCAAGTGCCCTTGACAAACACTGAGGCCACAGATTAAATAATGTAAGCAAAAGGCATAGC	14940
Db	84780	CTCCGCAAGTGCCCTTGACAAACACTGAGGCCACAGATTAAATAATGTAAGCAAAAGGCATAGC	84839
QY	14941	TTTCGATTTCAAGTCACCGGACAGTGAGTGGTGACATTTAGAAAGTTGTTGGCCACACATT	15000
Db	84840	TTTCGATTTCAAGTCACCGGACAGTGAGTGGTGACATTTAGAAAGTTGTTGGCCACACATT	84899
QY	15001	CAGCTGTGACTCAAGCCCGACCAATATGACAGCTGACCATTTCCCTATCACACACTAG	15060
Db	84900	CAGCTGTGACTCAAGCCCGACCAATATGACAGCTGACCATTTCCCTATCACACACTAG	84959
QY	15061	TACAGAAAAAGAAACCAACACAGGAGGAGCATTTTCAGGTATGAGAAATTTATTAG	15120
Db	84960	TACAGAAAAAGAAACCAACACAGGAGGAGCATTTTCAGGTATGAGAAATTTATTAG	85019
QY	15121	CCGGGGAATTCATCTTAACAAAACAGCAAAATGTTTATTCAAAATGCTATAGATTTCTGTT	15180
Db	85020	CCGGGGAATTCATCTTAACAAAACAGCAAAATGTTTATTCAAAATGCTATAGATTTCTGTT	85079
QY	15181	TGATTAACAATATATGATATGATGAGAGCCCTCGAAGATTTGCTCTCGCCCAAGGACAA	15240
Db	85080	TGATTAACAATATATGATATGATGAGAGCCCTCGAAGATTTGCTCTCGCCCAAGGACAA	85139
QY	15241	CCCGAAACCCAGAGTTTAACAAAGGCGCGGGGGAGACCGTGTGCGCGCGGAGGAGGAGC	15300
Db	85140	CCCGAAACCCAGAGTTTAACAAAGGCGCGGGGGAGACCGTGTGCGCGCGGAGGAGGAGC	85199
QY	15301	CTGGCCATATCAAGCAAAATAACGATCAGTGTCAAAATGCCCACACAGCTGATCCCGGTAG	15360
Db	85200	CTGGCCATATCAAGCAAAATAACGATCAGTGTCAAAATGCCCACACAGCTGATCCCGGTAG	85259
QY	15361	GCACGATGTGGCAAACTGACGGTTCACAGGATTTCCCTGAAACCAACAGTTAGAGCC	15420
Db	85260	GCACGATGTGGCAAACTGACGGTTCACAGGATTTCCCTGAAACCAACAGTTAGAGCC	85319
QY	15421	CCGGTAATCGGAACATTAATTCCTCGTGGGTGCTGAGAAATTAATTCATCCACAGAC	15480
Db	85320	CCGGTAATCGGAACATTAATTCCTCGTGGGTGCTGAGAAATTAATTCATCCACAGAC	85379
QY	15481	CATTTCAAAAGCGTCTCGAGTCTGCAACACAGACGACTAGTGTGTGTATCGGA	15540
Db	85380	CATTTCAAAAGCGTCTCGAGTCTGCAACACAGACGACTAGTGTGTGTATCGGA	85439
QY	15541	GGAACCAACGCTGAGAGGGTTCATCAAAACACACAGTGTGTCCGCTTATTTGTT	15600
Db	85440	GGAACCAACGCTGAGAGGGTTCATCAAAACACACAGTGTGTGTCCGCTTATTTGTT	85499
QY	15601	GGTTTGAAGATAGCTGATTCCTCGCCCGGGGTGTCACAGTCAAGCTCAAGCTCAATTGC	15660
Db	85500	GGTTTGAAGATAGCTGATTCCTCGCCCGGGGTGTCACAGTCAAGCTCAAGCTCAATTGC	85559
QY	15661	CCATAGTAATAATCTTATATATGATGATGACCCCATGATGACCGCGAGATGGCCACAGA	15720
Db	85560	CCATAGTAATAATCTTATATATGATGATGACCCCATGATGACCGCGAGATGGCCACAGA	85619
QY	15721	CACGCCATTAATCTGAGCGCAGAGAGGCCCGAAGATACGCTGATCTGCTGCGCG	15780
Db	85620	CACGCCATTAATCTGAGCGCAGAGAGGCCCGAAGATACGCTGATCTGCTGCGCG	85679
QY	15781	TCGTGTCCATCTTGATGACTTCCCGATACCGTCTCTTGATCACTTAACGAGCGGTCC	15840
Db	85680	TCGTGTCCATCTTGATGACTTCCCGATACCGTCTCTTGATCACTTAACGAGCGGTCC	85739
QY	15841	GAAAGGGGCTAAGCATTCGCGCGCCGAGCATGGAACCGCATTTTCCGCAACCTCAAG	15900
Db	85740	GAAAGGGGCTAAGCATTCGCGCGCCGAGCATGGAACCGCATTTTCCGCAACCTCAAG	85799

OY	15901	CGGAGCGCGACACACGGCGGACACACCGGACAAGACATCTTTCCGATGAGACGCAACCTA	15960
Db	85800	CGGAGCGCGACACACGGCGGACACACCGGACAAGACATCTTTCCGATGAGACGCAACCTA	85859
OY	15961	AAGACACGCGCGGTGAACGGAAATTGATGGGTAGGGAATTCCGTATCTTCCCAAGATC	16020
Db	85860	AAGACACGCGCGGTGAACGGAAATTGATGGGTAGGGAATTCCGTATCTTCCCAAGATC	85919
OY	16021	TTGCTCTTTCTTACGGCTCCAGACAGCGCCCTCGGCTTGACACAGCCGTGCTCTTCCA	16080
Db	85920	TTGCTCTTTCTTACGGCTCCAGACAGCGCCCTCGGCTTGACACAGCCGTGCTCTTCCA	85979
OY	16081	GAGCGCAGTGGGATGTGTCTTAACCTACAGATGAGCATTCATATGTTGACACCGTGGGTGA	16140
Db	85980	GAGCGCAGTGGGATGTGTCTTAACCTACAGATGAGCATTCATATGTTGACACCGTGGGTGA	86039
OY	16141	TAATCATAAATTGGGAAACGACGGTGGTGTAGCTGCCACACACGAGCTCGCTCTTGTCTCG	16200
Db	86040	TAATCATAAATTGGGAAACGACGGTGGTGTAGCTGCCACACACGAGCTCGCTCTTGTCTCG	86099
OY	16201	TTCTGCCAAAACAGCGCCGGGTACAGACACACTATGGCTTTTGAGCTCAGCCATTCTTG	16260
Db	86100	TTCTGCCAAAACAGCGCCGGGTACAGACACACTATGGCTTTTGAGCTCAGCCATTCTTG	86159
OY	16261	AGGGCCATGTGCATACAGATGGGCCCCCTTGATTTCCCAAGCGGCCATGATTAAGTCG	16320
Db	86160	AGGGCCATGTGCATACAGATGGGCCCCCTTGATTTCCCAAGCGGCCATGATTAAGTCG	86219
OY	16321	GCAACGTTTAAAAACCCATGTAAAGTTTCACTTAATTTAAAAATGACACAACTCCGCCAT	16380
Db	86220	GCAACGTTTAAAAACCCATGTAAAGTTTCACTTAATTTAAAAATGACACAACTCCGCCAT	86279
OY	16381	GCCTGTGCAAAACATTAAGAAAGTGGACACACGTGGCTTGGCCGTCTCTGCAATGAA	16440
Db	86280	GCCTGTGCAAAACATTAAGAAAGTGGACACACGTGGCTTGGCCGTCTCTGCAATGAA	86339
OY	16441	CCCCGCGCGTAAACATTACTTCTCTCCCATACGGTGGAGGTAGATATCAGATGTGCTTCC	16500
Db	86340	CCCCGCGCGTAAACATTACTTCTCTCCCATACGGTGGAGGTAGATATCAGATGTGCTTCC	86399
OY	16501	CGTTGTTCGGGAGACACACACCCGCTCCAGACGGTCCCTCTGTCCCGCTCTCATCTCC	16560
Db	86400	CGTTGTTCGGGAGACACACACCCGCTCCAGACGGTCCCTCTGTCCCGCTCTCATCTCC	86459
OY	16561	CGCGGCGACCGTTCTCTGACATCATCTACACATCATATGTCAGACAGTAGCGAAGTTTCAG	16620
Db	86460	CGCGGCGACCGTTCTCTGACATCATCTACACATCATATGTCAGACAGTAGCGAAGTTTCAG	86519
OY	16621	GGCAGTGGAGCATCCCATGTATTTTGGACTGATGAGACGGGACACATGAATAATCCACGC	16680
Db	86520	GGCAGTGGAGCATCCCATGTATTTTGGACTGATGAGACGGGACACATGAATAATCCACGC	86579
OY	16681	ACAAGTCAAGGGGGGGGACATCTCTCTGGAGTGGGCGATCTGGCAGAGTCCCTCAATATAG	16740
Db	86580	ACAAGTCAAGGGGGGGGACATCTCTCTGGAGTGGGCGATCTGGCAGAGTCCCTCAATATAG	86639
OY	16741	CAGAGATTCGAACGCTTGAGCGCGTGCGAAGGCCACAGCTCATAGTAATTTTCAGAAAT	16800
Db	86640	CAGAGATTCGAACGCTTGAGCGCGTGCGAAGGCCACAGCTCATAGTAATTTTCAGAAAT	86699
OY	16801	GTTGTGTCATATGCCGTCAATGTGGGTCTTCCAGGTTTTCACACAGATTCAGACTCCGT	16860
Db	86700	GTTGTGTCATATGCCGTCAATGTGGGTCTTCCAGGTTTTCACACAGATTCAGACTCCGT	86759
OY	16861	CATTAACACATATCAAACCTCTCTCGCATTTTCTGACAGGGCTGCAATCTGCCCTGAC	16920
Db	86760	CATTAACACATATCAAACCTCTCTCGCATTTTCTGACAGGGCTGCAATCTGCCCTGAC	86819
OY	16921	AAACTCGCAGGAATCACTGGGAGACGGCAAGAAACGTCATATGATTAATTCGGCAC	16980
Db	86820	AAACTCGCAGGAATCACTGGGAGACGGCAAGAAACGTCATATGATTAATTCGGCAC	86879

QY	1698	ACACAGGTGTCGGGACGTTTGGATCTCAGGAAGCCACATATATCGCACACCCGAGCGGC	1704
Db	8688	ACACAGGTGTCGGGACGTTTGGATCTCAGGAAGCCACATATATCGCACACCCGAGCGGC	86939
QY	1704	TCGCAAAATTTGAACTCCGACGTTCTCTCCAAAGTAAAAAAGATATACCTCAACACCGCC	17100
Db	8690	TCGCAAAATTTGAACTCCGACGTTCTCTCCAAAGTAAAAAAGATATACCTCAACACCGCC	86999
QY	1710	TAGCACAGGTTGCGCACAGAGTCTTGAGTCCGTTTGATTTCCGTTTATAAACGAGAC	17160
Db	8700	TAGCACAGGTTGCGCACAGAGTCTTGAGTCCGTTTGATTTCCGTTTATAAACGAGAC	87059
QY	1716	TCTCAGTGGCGCTTACCCCTCGGCGCGCTGTCTCTCGAAACATCTCTCTGACGCA	17220
Db	8706	TCTCAGTGGCGCTTACCCCTCGGCGCGCTGTCTCTCGAAACATCTCTCTGACGCA	87119
QY	1722	ACTGCCATGGAACAGTATGCAACGATGTGGTGGATGAGTTACACGATCGGAGCC	17280
Db	8712	ACTGCCATGGAACAGTATGCAACGATGTGGTGGATGAGTTACACGATCGGAGCC	87179
QY	1728	CACCGTAACCTCAGAGAGCAATTTGAAAAGTCTGTATCTTTCCCGACAGACGCCCGCCG	17340
Db	8718	CACCGTAACCTCAGAGAGCAATTTGAAAAGTCTGTATCTTTCCCGACAGACGCCCGCCG	87233
QY	1734	CTTGCCTGGCGGTGTACGTCCTCAATATCTGTGAGATCTCAGTCGATATATACATCT	17400
Db	8724	CTTGCCTGGCGGTGTACGTCCTCAATATCTGTGAGATCTCAGTCGATATATACATCT	87299
QY	1740	AATTTCTTAAATTTCTGGGCAATGTGAACCGGTTTGACACCGCCACGGCTGAGCAAAA	17466
Db	8730	AATTTCTTAAATTTCTGGGCAATGTGAACCGGTTTGACACCGCCACGGCTGAGCAAAA	87359
QY	1746	ATCTGCAAAATATCTTGTATTAATCTTATCGAGCGCATGTCGGTGCACCGGTTCCACG	17520
Db	8736	ATCTGCAAAATATCTTGTATTAATCTTATCGAGCGCATGTCGGTGCACCGGTTCCACG	87419
QY	1752	GACACGTAATATGTCCTGTCTCGTCATCCATTCCTACGCGGATATCGCTTAGACATC	17580
Db	8742	GACACGTAATATGTCCTGTCTCGTCATCCATTCCTACGCGGATATCGCTTAGACATC	87479
QY	1758	CAGCGCCGTCAATGACCAAGCTTTTAAATCATATGCGGTCGGCATCTCGGCTATTGCA	17640
Db	8748	CAGCGCCGTCAATGACCAAGCTTTTAAATCATATGCGGTCGGCATCTCGGCTATTGCA	87539
QY	1764	ATTACTCTGACCGAGCGGCTCAGTTAAATACGAGACCCCGCAACCCACGAGCTCCGTA	17700
Db	8754	ATTACTCTGACCGAGCGGCTCAGTTAAATACGAGACCCCGCAACCCACGAGCTCCGTA	87599
QY	1770	ACAAAAGAGTCTAGATCTGAAAAGAACCTTACTATATACGCCACGGGAAAACTCTGTA	17760
Db	8760	ACAAAAGAGTCTAGATCTGAAAAGAACCTTACTATATACGCCACGGGAAAACTCTGTA	87659
QY	1776	ACAAATGAAAAAATGTTCTCAGAAAAAGAGAGAAACCTGACGACACGCAATCTAG	17820
Db	8766	ACAAATGAAAAAATGTTCTCAGAAAAAGAGAGAAACCTGACGACACGCAATCTAG	87719
QY	1782	TCAACACGAAACCTAAAGGCGGTACGTGACCAATATCTTTCCGTCCTCCGAGGAGTGGG	17880
Db	8772	TCAACACGAAACCTAAAGGCGGTACGTGACCAATATCTTTCCGTCCTCCGAGGAGTGGG	87779
QY	1788	GTTTCTCACAATGCGGTGAGCAAAAGCAAGCTATATTAAGACAGTGTGAGAGGA	17940
Db	8778	GTTTCTCACAATGCGGTGAGCAAAAGCAAGCTATATTAAGACAGTGTGAGAGGA	87833
QY	1794	AAACTTTATTGACAGGACAGGCAAAAGCAAGCTGTGACAGGTATGTCACATG	18000
Db	8784	AAACTTTATTGACAGGACAGGCAAAAGCAAGCTGTGACAGGTATGTCACATG	87899
QY	1800	GGCGGCAATCCCGAGCGCGGCAAGACACTGTGTCGCAAAATTTGAAATGACAGGGGAT	18066
Db	8790	GGCGGCAATCCCGAGCGCGGCAAGACACTGTGTCGCAAAATTTGAAATGACAGGGGAT	87959
QY	1806	TGTGGGACAGGGCTCGGCTTCCGAGAGTGGGGAAGCCCTCTAGTGTGAGAGCAATAGCC	18120

18121 GGTGGAATTCGGTTCGCTGTCGCGGGGTGCTGACACCGCAGCTAGATATTTGGCGAG 18180
18020 GGGTGAATTCGGTTCGCTGTCGCGGGGTGCTGACACCGCAGCTAGATATTTGGCGAG 88079
18181 CGAAACACGCGCAGACACTCGCGCTGTTTAAATTAATCCACCGGCTCCAGCAGACTCC 18240
18080 CGAAACACGCGCAGACACTCGCGCTGTTTAAATTAATCCACCGGCTCCAGCAGACTCC 88139
18241 GTTACCAGAGAGAGGTGGAACGTAACCATATATCCGAATGTAATCCAGACCGCTC 18300
88140 GTTACCAGAGAGAGGTGGAACGTAACCATATATCCGAATGTAATCCAGACCGCTC 88199
18301 TGGTAAATCATCAACCCGCTATGATCTCTCTCCAGCAGCTATTTAGCATGCTCTCG 18360
88200 TGGTAAATCATCAACCCGCTATGATCTCTCTCCAGCAGCTATTTAGCATGCTCTCG 88259
18361 GTGAGGAAACATATCTGTGGGGTATGCGGCAACAGGGCTGTTCGGCCGAATGCGCCG 18420
88260 GTGAGGAAACATATCTGTGGGGTATGCGGCAACAGGGCTGTTCGGCCGAATGCGCCG 88319
18421 ACAAGGTGCTTGCAGTGGTGGCTTTGGCGCGGCAACAGGCGAAGCGCTTGGGCGA 18480
88320 ACAAGGTGCTTGCAGTGGTGGCTTTGGCGCGGCAACAGGCGAAGCGCTTGGGCGA 88379
18481 CCGGACCTCATGTTCCCAACCAACCGCCATAGTAAATAAACAACGCGGTAGATCA 18540
88380 CCGGACCTCATGTTCCCAACCAACCGCCATAGTAAATAAACAACGCGGTAGATCA 88439
18541 ACACGTCTCCGCTGCTGCCCTCCACAGGCGCTTGTACTCATCTCCGCGACCGAGATACG 18600
88440 ACACGTCTCCGCTGCTGCCCTCCACAGGCGCTTGTACTCATCTCCGCGACCGAGATACG 88499
18601 GATCTGGGGGTTTACCTGCTGGGTGACGTCAGAGACATGCGCGGTGGCATCCGCTTC 18660
88500 GATCTGGGGGTTTACCTGCTGGGTGACGTCAGAGACATGCGCGGTGGCATCCGCTTC 88559
18661 GTTACAGAGCGGGAAGATGTAACAAAGATCGGCAACAGGCGAATTAACGCGGCACTGTT 18720
88560 GTTACAGAGCGGGAAGATGTAACAAAGATCGGCAACAGGCGAATTAACGCGGCACTGTT 88619
18721 AGGCGCGCGCGCGAGAGTTCCTCCATGATGATATCTTGACAGGCTGACTGTCG 18780
88620 AGGCGCGCGCGCGAGAGTTCCTCCATGATGATATCTTGACAGGCTGACTGTCG 88679
18781 TATAGCGTGGCAACCACTTCTTACATTCCTCGAGCGTCAATCGTCTTAAACGCTG 18840
88680 TATAGCGTGGCAACCACTTCTTACATTCCTCGAGCGTCAATCGTCTTAAACGCTG 88739
18841 CCGTATGCTTAAATTAATGACATAGTCAGATACATGTTCTCTCATGCTCAGAGAGCG 18900
88740 CCGTATGCTTAAATTAATGACATAGTCAGATACATGTTCTCTCATGCTCAGAGAGCG 88799
18901 ACCCGCGCGCTTAAATGATTCAGAGTAAAGCAACAGAGTCTTTCTCATCCAGCA 18960
88800 ACCCGCGCGCTTAAATGATTCAGAGTAAAGCAACAGAGTCTTTCTCATCCAGCA 88859
18961 ATGATTCAGAGATGCTATCATTAATGCAACAATGAGCAACAGCATGCGCTCAGGCGA 19020
88860 ATGATTCAGAGATGCTATCATTAATGCAACAATGAGCAACAGCATGCGCTCAGGCGA 88919
19021 CGGCGGTTTACGCGGATGACCTTCGCTTCCTCCGCAATCTCTGAGGGTCCGCTCG 19080
88920 CGGCGGTTTACGCGGATGACCTTCGCTTCCTCCGCAATCTCTGAGGGTCCGCTCG 88979
19081 AATAACTGGCTTAAAAATTAATCCACCGCGCGCGCGCGCGCTTAAACGCTCTTTC 19140
88980 AATAACTGGCTTAAAAATTAATCCACCGCGCGCGCGCGCGCTTAAACGCTCTTTC 89039
19141 GGCACAGCGCTAGGGCTGGCAGGAGCGGACGACGACTATTTTCACTCTAGGCGCG 19200
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89040 GGCACAGCGCGTATGGGCTGGCAGGAGCGGACCCACGACACTATTTTCACTCTAGGCGCG 89099
19201 CCTACTAGCGGAATTCGGGCTCTACAAAATCCACCGAGCCGCGCAATGTACCATGAG 19260
89100 CCTACTAGCGGAATTCGGGCTCTACAAAATCCACCGAGCCGCGCAATGTACCATGAG 89159
19261 TCAATTCATCTGACAGATCACCAGGATGACAGGAGCTGGGGTCTTTTACTGAGACCG 19320
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89280 ACCGGCGAGTCTGCGCAGTACAGCCATACATAGAAATTTGAGATTTGACAGAGATC 89339
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89340 GCACAGCCGCTGTGGTGGTCCCTCTGCGCTGCTTCCCTGCGCAGGCAACCGTGTGC 89399
19501 TGGTCTGTTATCCACATACATCCCGAGCTCATTTGCGCAAAAAGAGCGCTCTCAC 19560
89400 TGGTCTGTTATCCACATACATCCCGAGCTCATTTGCGCAAAAAGAGCGCTCTCAC 89459
19561 ACCGTTTAAATCTCACACAGGTTCTCTGCTCGGCGTTTACGGGCGCATCCACT 19620
89460 ACCGTTTAAATCTCACACAGGTTCTCTGCTCGGCGTTTACGGGCGCATCCACT 89519
19621 GAGTTTGGAGCCCATCTATACGCTGCCATAGAAACATCTGTACCCGGTTTG 19680
89520 GAGTTTGGAGCCCATCTATACGCTGCCATAGAAACATCTGTACCCGGTTTG 89579
19681 GGTCTTGGGCTTATGCAATCGTACCCCTCTAGGCTCTGCGGAGCGTGTTCGCTACCA 19740
89580 GGTCTTGGGCTTATGCAATCGTACCCCTCTAGGCTCTGCGGAGCGTGTTCGCTACCA 89639
19741 GCGACCCAAATTAATAAATCTGTAATAGCGCCCAAAATGAGATGATCTGTGAT 19800
89640 GCGACCCAAATTAATAAATCTGTAATAGCGCCCAAAATGAGATGATCTGTGAT 89699
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19861 CAGCTCTCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 19920
89760 CAGCTCTCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 89819
19921 CCGCTCTAATTAATTAATGAGAGGCTCCGAATGACTATCTAAGATGACAGCATACCA 19980
89820 CCGCTCTAATTAATTAATGAGAGGCTCCGAATGACTATCTAAGATGACAGCATACCA 89879
19981 GCGGATCCAGCGGCGGCTCAAGTAAATAAATCTTCTCCGCAAAAACGCTTGTGTG 20040
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90000 GGCATCTCGACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 90059
20161 CCAAGGTGCAATGCACTACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20220
90060 CCAAGGTGCAATGCACTACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 90119
20221 CGTGCGACCAACAAGTGTGGGAAAGTGTGCTTCCAAATTTGAAATATCATC 20280
90120 CGTGCGACCAACAAGTGTGGGAAAGTGTGCTTCCAAATTTGAAATATCATC 90179
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OY	20281	TTCCAGGTATGTTGGTGGTATTTCATCTCGGTCTGTTGAACCTTGTCACGAAACT	20340
Db	90180	TTCCGACGATATTGTAGTGTATTTCATCTCGGTCTGTTGAACCTTGTCACGAAACT	90239
OY	20341	AACCTCAAAAGCCTCACCACTCCCCTAACCCTAGCTGAATTTTATGTCACCTTAAG	20400
Db	90240	AACCTCAAAAGCCTCACCACTCCCCTAACCCTAGCTGAATTTTATGTCACCTTAAG	90299
OY	20401	GTCGACGTGATACGATATGCCCCGTGAAAACTCGACTTCGCATTAATTTATCCCAA	20460
Db	90300	GTCGACGTGATACGATATGCCCCGTGAAAACTCGACTTCGCATTAATTTATCCCAA	90359
OY	20461	GCGTTTGGGGTCCGTCACCTAACTAAGTGAAGCTTACAGGTTTCATAGTCCCGGT	20520
Db	90360	GCGTTTGGGGTCCGTCACCTAACTAAGTGAAGCTTACAGGTTTCATAGTCCCGGT	90419
OY	20521	TTGCCCATCTCCCCCAGCAGAACGAAAGCTTCAATTTTAAAGGGCACCAAGCTC	20580
Db	90420	TTGCCCATCTCCCCCAGCAGAACGAAAGCTTCAATTTTAAAGGGCACCAAGCTC	90479
OY	20581	AACCTTATTTAAGAGAAAAAAACACCGCATCAGAAGTTTTCCGACGACACACCC	20640
Db	90480	AACCTTATTTAAGAGAAAAAAACACCGCATCAGAAGTTTTCCGACGACACACCC	90539
OY	20641	CAGACATAATTCCTGGCAGTTCCGGCAGCAGCTGATTTTTTCTGATTTATTTGTAATTC	20700
Db	90540	CAGACATAATTCCTGGCAGTTCCGGCAGCAGCTGATTTTTTCTGATTTATTTGTAATTC	90599
OY	20701	GCATCCAAATGGCCCCAAACTACTCAATTAATAAAAACCGTAAACACACACACTGCTGAA	20760
Db	90600	GCATCCAAATGGCCCCAAACTACTCAATTAATAAAAACCGTAAACACACACACTGCTGAA	90659
OY	20761	CAAAATATGCGTTCTTGCCGCCCAAGACGTGCGTAGCAGCAGCAGCAGCGCTGTAA	20820
Db	90660	CAAAATATGCGTTCTTGCCGCCCAAGACGTGCGTAGCAGCAGCAGCAGCGCTGTAA	90719
OY	20821	AACCTAACAAGGCTTAAACGTTTGACGGAACACAGAGTCGAGGCAACAAAAAGCCC	20880
Db	90720	AACCTAACAAGGCTTAAACGTTTGACGGAACACAGAGTCGAGGCAACAAAAAGCCC	90779
OY	20881	AACGTGGAAGCAAAAAAATAGTGTACAAGTCCGAGAGAGAGAGGCGTGTCAAGGCCAAC	20940
Db	90780	AACGTGGAAGCAAAAAAATAGTGTACAAGTCCGAGAGAGAGAGGCGTGTCAAGGCCAAC	90839
OY	20941	AGACAGCGTACCCGCGCGCCCTCCAATCAAAACAGTCAGAGATAAAGTCCCATCC	21000
Db	90840	AGACAGCGTACCCGCGCGCCCTCCAATCAAAACAGTCAGAGATAAAGTCCCATCC	90899
OY	21001	ACACACCTCAAGCGCTTGCTTTATAGAGTATGTGATGTACCGGCTTAGAGSTAGAGAAA	21060
Db	90900	ACACACCTCAAGCGCTTGCTTTATAGAGTATGTGATGTACCGGCTTAGAGSTAGAGAAA	90959
OY	21061	AATTGCATGAGCGTGCAGAGCGCGCTCATAAAGCGAGTGTGACCGAGCGCTGTGAG	21120
Db	90960	AATTGCATGAGCGTGCAGAGCGCGCTCATAAAGCGAGTGTGACCGAGCGCTGTGAG	91019
OY	21121	TGAACAAAGCCACCTTCTATTAAGGGCACAGGGGACGAAAAACACCGGGGCTAAAAA	21180
Db	91020	TGAACAAAGCCACCTTCTATTAAGGGCACAGGGGACGAAAAACACCGGGGCTAAAAA	91079
OY	21181	AAGGTCTTAAAGAACTAAAAAATATATACACCGAAGCGCTGTAAAAATCCAAAGTTCTGA	21240
Db	91080	AAGGTCTTAAAGAACTAAAAAATATATACACCGAAGCGCTGTAAAAATCCAAAGTTCTGA	91139
OY	21241	GTAATCTGTGGGCAATCGTGGGGCACAAAATATACACAGTCATTCGCGCAACAACAGAG	21300
Db	91140	GTAATCTGTGGGCAATCGTGGGGCACAAAATATACACAGTCATTCGCGCAACAACAGAG	91199
OY	21301	CAGCAGCAGACGAGCAGACCCCAACAAAAATGGAACGTGAACCCATGGAAGTCAACGCC	21360
Db	91200	CAGCAGCAGACGAGCAGACCCCAACAAAAATGGAACGTGAACCCATGGAAGTCAACGCC	91259

D	92340	CCCCGATGGCGATGGTCGTCCTACAAACTGGCGCTTCTCTCCGGCTCCGACTGCTCCC	92399	
Q	22501	CGTGTGTGATGAGACGGCAGCTTCATTTCCGCAATGTTAACTCCAAACATCTCAGGGGTGT	22560	
D	92400	CGTGGTGTGATGAGACGGCAGCTTCATTTCCGCAATGTTAACTCCAAACATCTCAGGGGTGT	92459	
Q	22561	GTGTGAAGCTGTTCCTCAGAGGAGGTGTTCGAAAGCTAAAGCTAACCTGTCCGTATGT	22620	
D	92460	GTGTGAAGCTGTTCCTCAGAGGAGGTGTTCGAAAGCTAAAGCTAACCTGTCCGTATGT	92519	
Q	22621	CAGAAATATACATCAGACGGCGCAGTATTTTAAAGCTGAGACCGAGAGACGGCGGT	22680	
D	92520	CAGAAATATACATCAGACGGCGCAGTATTTTAAAGCTGAGACCGAGAGACGGCGGT	92579	
Q	22681	CCCCCAGCGTGGAGAGACAGCTTAAGAGACGGGGGCCCTGGCCCTGGCCGCTGATCTGTATA	22740	
D	92580	CCCCCAGCGTGGAGAGACAGCTTAAGAGACGGGGGCCCTGGCCCTGGCCGCTGATCTGTATA	92639	
Q	22741	CGCCTTTCTTAACGATGCCCTTAATGTGTCGTAACCTGCTAATGCTGCCAGCGCAT	22800	
D	92640	CGCCTTTCTTAACGATGCCCTTAATGTGTCGTAACCTGCTAATGCTGCCAGCGCAT	92699	
Q	22801	CGACGTCACACCTGGGGCCGCTAATGAAGAGACAGGGCTAGGGTAAGGGGAATTAAAC	22860	
D	92700	CGACGTCACACCTGGGGCCGCTAATGAAGAGACAGGGCTAGGGTAAGGGGAATTAAAC	92759	
Q	22861	CCTAAAAAGAGAGAGAAATGGCAAAACAGACAGACAGCGCTTCATGTTCAACCTTT	22920	
D	92760	CCTAAAAAGAGAGAGAAATGGCAAAACAGACAGACAGCGCTTCATGTTCAACCTTT	92819	
Q	22921	TAAATGAGCTCTGGCCCGGGAAAAATGAGTAACATGGGACACATGGGGACTACAGATCAT	22980	
D	92820	TAAATGAGCTCTGGCCCGGGAAAAATGAGTAACATGGGACACATGGGGACTACAGATCAT	92879	
Q	22981	ATGAAGGATGTGACATATTTCAGAAATATACAGCTCAAAAAAGTTACACTCTGTGGCACT	23040	
D	92880	ATGAAGGATGTGACATATTTCAGAAATATACAGCTCAAAAAAGTTACACTCTGTGGCACT	92939	
Q	23041	CGTATACGACAAAGGACACGCGTTTGGGGGGGGGCGACGAAACAGGGGGGATGTTAT	23100	
D	92940	CGTATACGACAAAGGACACGCGTTTGGGGGGGGGCGACGAAACAGGGGGGATGTTAT	92999	
Q	23101	TGACTTTGAATCTGTCGGCCGCTGCGCCCTGCGCAAAAACTGCTGATGTCCTCCAGCTTCAC	23160	
D	93000	TGACTTTGAATCTGTCGGCCGCTGCGCCCTGCGCAAAAACTGCTGATGTCCTCCAGCTTCAC	93059	
Q	23161	CATGTTCAAGCTCTCGGCTCTTGGAAAGAAATAACAGAGTCTCTATCTCCACGGCTTCGCG	23220	
D	93060	CATGTTCAAGCTCTCGGCTCTTGGAAAGAAATAACAGAGTCTCTATCTCCACGGCTTCGCG	93119	
Q	23221	AAAGAGCCGCTGATGTATGACAGAGGAGGGATTCGTCGCGAGATCAGTGTGTTGA	23280	
D	93120	AAAGAGCCGCTGATGTATGACAGAGGAGGGATTCGTCGCGAGATCAGTGTGTTGA	93179	
Q	23281	CAGCAAGCTGGGGCCCTGCTGTGTGACAGCTGTCCTCGGAGATGTAGTCTTACCCAG	23340	
D	93180	CAGCAAGCTGGGGCCCTGCTGTGTGACAGCTGTCCTCGGAGATGTAGTCTTACCCAG	93239	
Q	23341	GCACACCCCGCAGATTCCTCCGAAAGGGAAGAAAGTCTATAGAGTAAATGAACCTAT	23400	
D	93240	GCACACCCCGCAGATTCCTCCGAAAGGGAAGAAAGTCTATAGAGTAAATGAACCTAT	93299	
Q	23401	AAAGTATATCCCTTCGATTAACAGAGACAGACCTTCTCGCCCGCGGTGGTGGCTT	23460	
D	93300	AAAGTATATCCCTTCGATTAACAGAGACAGACCTTCTCGCCCGCGGTGGTGGCTT	93359	
Q	23461	GGGCACTGGGGAATGACAGCACTCATCTTCTCGCCAGAGGTAGGCTCTGCACATATTT	23520	
D	93360	GGGCACTGGGGAATGACAGCACTCATCTTCTCGCCAGAGGTAGGCTCTGCACATATTT	93419	
Q	23521	TTTGCATTAATCATTAAGTCCCGCGATTAACGGCAAAAAATTAAGTTAGATGTGGC	23580	

D	93420	TTTGCATTAATCATTAAGTCCCGCGATTAACGGCAAAAAATTAAGTTAGATGTGGC	93479	
Q	23581	ATACACTTTCGGTGAGTGTTCCTCATGAGCTACTGTTGGCGTAATAGTGGTCACTG	23640	
D	93480	ATACACTTTCGGTGAGTGTTCCTCATGAGCTACTGTTGGCGTAATAGTGGTCACTG	93539	
Q	23641	GTGATTTGCACTCTTTAATAGTCTTCAGATGTTAAAGTTTACAGACTCTCGCCAT	23700	
D	93540	GTGATTTGCACTCTTTAATAGTCTTCAGATGTTAAAGTTTACAGACTCTCGCCAT	93599	
Q	23701	ACCCAAAAATGTGAAGAGAACTGTAATACTCCATGCTGGGACTCAATAGTCGAC	23760	
D	93600	ACCCAAAAATGTGAAGAGAACTGTAATACTCCATGCTGGGACTCAATAGTCGAC	93659	
Q	23761	CTCATCGAGTCTCTGTCGAGGAAATTTGACTGGGGAACATCTGTTCTGCCATGCTC	23820	
D	93660	CTCATCGAGTCTCTGTCGAGGAAATTTGACTGGGGAACATCTGTTCTGCCATGCTC	93719	
Q	23821	CTGGGTGAGTGTCTTAAACCAGGGTGTGCTCGGCTACAGAAACCGATCTGGGACTC	23880	
D	93720	CTGGGTGAGTGTCTTAAACCAGGGTGTGCTCGGCTACAGAAACCGATCTGGGACTC	93779	
Q	23881	CATGGGGGGGTTACTATGACAGGCAACATACCTTGTCCGCTCACCGTCCGCTTT	23940	
D	93780	CATGGGGGGGTTACTATGACAGGCAACATACCTTGTCCGCTCACCGTCCGCTTT	93839	
Q	23941	TGTACGAGTTAGACTCCGCCCTCTGTGAAGAGATGTTGTACCCACAGCATGATTAAG	24000	
D	93840	TGTACGAGTTAGACTCCGCCCTCTGTGAAGAGATGTTGTACCCACAGCATGATTAAG	93899	
Q	24001	CAGTCAGGGCAATTAAGTTTCTGCTTCTCAATTCGACATTAATACGATAGGTTT	24060	
D	93900	CAGTCAGGGCAATTAAGTTTCTGCTTCTCAATTCGACATTAATACGATAGGTTT	93959	
Q	24061	AACTAGCTGTATCCGGTCAAGAGCAAGTCTCAATTAAGTCCGCGCTGGCTGCTGC	24120	
D	93960	AACTAGCTGTATCCGGTCAAGAGCAAGTCTCAATTAAGTCCGCGCTGGCTGCTGC	94019	
Q	24121	TCCTCTTTAAAAAGAAATTAAGCAGCTGACTGTGCTCAAAATGAGACCCGCGACCG	24180	
D	94020	TCCTCTTTAAAAAGAAATTAAGCAGCTGACTGTGCTCAAAATGAGACCCGCGACCG	94079	
Q	24181	GGCGGCTCCACTGCTTAATGGGAGTAAATGAAGGCCGTCAAAAAATCTGTATGCTG	24240	
D	94080	GGCGGCTCCACTGCTTAATGGGAGTAAATGAAGGCCGTCAAAAAATCTGTATGCTG	94139	
Q	24241	TCCTTCAGGGGTTCTGGAATGAAGCAACGTCACCTCCGTAACGGCGCACCGTTGCAGG	24300	
D	94140	TCCTTCAGGGGTTCTGGAATGAAGCAACGTCACCTCCGTAACGGCGCACCGTTGCAGG	94199	
Q	24301	TCACAGGCTTCACTCTCTTAAAAAAAGTCACTGTTGGCTTCAAGATCTCTTCTGCTG	24360	
D	94200	TCACAGGCTTCACTCTCTTAAAAAAAGTCACTGTTGGCTTCAAGATCTCTTCTGCTG	94259	
Q	24361	GTGACCTTGATGATGATATGSCAAAGAAAGGATTAATGCTTGGGTGATCCCGTAAGC	24420	
D	94260	GTGACCTTGATGATGATATGSCAAAGAAAGGATTAATGCTTGGGTGATCCCGTAAGC	94319	
Q	24421	TGAGAGGTTCCGCGGCTTGGGATCAGCGCCAAAAAGTGGCTGTTAAAAATTCATGCTGG	24480	
D	94320	TGAGAGGTTCCGCGGCTTGGGATCAGCGCCAAAAAGTGGCTGTTAAAAATTCATGCTGG	94379	
Q	24481	GCAATGCTGCGCCCAAGCTGCTCCCATCTCTCAAGAGGAGGTGGAGCGCTTAACGCCG	24540	
D	94380	GCAATGCTGCGCCCAAGCTGCTCCCATCTCTCAAGAGGAGGTGGAGCGCTTAACGCCG	94439	
Q	24541	TCCACAGTTTGGCAGTGAACACACCTGAGCAATTCACCTCCCATCAGAGAAC	24600	
D	94440	TCCACAGTTTGGCAGTGAACACACCTGAGCAATTCACCTCCCATCAGAGAAC	94499	
Q	24601	GGAGTCCCTGCGCCAGTAAAAACAATCTCATGCTGTTTGGACCGCGTAAATATCAT	24660	
D	94500	GGAGTCCCTGCGCCAGTAAAAACAATCTCATGCTGTTTGGACCGCGTAAATATCAT	94559	

QY 24661 GCCTGAAAAATCTCCACGCTGAGCTTGCGCTCTCGGCGTCAAGTAGCCAAAGCCAGT 24720
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Db 94560 GCGTGAATAATCTCCAGCTCCAGCTTGCGGCTCTCGGCGTCAAGTAGCCAAAGCCAGT 94619
QY 24721 TCGGCAACACAGTCGGCCAGTCTTGAGCGCCAAATGCCATGTATCGTTCCTCGGCGG 24780
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Db 94620 TCGGCAACACAGTCGGCCAGTCTTGAGCGCCAAATGCCATGTATCGTTCCTCGGCGG 94679
QY 24781 CGGCTAAGGCTGCGGTAAGGGCGGCTCGCGCCAAATGACGAGATTGACATATACT 24840
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Db 94680 CGGCTAAGGCTGCGGTAAGGGCGGCTCGCGCCAAATGACGAGATTGACATATACT 94739
QY 24841 GCGGCTCCACGCGCATCATCGACGAGTTCAAACCAATGTATCATCCCCCTCCAGGC 24900
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Db 94740 GCGGCTCCACGCGCATCATCGACGAGTTCAAACCAATGTATCATCCCCCTCCAGGC 94799
QY 24901 TCCACACCAACTCTCCCTGTGGGCTGACGCACTTGGTAGCCTAATGTTGCCAG 24960
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Db 94800 TCCACACCAACTCTCCCTGTGGGCTGACGCACTTGGTAGCCTAATGTTGCCAG 94859
QY 24961 TTACACAGGAAGCTGACCTGGGCTTGGTGCAGAGATTGCGACAGAGATTAGAACAG 25020
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Db 94860 TTACACAGGAAGCTGACCTGGGCTTGGTGCAGAGATTGCGACAGAGATTAGAACAG 94919
QY 25021 TTTATGGCGCTGCCCTTGCGTCTCACACCAAGTGTGTTGTTGAGCGCCTCCTTAGCAG 25080
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Db 94920 TTTATGGCGCTGCCCTTGCGTCTCACACCAAGTGTGTTGTTGAGCGCCTCCTTAGCAG 94979
QY 25081 ACGTAGGAGTCCCGGCTTAAATGACAGTGTAAATAGGGCATATCATGATTTTAAAC 25140
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Db 94980 ACGTAGGAGTCCCGGCTTAAATGACAGTGTAAATAGGGCATATCATGATTTTAAAC 95039
QY 25141 GGCACGAGTAAAGTGTTCGACGGCGCACTAGTGTGTATTCATCTCAATTCG 25200
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Db 95040 GGCACGAGTAAAGTGTTCGACGGCGCACTAGTGTGTATTCATCTCAATTCG 95099
QY 25201 GCACCGTAGAGTTTTAGAGATTTGGCGCCACTCTGCGCAACAGGTGCACTGGCCA 25260
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Db 95100 GCACCGTAGAGTTTTAGAGATTTGGCGCCACTCTGCGCAACAGGTGCACTGGCCA 95159
QY 25261 TCTGGGTTTGTTCGTACAGTCGGAATAAAGCTCCGGCACACACGCGCTGAAACAG 25320
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QY 25321 TTTGACACGCGCTCTGATTCGCGCATCTTCGCGTTCAAAAATGCAAAATCGATGA 25380
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Db 95220 TTTGACACGCGCTCTGATTCGCGCATCTTCGCGTTCAAAAATGCAAAATCGATGA 95279
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QY 25441 CCAACGTGGCGCTTATTTAAACAGCTGATGTTCTGTGTCCGCAAAAGAC 25500
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Db 95340 CCAACGTGGCGCTTATTTAAACAGCTGATGTTCTGTGTCCGCAAAAGAC 95399
QY 25501 GAGACATCTATCCGACGCGCTGCTAGCGAAGGGGGGACATTTCTCATGAGT 25560
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Db 95400 GAGACATCTATCCGACGCGCTGCTAGCGAAGGGGGGACATTTCTCATGAGT 95459
QY 25561 GCTTTGAGGCTTTGTCTTCGGTGGCATGAGCGGCTTAAATAAACACGTAAGAAC 25620
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Db 95460 GCTTTGAGGCTTTGTCTTCGGTGGCATGAGCGGCTTAAATAAACACGTAAGAAC 95519
QY 25621 TGACCTCGGAGAGCCGGCTGACCTTAATACAGCGTTGCGACAGCACACATCTGTAC 25680
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Db 95520 TGACCTCGGAGAGCCGGCTGACCTTAATACAGCGTTGCGACAGCACACATCTGTAC 95579
QY 25681 GAGATGTAATGGAAGCGGTACCAACAGGTACATCTCATCAGTCGCTTCGCTCC 25740
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Db 95580 GAGATGTAATGGAAGCGGTACCAACAGGTACATCTCATCAGTCGCTTCGCTCC 95639

QY 25741 ACCAGTGTCTGAGGCTCTCCCGAAACACGGAATTTTATACACTGACAGCCACAAA 25800
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Db 95640 ACCAGTGTCTGAGGCTCTCCCGAAACACGGAATTTTATACACTGACAGCCACAAA 95699
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Db 95820 GTGTATGCTTCTCTGCTTAAAGTCTGTAAAGACCGTCAGAGCGCTTCGTGTTT 95879
QY 25981 GACATTAACGGCGCAACCTCGTCCGTTAGCCTTTCCCGAATACCAGCATAGTCTCC 26040
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Db 95880 GACATTAACGGCGCAACCTCGTCCGTTAGCCTTTCCCGAATACCAGCATAGTCTCC 95939
QY 26041 ACCGTAAACAGGCACTGCTCCATTAATCTGTGCGCAAGAGACCGGTTAGTAGTTG 26100
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Db 96180 AAGACCCCGGATTTGAAACCAACTCCGTAATTTTAAACCGGTAAAGCAGCCCTTTAA 96239
QY 26341 AGTGAAGCTTTGAAAGATGTTGTAAACCGGAAGGACGCTTCCAGTCTGCAAACTA 26400
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QY 26401 CGCGAAGCAGGCTTATTTATACAGTATCTGAGCTGAATGATTTGGTGGCAA 26460
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QY 26461 TCACGCGCTGTAAATAATCCCTCAATTTGGGACGTAATTCACAAATATCCTTACGACT 26520
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QY 26581 AAATAGACGAGTGGGCGGGGCAAGGCTGTGCGCAGGCTGGACGCGGATGATGATCTA 26640
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Db 96600 CGACTACGTTGCCCTTTAAGCAGACGTCACCTTGTGTACAAACGTAATGTGTGACCGTTT 96659
QY 26761 GAACCAAGGGCCGACCGGCGCAAGAACTGATGAAGGAGCGCGGTTCCAAACATTTCTT 26820
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Db 96720 CAAAATGGGTATGGGTCAAGTAGACCGCTCTGGCCGTACCAACACACGCTATTTC 96779
Qy 26881 TGTGGTCTGGGGGAGAGTCCGCTCCATCTTAGACAGTCCGGCAGGAGCTAGGCG 26940
Db 96780 TGTGGTCTGGGGGAGAGTCCGCTCCATCTTAGACAGTCCGGCAGGAGCTAGGCG 96839
Qy 26941 TGAATTAACATGTCATGAGAGACCCAGTGTCACTGTGTTTAAAGAAACAGGTAGGTGC 27000
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Qy 27301 AGAACCGGGGCGGCTTTACAAATTAACGACAACTCTAGTGTGACCGGAGTCTGAC 27360
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Qy 27901 AACTGCAACTGGACACCGCCCTTATTCACCTGTGACGAACTGGCCGCTGCTGG 27960
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Qy 27961 TTACCGGCAACCAAGATTGTTTGTCCCTATGACAGTCACTGGAAGCTATCATCACA 28020
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Qy 28381 CATTGATGATGATGACCGGACGAGACGCAACGCAAGGGGAAATTTTACGAGATTGT 28440
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Qy 28441 TAGAAATGCTAAACCAATTAACACTATACGGGTTCTATTTTTACGAGTCTTAAACAGT 28500
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Qy 28621 AATTGAACAACGTGCTGGGTTTTTTTAAAGCTTAAGCAACCCCGTGGCAACGCTACAAAAA 28680
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Db 98700 CAGACCAAGGTCCTGCTCGGCCAGGTTATGCAAAATATTGACGCGTCTCCAAATAA 98759
Qy 28861 GCGCGACAGATTATGACGAGCATGCTTCCAGCCCGGGATTTCGCGCGGAGTTCAATTA 28920
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Qy 28921 AAACAAAACTGTATCCGATCTTAAAGGAGTGTGCTGAAACGTCGCAAAAATATGAT 28980
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Qy 28981 CGCTATTCCAAATTTAGATGCTATAGTCTTGGCGGACAGAGACGCAAGACCTTAGGCC 29040
Db 98880 CGCTATTCCAAATTTAGATGCTATAGTCTTGGCGGACAGAGACGCAAGACCTTAGGCC 98939
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QY	2904.1	CTATCAGACGCTCGCTGGCCCTGGCGTATTTTCAAAATAATGACATTTTGGAAAGAAAC	29100
Db	9894.0	CTATCAGACGCTCGCTGGCCCTGGCGTATTTTCAAAATAATGACATTTTGGAAAGAAAC	98999
QY	29101	ATTCTCGGAGTCTTTTACAACCGTCGAGACTATCTTCAGGAAACATTTAGTGCATAC	29160
Db	99000	ATTCTCGGAGTCTTTTACAACCGTCGAGACTATCTTCAGGAAACATTTAGTGCATAC	99059
QY	29161	GACAGGTATACCGGAAGCCACGTCGCCACAAGAAATTTCTACAAATCTGTTTACTTTTC	29220
Db	99060	GACAGGTATACCGGAAGCCACGTCGCCACAAGAAATTTCTACAAATCTGTTTACTTTTC	99119
QY	29221	AAACATTTCCATACGACGAGCTTCATTTCAACATCCATGACCTTTGTAGACGACTGA	29280
Db	99120	AAACATTTCCATACGAGGACTTCATTTCAACATCCATGACCTTTGTAGACGACTGA	99179
QY	29281	AAAGGGATCCCGGTAATACGAGACCTGTCTCCATAGTCCCGGCTTTTAAACATGA	29340
Db	99180	AAAGGGATCCCGGTAATACGAGACCTGTCTCCATAGTCCCGGCTTTTAAACATGA	99239
QY	29341	AACTACTGTACGATTTCAACGCGTAGACACCCTGCAGATTTCCACAGGAAGGCAACCCA	29400
Db	99240	AACTACTGTACGATTTCAACGCGTAGACACCCTGCAGATTTCCACAGGAAGGCAACCCA	99299
QY	29401	TCGTGCTGAGCATGTTTCGTATTTCAAAATCCACGATTCGCTCCTCGAAGACTTTACAG	29460
Db	99300	TCGTGCTGAGCATGTTTCGTATTTCAAAATCCACGATTCGCTCCTCGAAGACTTTACAG	99359
QY	29461	AAGCGGTATGCGCGTTAATCTAAAGTCGGAACCGATGACGAGGCAACATCCGCTGA	29520
Db	99360	AAGCGGTATGCGCGTTAATCTAAAGTCGGAACCGATGACGAGGCAACATCCGCTGA	99419
QY	29521	TGCAACACCTCAGTACATGCAAAAAGATGCCGGACACGCAAAATATGACCACACAATTC	29580
Db	99420	TGCAACACCTCAGTACATGCAAAAAGATGCCGGACACGCAAAATATGACCACACAATTC	99479
QY	29581	CATCGGTGTTTACGCAAAATACACGAGGATATTTGACAGTGTTTTAAAGCTTTTAAACGTC	29640
Db	99480	CATCGGTGTTTACGCAAAATACACGAGGATATTTGACAGTGTTTTAAAGCTTTTAAACGTC	99539
QY	29641	TCATGTTACAGTTACGGGAACCTGCTGTACTCAGTACGAGGATCTTGTGATTCCTAT	29700
Db	99540	TCATGTTACAGTTACGGGAACCTGCTGTACTCAGTACGAGGATCTTGTGATTCCTAT	99599
QY	29701	ATCAACCCCCCTTAATACCGATACCATGTAACAAAAATTTTAACTTTAAACGACAAA	29760
Db	99600	ATCAACCCCCCTTAATACCGATACCATGTAACAAAAATTTTAACTTTAAACGACAAA	99659
QY	29761	CGGACACAAACGACGACATCTTAAAGAGCTGTACAGCCCGTGAAGACAAAGACCTCTAT	29820
Db	99660	CGGACACAAACGACGACATCTTAAAGAGCTGTACAGCCCGTGAAGACAAAGACCTCTAT	99719
QY	29821	CGGCTGAAAAACAAGATAGCACTCGACTCTCAAAAAACAAGCTGTGAGCGCTCAAAAAAC	29880
Db	99720	CGGCTGAAAAACAAGATAGCACTCGACTCTCAAAAAACAAGCTGTGAGCGCTCAAAAAAC	99779
QY	29881	TGTACGACGACTTTGGAGCCGCTCCACAACAAATTAACCCACCTCTATTAAACTTGAAT	29940
Db	99780	TGTACGACGACTTTGGAGCCGCTCCACAACAAATTAACCCACCTCTATTAAACTTGAAT	99839
QY	29941	ATTGGGGTAAATTAATACGAAACACAAGTGTCCGTAGATTGGAGCACATATTAACCTGTGA	30000
Db	99840	ATTGGGGTAAATTAATACGAAACACAAGTGTCCGTAGATTGGAGCACATATTAACCTGTGA	99899
QY	30001	CATACACGCAACCCGACGATAGCTTAAATTTCAACCCGGTTTAAACAGGAGGCACTAGATC	30060
Db	99900	CATACACGCAACCCGACGATAGCTTAAATTTCAACCCGGTTTAAACAGGAGGCACTAGATC	99959
QY	30061	GCATGTTTGCAGAAATTAACGATGGAATTCGCCCAATTTTTCGAAATTTTAAANATGAGG	30120
Db	99960	GCATGTTTGCAGAAATTAACGATGGAATTCGCCCAATTTTTCGAAATTTTAAANATGAGG	100019

QY	30121	GGGTGGCAACGACGACACCGACGGCCGACTGCAGTTCGGACAAATACGCCGCGTCCGACAGCT	30180
Db	100020	GGGTGGCAACGACGACACCGACGGCCGACTGCAGTTCGGACAAATACGCCGCGTCCGACAGCT	100079
QY	30181	TAGCAACAGCGCTTATCTACTCTGCGCAAAAGTTATTTCAATAGAGATCCCCGCTGACGG	30240
Db	100080	TAGCAACAGCGCTTATCTACTCTGCGCAAAAGTTATTTCAATAGAGATCCCCGCTGACGG	100133
QY	30241	ACACTAACGACCTCGACGACGTTTTACGGCCAAAGGGGCGAGCTTGGACTTTATCTGAGAC	30300
Db	100140	ACACTAACGACCTCGACGACGTTTTACGGCCAAAGGGGCGAGCTTGGACTTTATCTGAGAC	100199
QY	30301	GGTCCGGGACGCTCGGCTATTAACCAATATGCCAACTGCACACCATTAACCGAGCTTTATCA	30360
Db	100200	GGTCCGGGACGCTCGGCTATTAACCAATATGCCAACTGCACACCATTAACCGAGCTTTATCA	100255
QY	30361	AGACCAAGAGTGGAGCCGGGGCCATCTTTCATCTCAGAGAGTACTTTGGACTTAATGGAC	30420
Db	100260	AGACCAAGAGTGGAGCCGGGGCCATCTTTCATCTCAGAGAGTACTTTGGACTTAATGGAC	100315
QY	30421	TTGACGCGGCGCATTCGCGCAACCTTTCATCGAAATCCCTAAATATGATCCTTAACGGAATT	30480
Db	100320	TTGACGCGGCGCATTCGCGCAACCTTTCATCGAAATCCCTAAATATGATCCTTAACGGAATT	100379
QY	30481	ACGCCGGGACCGCTTCATATCTTTCTGTTTATATGCGCGCAAAAGCCGGGCGCTAATTA	30540
Db	100380	ACGCCGGGACCGCTTCATATCTTTCTGTTTATATGCGCGCAAAAGCCGGGCGCTAATTA	100435
QY	30541	TCAAAACAAAAGTTTTACCTGTTGGATGCCCATTTGGCGTACGCCACGCTACCAAAATAGTC	30600
Db	100440	TCAAAACAAAAGTTTTACCTGTTGGATGCCCATTTGGCGTACGCCACGCTACCAAAATAGTC	100499
QY	30601	CGGACACAGCTAATCACTTCGTGTCGAGACCCGACCGCATACTAGATAGTACGTGTCACCGCAG	30660
Db	100500	CGGACACAGCTAATCACTTCGTGTCGAGACCCGACCGCATACTAGATAGTACGTGTCACCGCAG	100555
QY	30661	ACAGGATATACACTGGCACTTTTCTATACATTATGCCCAGCGAAATGTATAATCCAGAGC	30720
Db	100560	ACAGGATATACACTGGCACTTTTCTATACATTATGCCCAGCGAAATGTATAATCCAGAGC	100619
QY	30721	ACTACATTCACCAACCACTATAGAACTATAAGTTGCGCAAAAGTACAGGGCCGACATAG	30780
Db	100620	ACTACATTCACCAACCACTATAGAACTATAAGTTGCGCAAAAGTACAGGGCCGACATAG	100677
QY	30781	ATATATCCACCGGCATAGAGCCGTGACCACTGCAGACATGCCAAGCCCGCGGATCGC	30840
Db	100680	ATATATCCACCGGCATAGAGCCGTGACCACTGCAGACATGCCAAGCCCGCGGATCGC	100733
QY	30841	CGGATGTGACGTCAAAATCATCCACCTCGCACCGCTGCCGAGAACCCACACCGACAGCT	30900
Db	100740	CGGATGTGACGTCAAAATCATCCACCTCGCACCGCTGCCGAGAACCCACACCGACAGCT	100795
QY	30901	CGAGGGCCAAACCCCCACGGGGAGGCTATCCGGTTTACGGGGCGGGAAACACCGCA	30960
Db	100800	CGAGGGCCAAACCCCCACGGGGAGGCTATCCGGTTTACGGGGCGGGAAACACCGCA	100855
QY	30961	GCTACCCAGACCCCGGCAACCAAGAGGCGGACACAAAACTTTAATCTCCGCTCCACGCG	31020
Db	100860	GCTACCCAGACCCCGGCAACCAAGAGGCGGACACAAAACTTTAATCTCCGCTCCACGCG	100911
QY	31021	AAACGGCGGTGCACACCCCGGAATTCCAACAACACCTGGAGCCAGCTACTTTTCAG	31080
Db	100920	AAACGGCGGTGCACACCCCGGAATTCCAACAACACCTGGAGCCAGCTACTTTTCAG	100975
QY	31081	AACCTGCGGCATTCAGAGGGTGGAAAGCGAAGCTTTCAGGCTTTCAGGCGATTTTGGATTT	31140
Db	100980	AACCTGCGGCATTCAGAGGGTGGAAAGCGAAGCTTTCAGGCTTTCAGGCGATTTTGGATTT	101035
QY	31141	CCGAGAAACGCTGCTGTGACGACGAAGGGGCCCCACGTAAGGCGCGTACACAGAGATGCGA	31200
Db	101040	CCGAGAAACGCTGCTGTGACGACGAAGGGGCCCCACGTAAGGCGCGTACACAGAGATGCGA	101099
QY	31201	TATCCGCGAGGCTGATCTGGAATGACAGACGATATATCTCTATATTCACCGTCGGCGA	31260

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Db 101100 TATCCCGAGGGATCTGGATGAGACGATATATCTCTCTATATTCACCTCGCGCA 101159
QY 31261 CTCATCGTTTGAAGCAGTGTTCGACAGCCCCCAATGAGCCGGAGTTTACATAGCA 31320
Db 101160 CTCATCGTTTGAAGCAGTGTTCGACAGCCCCCAATGAGCCGGAGTTTACATAGCA 101219
QY 31321 AGCGCAGAGAGACAGCATGGCGGCTTTCAGACAGATGCTCGAGAGCGGAAACGC 31380
Db 101220 ACCCGACAGAGAGACAGCATGGCGGCTTTCAGACAGATGCTCGAGAGCGGAAACGC 101279
QY 31381 CGTTCCTGCGTTCGAGCAGCTTATACGAGACGACATTTCTTCCCTGATATAAAAA 31440
Db 101280 CGTTCCTGCGTTCGAGCAGCTTATACGAGACGACATTTCTTCCCTGATATAAAAA 101339
QY 31441 TAGAACGTTTAAATCAAGTACGAAGCGCCTCGCAGCAGCTGCCAAACATTCGAGAAC 31500
Db 101340 TAGAACGTTTAAATCAAGTACGAAGCGCCTCGCAGCAGCTGCCAAACATTCGAGAAC 101399
QY 31501 AAAACGGGGGAGCGCGTCCGAGAAAGCGGGCGCTCCAGAGCATGAGCAAAATTTATGTTA 31560
Db 101400 AAAACGGGGGAGCGCGTCCGAGAAAGCGGGCGCTCCAGAGCATGAGCAAAATTTATGTTA 101459
QY 31561 ATATCACTTGAACACGGCTCTAATTACAGACGCGAGGGCGGGGACCGCGCGTCA 31620
Db 101460 ATATCACTTGAACACGGCTCTAATTACAGACGCGAGGGCGGGGACCGCGCGTCA 101519
QY 31621 AAAACGTTCTCAATTTTTCATCTGTGGGAGAAAAACTCAACATACCAATTAAGGAGC 31680
Db 101520 AAAACGTTCTCAATTTTTCATCTGTGGGAGAAAAACTCAACATACCAATTAAGGAGC 101579
QY 31681 CCAAGCAGGTCCCTAGACATCGATCTGCACTGATACCGTTACTATACGGCTATACGGAAG 31740
Db 101580 CCAAGCAGGTCCCTAGACATCGATCTGCACTGATACCGTTACTATACGGCTATACGGAAG 101639
QY 31741 GAAATTTCAACAGGGGGGCTTCAAAAAACACTTAACAATAAACAACCGGTCTG 31800
Db 101640 GAAATTTCAACAGGGGGGCTTCAAAAAACACTTAACAATAAACAACCGGTCTG 101699
QY 31801 CGTCAATGAGGGCCACGACGACGATGCGCAAAAAAACTGGCGGCTTTCACAGTGC 31860
Db 101700 CGTCAATGAGGGCCACGACGACGATGCGCAAAAAAACTGGCGGCTTTCACAGTGC 101759
QY 31861 AAGGCTCACAGATTTGCTCAGAGAGACCAAAATATCATGTCGGGGCTGGAAGAACAGA 31920
Db 101760 AAGGCTCACAGATTTGCTCAGAGAGACCAAAATATCATGTCGGGGCTGGAAGAACAGA 101819
QY 31921 TGGCCAAACCACTGATCCAGGCTTTTAGCGGTACTCCGGGACGAGGTAAACATC 31980
Db 101820 TGGCCAAACCACTGATCCAGGCTTTTAGCGGTACTCCGGGACGAGGTAAACATC 101879
QY 31981 TACGGGATAAAAATTCAGACCTTAAAAACAGGATCGAGAGCGCAACAAAGAAATCCAC 32040
Db 101880 TACGGGATAAAAATTCAGACCTTAAAAACAGGATCGAGAGCGCAACAAAGAAATCCAC 101939
QY 32041 AGGAAGAATGTTTTTATGCGATGCTCAGACGCTCGACAGCTTCGAACCCCTCCGA 32100
Db 101940 AGGAAGAATGTTTTTATGCGATGCTCAGACGCTCGACAGCTTCGAACCCCTCCGA 101999
QY 32101 AAACGCAATTTTCAATGAGATCTTTCGACACGTTAAAAACGAAAGTTATGCTGCACAC 32160
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Db 102060 TGGCGTCAATTAACACAGATTAACGAGAGCGCACCGGAAGCCCTCAACAAATTTACTG 102119
QY 32221 AAGACCCCGCCGACCAAGAGACGACATTAACAACATTTCCAAATTTTATCCATCGTG 32280
Db 102120 AAGACCCCGCCGACCAAGAGACGACATTAACAACATTTCCAAATTTTATCCATCGTG 102179
QY 32281 CAATATCATATCAAGTAAATAATCTTAAGTACGCAAAAAAGCATGCAATTTAAAG 32340
Db 102180 CAATATCATATCAAGTAAATAATCTTAAGTACGCAAAAAAGCATGCAATTTAAAG 102239
QY 32341 TAAAGCCCATGAGCAAGGTACAGGCGTCAAGCTGTGTGATCCTCGAGGCGAGTTAGCAACA 32400
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QY 32401 TCTTTAATTTAGAGTGGCCATACGAAACCGTGCACCGGTTTCAAGAAATGCCCCCTGTG 32460
Db 102300 TCTTTAATTTAGAGTGGCCATACGAAACCGTGCACCGGTTTCAAGAAATGCCCCCTGTG 102359
QY 32461 CGCGGGGGAAGAAAAATGGAATCGTTAACAATAATGAAAAAGCAACAGAGCTCTG 32520
Db 102360 CGCGGGGGAAGAAAAATGGAATCGTTAACAATAATGAAAAAGCAACAGAGCTCTG 102419
QY 32521 ACCAAATTAAGGAGAGCGCGAAACGTTACTTGACACAAATTAACCGCAATCCGAGATG 32580
Db 102420 ACCAAATTAAGGAGAGCGCGAAACGTTACTTGACACAAATTAACCGCAATCCGAGATG 102479
QY 32581 AGAACCCGGTCCCGCCATGTCATACCGATACGAGACCTGATTAACAACGACGCG 32640
Db 102480 AGAACCCGGTCCCGCCATGTCATACCGATACGAGACCTGATTAACAACGACGCG 102539
QY 32641 CCCTGATAGGCAATTCGAAACACAGGGTTGAAAAAACHCAAGCGCCCATCACAGAC 32700
Db 102540 CCCTGATAGGCAATTCGAAACACAGGGTTGAAAAAACHCAAGCGCCCATCACAGAC 102599
QY 32701 TGGCATATCGAGTGGTTCATATATATGCTGTAAACAACAGCGGCTTGATACATAT 32760
Db 102600 TGGCATATCGAGTGGTTCATATATATGCTGTAAACAACAGCGGCTTGATACATAT 102659
QY 32761 CAGACATCTGGCCAGATTCGAGGCGATCTGACCAACAACACATGTTTCTTCAAAAG 32820
Db 102660 CAGACATCTGGCCAGATTCGAGGCGATCTGACCAACAACACATGTTTCTTCAAAAG 102719
QY 32821 CCACTGTAGCAAAAGCTCACAACGCTGGGAGGACGACCTAATACCGAATGCGTAGAG 32880
Db 102720 CCACTGTAGCAAAAGCTCACAACGCTGGGAGGACGACCTAATACCGAATGCGTAGAG 102779
QY 32881 CGCTAATAAAGAGGCCCTCTTCCCTCAACAAGCGCGCTCTCTCGGGGTTCAAAACA 32940
Db 102780 CGCTAATAAAGAGGCCCTCTTCCCTCAACAAGCGCGCTCTCTCGGGGTTCAAAACA 102839
QY 32941 TACTGGGGACAGCGTCCGTTCCGATACAGAGCGCTGACGGCAATCGTTCCGGGGTGC 33000
Db 102840 TACTGGGGACAGCGTCCGTTCCGATACAGAGCGCTGACGGCAATCGTTCCGGGGTGC 102899
QY 33001 CCAAGCCACAAAAAGATCCGCTGGGAGATGATCAATAGTGGAGCGAGTAAACGGTTC 33060
Db 102900 CCAAGCCACAAAAAGATCCGCTGGGAGATGATCAATAGTGGAGCGAGTAAACGGTTC 102959
QY 33061 ACCTAAAGAGCTGAAGCTGTGATACCAATCGCTGTGCAAAAGCCACAGCGCA 33120
Db 102960 ACCTAAAGAGCTGAAGCTGTGATACCAATCGCTGTGCAAAAGCCACAGCGCA 103019
QY 33121 AACTGTTAATGATTAATTAACCCGTAAGTCAAGAGCGGAGGCTGTCAGAGAAACGGTTC 33180
Db 103020 AACTGTTAATGATTAATTAACCCGTAAGTCAAGAGCGGAGGCTGTCAGAGAAACGGTTC 103079
QY 33181 TGGAAACAGGTGGGCAAGAAACGCTCTAAAGTTTCAACCGTGCAGTCCAAAGAAATG 33240
Db 103080 TGGAAACAGGTGGGCAAGAAACGCTCTAAAGTTTCAACCGTGCAGTCCAAAGAAATG 103139
QY 33241 AAGACTTTTACAGTGGGACCGTACGACAAAGGCCGGAATTCGAGAAAAACACTTAC 33300
Db 103140 AAGACTTTTACAGTGGGACCGTACGACAAAGGCCGGAATTCGAGAAAAACACTTAC 103199
QY 33301 GGAAGCTGATACCAATTCACGGGACAGAGGACCGCGTCCAGGCGCACCGCGCTTC 33360
Db 103200 GGAAGCTGATACCAATTCACGGGACAGAGGACCGCGTCCAGGCGCACCGCGCTTC 103259
QY 33361 CCATGGAATACAGCGCCGACCATATCCACAGGCAACAGGCGGTTTACGGGCTACCGGG 33420
Db 103260 CCATGGAATACAGCGCCGACCATATCCACAGGCAACAGGCGGTTTACGGGCTACCGGG 103319
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OY	33421	AAAAGGAAAGGCGCATGGAATATAAATTCAACAGGCGCTTTAGGATTTCAACTTTCAACC	33480
Db	103320	AAAAGGAAAGGCGCATGGAATATAAATTCAACAGGCGCTTTAGGATTTCAACTTTCAACC	103379
OY	33481	TCATCGACGCTTCGGATTGGCAAGAGATGGCAATCGAAGTAATCTCCAGACACGGCTGGTCCC	33540
Db	103380	TCATCGACGCTTCGGATTGGCAAGAGATGGCAATCTCGAAGTAATCTCCAGACACGGCTGGTCCC	103439
OY	33541	TTTCCTGTAGCGTTGGACCAAGCTGTGCGCTTACGTGAGAGACATCTCAACACCCTGG	33600
Db	103440	TTTCCTGTAGCGTTGGACCAAGCTGTGCGCTTACGTGAGAGACATCTCAACACCCTGG	103499
OY	33601	ACGACATCTTCACGACGAAAGCTGGCATCTCTGCTCTCCAAACGGGCGCGGTTCAAGACCCC	33660
Db	103500	ACGACATCTTCACGACGAAAGCTGGCATCTCTGCTCTCCAAACGGGCGCGGTTCAAGACCCC	103559
OY	33661	CAGCGTTTGACTGATTCGCGCGCTTATCAAAACAGGGTAACCGTGTTTCTTAAAAACCATATG	33720
Db	103560	CAGCGTTTGACTGATTCGCGCGCTTATCAAAACAGGGTAACCGTGTTTCTTAAAAACCATATG	103619
OY	33721	GCGTGGCCATGTGTGGCAACCTGGCGGGACAGATCATCTACCAATGGCCAACTGTGATTC	33780
Db	103620	GCGTGGCCATGTGTGGCAACCTGGCGGGACAGATCATCTACCAATGGCCAACTGTGATTC	103679
OY	33781	ACGCGGTGCAATCCCGACACCTTTCAAACAGCGCCAGGTGGGAACAAGTTTAGAACACACCG	33840
Db	103680	ACGCGGTGCAATCCCGACACCTTTCAAACAGCGCCAGGTGGGAACAAGTTTAGAACACACCG	103739
OY	33841	CGGCGGAATACTGTGGAATTACTCTGTGACATGACAGTAGTGGCTTCAACGACCAAGGANTCG	33900
Db	103740	CGGCGGAATACTGTGGAATTACTCTGTGACATGACAGTAGTGGCTTCAACGACCAAGGANTCG	103799
OY	33901	CGGTAAAGTCGGAGGCGCGGGGCTACAGGAGGACATCAACTCGCGCGGCAACGTGTGA	33960
Db	103800	CGGTAAAGTCGGAGGCGCGGGGCTACAGGAGGACATCAACTCGCGCGGCAACGTGTGA	103859
OY	33961	CTCCCGCGAAACCCAACTAGAAAGCCCGCAAGAACTAATTAACGGCACTGAAGGCCCTTA	34020
Db	103860	CTCCCGCGAAACCCAACTAGAAAGCCCGCAAGAACTAATTAACGGCACTGAAGGCCCTTA	103919
OY	34021	CCGTGAGAGACTTTCACAATTTCTCTAAAAAGCTCAATCTTTAAACAGAGACAGCGACTCA	34080
Db	103920	CCGTGAGAGACTTTCACAATTTCTCTAAAAAGCTCAATCTTTAAACAGAGACAGCGACTCA	103979
OY	34081	TTGGCGCTCAGAGACGCGAATTTTCAGCAACTAGAGCGCAGCATCTCGCGCGCGCAAGCGC	34140
Db	103980	TTGGCGCTCAGAGACGCGAATTTTCAGCAACTAGAGCGCAGCATCTCGCGCGCGCAAGCGC	104039
OY	34141	TCGCGCAATCCACCCGTCGACGAGATGCGAGGCAAGATGGCAACCGCTATCAGCAACTCT	34200
Db	104040	TCGCGCAATCCACCCGTCGACGAGATGCGAGGCAAGATGGCAACCGCTATCAGCAACTCT	104099
OY	34201	TACCCCGGGCGCCGCTCGCAATATCATGAGACCGTGTGAATCTTATAAAAAGCTATGACT	34260
Db	104100	TACCCCGGGCGCCGCTCGCAATATCATGAGACCGTGTGAATCTTATAAAAAGCTATGACT	104159
OY	34261	TTTTGAGTTCAACGGTATATCGACAATAATCTTGACAAAGGAGCGCTTACGAGACGCCATAG	34320
Db	104160	TTTTGAGTTCAACGGTATATCGACAATAATCTTGACAAAGGAGCGCTTACGAGACGCCATAG	104219
OY	34321	CGGGATTTGGCGGTGTGGAAATCGGAGCAAAATCGGTATGTGCTACACTCAACAAAGG	34380
Db	104220	CGGGATTTGGCGGTGTGGAAATCGGAGCAAAATCGGTATGTGCTACACTCAACAAAGG	104279
OY	34381	AAACGCAACAGTTTAAACGTACTGTGAGCGAGGTAGAAATAACAGACACCGTGGCGCAGC	34440
Db	104280	AAACGCAACAGTTTAAACGTACTGTGAGCGAGGTAGAAATAACAGACACCGTGGCGCAGC	104339
OY	34441	GTCCTACAGATTTGGAACGTGTGGCGGAAAAACACGAGACGACTTAAAGGTGCTGAACAGG	34500
Db	104340	GTCCTACAGATTTGGAACGTGTGGCGGAAAAACACGAGACGACTTAAAGGTGCTGAACAGG	104399

OY	34501	GGCTGTAGAGAACTCGCGGCCCTCAGAGGTAAAGGGCGGAAAAACCCAGTAAAGCGCTGGG	34560
Db	104400	CGGTAGAGAACTCGCGGCCCTCAGAGGTAAAGGGCGGAAAAACCCAGTAAAGCGCTGGG	104459
OY	34561	AACAAAAACTGGAAGACATAGAAATCCCTCTTCGCGCCACGAGAGACGGCAGCGAATAT	34620
Db	104460	AACAAAAACTGGAAGACATAGAAATCCCTCTTCGCGCCACGAGAGACGGCAGCGAATAT	104519
OY	34621	CATCGAGACTTGGAAAGCAATCGGCACACAGCGGTTTGGACCAATCACCCTGCCGATTTAG	34680
Db	104520	CATCGAGACTTGGAAAGCAATCGGCACACAGCGGTTTGGACCAATCACCCTGCCGATTTAG	104579
OY	34681	GAACTCTTCGATTAATGCGGGGAAGCCGCAATTTCTCTCAGACAGCCAGTCTACCCG	34740
Db	104580	GAACTCTTCGATTAATGCGGGGAAGCCGCAATTTCTCTCAGACAGCCAGTCTACCCG	104639
OY	34741	AAGGCTTCGAGCAATAGGCAAAAACCTAGGAGGCTTCAAGGCTCAATTAAGTACAAA	34800
Db	104640	AAGGCTTCGAGCAATAGGCAAAAACCTAGGAGGCTTCAAGGCTCAATTAAGTACAAA	104699
OY	34801	AACAGTTTCTGGAGATTTTGAACAAACCACGCTTAACGCTTTCACGCTTCCGCTAT	34860
Db	104700	AACAGTTTCTGGAGATTTTGAACAAACCACGCTTAACGCTTTCACGCTTCCGCTAT	104759
OY	34861	CCCAAAACATTAACGAAACGTTCCGGCGCCCGCGGATGACCTGCTGGCCAGACTGA	34920
Db	104760	CCCAAAACATTAACGAAACGTTCCGGCGCCCGCGGATGACCTGCTGGCCAGACTGA	104819
OY	34921	CCAATCACCCTTACGTTGGCGGCGAGCGGCCCCACTTTCACATCGTGATTAAGAAACGCTAC	34980
Db	104820	CCAATCACCCTTACGTTGGCGGCGAGCGGCCCCACTTTCACATCGTGATTAAGAAACGCTAC	104879
OY	34981	CGACCGTGCATCCGGAAGAAACCAACTCAGCTCCCGCGCAGCAGGAGAGGCCCTCTCACC	35040
Db	104880	CGACCGTGCATCCGGAAGAAACCAACTCAGCTCCCGCGCAGCAGGAGAGGCCCTCTCACC	104939
OY	35041	GCCAGATCACTAGTCAAAAGTCTTAGAGGCGTTGTTTCATTAATTTCCACCAGCTAA	35100
Db	104940	GCCAGATCACTAGTCAAAAGTCTTAGAGGCGTTGTTTCATTAATTTCCACCAGCTAA	104999
OY	35101	C 35101	
Db	105000	C 105000	
RESULT 3			
AAL35004			
ID	AAL35004	standard; cDNA; 370 BP.	
AC	AAL35004;		
DT	08-JAN-2002	(first entry)	
DE	Human musculoskeletal system related polynucleotide SEQ ID NO 346.		
XX	Cytostatic; immunosuppressive; nocotropic; neuroprotective; antiviral;		
KM	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;		
KM	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;		
KM	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;		
KM	neurological disease; infection; human; secreted protein;		
KM	musculoskeletal system; ss.		
OS	Homo sapiens.		
XX	WO200155367-A1.		
PD	02-AUG-2001.		
PF	17-JAN-2001;	2001WO-US01338.	
XX	31-JAN-2000;	2000US-0179065.	
PR	04-FEB-2000;	2000US-0180628.	
PR	24-FEB-2000;	2000US-0184664.	

PS Claim 1; SEQ ID NO 346; 781pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABR03087-ABR04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 370 BP; 107 A; 71 C; 74 G; 115 T; 3 other;

Query Match 0.1%; Score 23; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4250 TTAAACATGCGATTATTATAA 4272
Dn 73 TTAAACATGCGATTATTATAA 95

RESULT 4
ID ABR57992 standard; cDNA: 370 BP.
XX
AC ABR57992:
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding novel human musculoskeletal system antigen #336.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW post-operative tissue repair; limb regeneration; neuronal growth;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW AIDS-related complex; chondrocyte growth; bone regeneration;
KW periodontal regeneration; tissue transport; bone graft; skin aging;
KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW cell growth; organ transplant; cell differentiation; body height;
KW weight; hair colour; eye colour; skin; percentage of adipose tissue;
KW pigmentation; cosmetic surgery; metabolism; biorythm; cardiac rhythm;
KW depression; tendency for violence; pain; reproductive capability;
KW hormone level; endocrine level; appetite; libido; memory; stress;
KW storage capability; fat content; lipid content; protein content;
KW carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX
XX Homo sapiens.
OS
XX
PN US2002147140-A1.
XX
PD 10-OCT-2002.
XX
XX 17-JAN-2001; 2001US-0764877.
XX
XX 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.

PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226688P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234974P.
PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239335P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251858P.
PR 08-DEC-2000; 2000US-251869P.

PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
XX WPI: 2003-128199/12.
DR P-PSDB: ABR12716.
XX
XX
PT Isolated nucleic acid molecules encoding musculoskeletal system
XX associated polypeptides, useful for detecting disorders, e.g. cancer -
PS Claim 1; SEQ ID NO 346; 321pp; English.
XX
XX The invention describes an isolated nucleic acid molecule comprising a
XX sequence encoding musculoskeletal system associated polypeptides useful
XX for detecting disorders, e.g., cancer or cancer metastases, in animals
XX or humans. The nucleic acid; stimulates re-vascularisation of ischemic
XX tissues associated with conditions such as thrombosis, arteriosclerosis,
XX and other cardiovascular conditions; treats wounds due to injuries,
XX burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
XX and limb regeneration; stimulates neuronal growth; can treat and prevent
XX neuronal damage occurring in certain disorders or neurodegenerative
XX conditions, such as, Alzheimer's disease, Parkinson's disease, and
XX AIDS-related complex; stimulates chondrocyte growth, thus they can be
XX used to enhance bone and periodontal regeneration and aid in tissue
XX transports or bone grafts; prevents skin aging due to sunburn by

CC	stimulating keratinocyte growth; prevents hair loss, since FGF family
CC	members activate hair-forming cells and promotes melanocyte growth;
CC	stimulates growth and differentiation of hematopoietic cells and bone
CC	marrow cells when used in combination with other cytokines; maintains
CC	organs before transplantation or for supporting cell culture of primary
CC	tissues; induces tissue of mesodermal origin to differentiate in early
CC	embryos; increases or decreases the differentiation or proliferation of
CC	hematopoietic stem cells, besides, hematopoietic lineage; modulates
CC	mammalian characteristics, such as, body height, weight, hair colour, eye
CC	colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC	(e.g., cosmetic surgery); modulates mammalian metabolism; changes
CC	mammal's metal state or physical state by influencing biorhythms,
CC	cardiac rhythms, depression, tendency for violence, tolerance for pain,
CC	reproductive capabilities, hormonal or endocrine levels, appetite,
CC	lipido, memory, or stress; increases or decreases storage capabilities,
CC	fat content, lipid, protein, carboxylate, vitamins, minerals, cofactors
CC	or other nutritional components. This sequence encodes a novel human
CC	musculoskeletal system antigen.
CC	Note: The sequence data for this patent did not form part of the
CC	printed specification, but was obtained in electronic format directly
CC	from the US patent office at
CC	ftp.segdata.uspto.gov/sequence.html?DocID=20020141140.
CC	
XX	
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SO	Sequence 370 BP; 107 A; 71 C; 74 G; 115 T; 3 other:
Qy	Query Match 0.1%; Score 23; DB 25; Length 370;
	Best Local Similarity 100.0%; Pred. No. 64;
Db	Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	4250 TTAAACATGGCATTATTTTAAA 4272
	73 TTAAACATGGCATTATTTTAAA 95
RESULT 5	
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ID	AAL37650 standard; DNA; 2004 BP.
XX	
AC	AAL37650;
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DT	08-JAN-2002 (first entry)
XX	
XX	
DE	Human musculoskeletal system related polynucleotide SEQ ID NO 4015.
XX	
KW	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiviral;
KW	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW	neurological disease; infection; human; secreted protein;
XX	musculoskeletal system; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO20015367-A1.
XX	
PD	02-AUG-2001.
XX	
XX	
PF	17-JAN-2001; 2001WO-US01338.
XX	
XX	
PR	31-JAN-2000; 2000US-0179065.
PR	04-FEB-2000; 2000US-0180628.
PR	24-FEB-2000; 2000US-0184664.
PR	02-MAR-2000; 2000US-0186350.
PR	16-MAR-2000; 2000US-0189874.
PR	17-MAR-2000; 2000US-0189076.
PR	18-APR-2000; 2000US-0198123.
PR	19-MAY-2000; 2000US-0205515.
PR	07-JUN-2000; 2000US-0209467.
PR	28-JUN-2000; 2000US-0214886.
PR	30-JUN-2000; 2000US-0215135.
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PR	07-JUL-2000; 2000US-0216880.
PR	11-JUL-2000; 2000US-0217487.

PR	11-JUL-2000	2000US-02174.96
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PR	26-JUL-2000	2000US-02203.63
PR	26-JUL-2000	2000US-02205.56
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 PR 08-SEP-2000; 2000US-0232080.
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 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.

PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
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 PR 17-NOV-2000; 2000US-0249217.
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 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251899.
 PR 08-DEC-2000; 2000US-0251990.
 PR 08-DEC-2000; 2000US-0251997.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-451937/48.
 XX
 PT Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the musculoskeletal system including
 PT musculoskeletal cancers and also for testing and detection e.g.
 PT diagnosis -
 XX
 PS Example 2; SEQ ID NO 4016; 781pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ALJ34669-ALJ37666) and proteins
 CC (ABB03087-ABB04109) associated with the musculoskeletal system useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 CC other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX Sequence 2004 BP; 632 A; 428 C; 351 G; 593 T; 0 other;
 SQ

Query Match

0.1%; Score 23; DB 22; Length 2004;

Best Local Similarity 100.0%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4250 TTAACATGCATTTTAAA 4272
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Db 439 TTAACATGCATTTTAAA 417

RESULT 7

ABX60638/c
ID ABX60638 standard; cDNA; 2004 BP.

AC ABX60638;

DT 26-FEB-2003 (first entry)

DE cDNA encoding novel human musculoskeletal system antigen #2982.

XX Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KM re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KM cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KM post-operative tissue repair; limb regeneration; neuronal growth;
KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KM AIDS-related complex; chondrocyte growth; bone regeneration;
KM periodontal regeneration; tissue transport; bone graft; skin aging;
KM keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KM cell growth; organ transplant; cell differentiation; body height;
KM weight; hair colour; eye colour; skin; percentage of adipose tissue;
KM pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm;
KM depression; tendency for violence; pain; reproductive capability;
KM hormone level; endocrine level; appetite; libido; memory; stress;
KM storage capability; fat content; lipid content; protein content;
KM carbohydrate content; vitamin content; cofactor content;
KM nutritional component.

OS Homo sapiens.

PN US2002147140-A1.

PD 10-OCT-2002.

XX 17-JAN-2001; 2001US-0764877.

XX 31-JAN-2000; 2000US-179065P.

PR 04-FEB-2000; 2000US-180628P.

PR 28-JUN-2000; 2000US-214886P.

PR 07-JUL-2000; 2000US-216647P.

PR 07-JUL-2000; 2000US-216880P.

PR 11-JUL-2000; 2000US-217487P.

PR 11-JUL-2000; 2000US-217496P.

PR 14-JUL-2000; 2000US-218290P.

PR 26-JUL-2000; 2000US-220963P.

PR 14-AUG-2000; 2000US-220964P.

PR 14-AUG-2000; 2000US-224518P.

PR 14-AUG-2000; 2000US-224519P.

PR 14-AUG-2000; 2000US-225267P.

PR 14-AUG-2000; 2000US-225268P.

PR 14-AUG-2000; 2000US-225270P.

PR 14-AUG-2000; 2000US-225447P.

PR 14-AUG-2000; 2000US-225757P.

PR 22-AUG-2000; 2000US-226868P.

PR 30-AUG-2000; 2000US-228924P.

PR 01-SEP-2000; 2000US-229287P.

PR 01-SEP-2000; 2000US-229343P.

PR 01-SEP-2000; 2000US-229344P.

PR 01-SEP-2000; 2000US-229345P.

PR 05-SEP-2000; 2000US-229509P.

PR 05-SEP-2000; 2000US-229513P.

PR 08-SEP-2000; 2000US-231413P.

PR 21-SEP-2000; 2000US-234223P.

PR 21-SEP-2000; 2000US-234274P.

PR 25-SEP-2000; 2000US-234997P.

PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239335P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.

XX (ROSE/) ROSEN C. A.
PA (RUBE/) RUBEN S. M.
PA (BARA/) BARASH S. C.
XX Rosen CA, Ruben SM, Barash SC;
DR WPI; 2003-128199/12.
XX Isolated nucleic acid molecules encoding musculoskeletal system
PT associated polypeptides, useful for detecting disorders, e.g. cancer -
XX Disclosure; SEQ ID NO 4015; 321pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence encoding musculoskeletal system associated polypeptides useful
CC for detecting disorders, e.g., cancer or cancer metastases, in animals
CC or humans. The nucleic acid; stimulates re-vascularisation of ischaemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and
CC AIDS-related complex; stimulates chondrocyte growth, thus they can be
CC used to enhance bone and periodontal regeneration and aid in tissue
CC transports or bone grafts; prevents skin aging due to sunburn by
CC stimulating keratinocyte growth; prevents hair loss, since FGF family
CC members activate hair-forming cells and promotes melanocyte growth;
CC stimulates growth and differentiation of hematopoietic cells and bone
CC marrow cells when used in combination with other cytokines; maintains
CC organs before transplantation or for supporting cell culture of primary
CC tissues; induces tissue of mesodermal origin to differentiate in early
CC embryos; increases or decreases the differentiation or proliferation of
CC embryonic stem cells, besides, haematopoietic lineage; modulates
CC mammalian characteristics, such as, body height, weight, hair colour, eye
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC (e.g., cosmetic surgery); modulates mammalian metabolism, changes
CC mammal's metal state or physical state by influencing biorhythms,
CC cardiac rhythms, depression, tendency for violence, tolerance for pain,
CC reproductive capabilities, hormonal or endocrine levels, appetite,
CC libido, memory, or stress; increases or decreases storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC or other nutritional components. This sequence encodes a novel human
CC musculoskeletal system antigen.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140.

XX Sequence 2004 BP; 629 A; 429 C; 353 G; 593 T; 0 other;

Query Match 0.1%; Score 23; DB 25; Length 2004;

Best Local Similarity 100.0%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4250 TTAACATGATGATTTTAA 4272
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Db 439 TTAACATGATGATTTTAA 417

RESULT 8

ABX60639/c
ID ABX60639 standard; cDNA; 2004 BP.

AC ABX60639;

DT 26-FEB-2003 (first entry)

XX cDNA encoding novel human musculoskeletal system antigen #2983.

Gene: ss: musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;
cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
post-operative tissue repair; limb regeneration; neuronal growth;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
AIDS-related complex; chondrocyte growth; bone regeneration;
periosteal regeneration; tissue transport; bone graft; skin aging;
keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
cell growth; organ transplant; cell differentiation; body height;
weight; hair colour; eye colour; skin; percentage of adipose tissue;
pigmentation; cosmetic surgery; metabolism; biohythm; circadian rhythm;
depression; tendency for violence; pain; reproductive capability;
hormone level; endocrine level; appetite; libido; memory; stress;
storage capability; fat content; lipid content; protein content;
carbohydrate content; vitamin content; cofactor content;
nutritional component.

XX Homo sapiens.

XX US2002147140-A1.

XX 10-OCT-2002.

XX 17-JAN-2001; 2001US-0764877.

XX 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226868P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 25-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234997P.

PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 13-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239935P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.

(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
Rosen CA, Ruben SM, Barash SC;
WPI; 2003-128199/12.
Isolated nucleic acid molecules encoding musculoskeletal system
associated polypeptides, useful for detecting disorders, e.g. cancer -
Disclosure; SEQ ID NO 4016; 321pp; English.

The invention describes an isolated nucleic acid molecule comprising a
sequence encoding musculoskeletal system associated polypeptides useful
for detecting disorders, e.g., cancer or cancer metastases, in animals
or humans. The nucleic acid stimulates re-vascularisation of ischemic
tissues associated with conditions such as thrombosis, arteriosclerosis,
and other cardiovascular conditions; treats wounds due to injuries,
burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
and limb regeneration; stimulates neuronal growth; can treat and prevent
neuronal damage occurring in certain disorders or neurodegenerative
conditions, such as, Alzheimer's disease, Parkinson's disease, and
AIDS-related complex; stimulates chondrocyte growth, thus they can be
used to enhance bone and periosteal regeneration and aid in tissue
transports or bone grafts; prevents skin aging due to sunburn by
stimulating keratinocyte growth; prevents hair loss, since RGF family
members activate hair-forming cells and promotes melanocyte growth;
stimulates growth and differentiation of hematopoietic cells and bone
marrow cells when used in combination with other cytokines; maintains
organs before transplantation or for supporting cell culture of primary
tissues; induces tissue of mesodermal origin to differentiate in early
embryos; increases or decreases the differentiation or proliferation of
embryonic stem cells, besides, haematopoietic lineage; modulates
mammalian characteristics, such as, body height, weight, hair colour, eye
colour, skin, percentage of adipose tissue, pigmentation, size, and shape
(e.g., cosmetic surgery); modulates mammalian metabolism; changes
mammal's metal state or physical state by influencing biorythms,
circadian rhythms, depression, tendency for violence, tolerance for pain,
reproductive capabilities, hormonal or endocrine levels, appetite,
libido, memory, or stress; increases or decreases storage capabilities,
fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
or other nutritional components. This sequence encodes a novel human
musculoskeletal system antigen.

Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from the US patent office at
ftp:seqdata.uspto.gov/sequence.html?DocID=20020147140.

Sequence 2004 BP; 632 A; 428 C; 351 G; 593 T; 0 other;

Query Match

0.1%, Score 23; DB 25; Length 2004;

Best Local Similarity 100.0%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4250 TTAACATGTCATTATTATAA 4272
|||||
DB 439 TTAACATGTCATTATTATAA 417

RESULT 9

AB070267
ID AB070267 standard; DNA; 917 BP.

AC AB070267;

DT 29-AUG-2002 (first entry)

DE Listeria monocytogenes 4b contig DNA sequence #209.

KW Antibacterial; Listeria; food contamination; mutational analysis;
infection; ds.

OS Listeria monocytogenes 4b.

PN WO200228891-A2.

PD 11-APR-2002.

PE 04-OCT-2001; 2001WO-FR03061.

PR 04-OCT-2000; 2000FR-0012697.

PA (INSP) INST PASTEUR.
(CNRS) CNRS CENT NAT RECH SCI.

PI Kunst F, Glaser P;

DR WPI; 2002-332479/37.

PT New genomic sequences from Listeria species, useful for detection,
treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -
XX

PS Claim 14; SEQ ID 3080; 180pp; French.

CC The present invention relates to nucleic acid sequences

CC (AB067188-AB071212) from Listeria sp. The sequences are useful as probes

CC and primers for identification and/or detection of Listeria (e.g. as

CC contaminants in foods, or mutational analysis) and for analysis of

CC gene expression. Proteins encoded by the nucleic acid sequences can be

CC used to screen for compounds that modulate gene expression, replication

CC and pathogenicity of Listeria (potential therapeutic agents), also for

CC treating infections by Listeria, and are useful as immunogens in

CC anti-Listeria vaccines.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 917 BP; 211 A; 178 C; 164 G; 360 T; 4 other;

Query Match 0.1%; Score 22; DB 24; Length 917;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2808 TATCAGCTTTTGAGCTGCTTG 2829
|||||

DB 279 TATCAGCTTTTGAGCTGCTTG 300

RESULT 10

ABK74889/C
ID ABK74889 standard; DNA; 1393 BP.

XX
AC ABK74889;

XX 13-AUG-2002 (first entry)

DT Bacillus licheniformis genomic sequence tag (GST) #2180.

DE Differential gene expression; genomic sequenced tag; GST;

KW altered culture condition; environmental stress;

KW physiological provocation; ds.

OS Bacillus licheniformis.

PN WO200229113-A2.

PD 11-APR-2002.

PE 05-OCT-2001; 2001WO-US31437.

PR 06-OCT-2000; 2000US-0680598.

PR 27-MAR-2001; 2001US-279526P.

PA (NOVO) NOVOZYMES BIOTECH INC.

PA (NOVO) NOVOZYMES AS.

PI Berka R, Clausen IG;

DR WPI; 2002-416684/44.

PS Claim 4; SEQ ID NO 2180; 200pp; English.

CC The invention describes a method of monitoring differential expression of

CC genes in a first Bacillus cell relative to expression of the genes in

CC other Bacillus cells, comprising hybridising labelled nucleic acid probes

CC isolated from Bacillus cells to a substrate containing array of Bacillus

CC genomic sequenced tags (GST), examining the array, and determining

CC relative gene expression by an observed hybridisation reporter signal of

CC a spot in the array. The method is useful for measuring the expression of

CC genes in a first Bacillus cell relative to expression of the same genes

CC in one or more second Bacillus cells. The method is useful for monitoring

CC global expression of several genes from a Bacillus cell, discovering new

CC genes, identifying possible functions of unknown open reading frames and

CC monitoring gene copy number variation and stability. Monitoring changes

CC in expression of genes may be used to provide a representation of the way

CC in which Bacillus cells adapt to changes in culture conditions,

CC environmental stress or other physiological provocation. Extensive

CC follow-up characterisation is unnecessary, when one spot on an array

CC equals one gene or one open reading frame, since sequence information is

CC available. This sequence represents a genomic sequence tag (GST) used in

CC the method of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at
ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1393 BP; 346 A; 319 C; 352 G; 375 T; 1 other;

Query Match 0.1%; Score 22; DB 24; Length 1393;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7457 TCCGTGATGGCCAGCTCTCGG 7478
|||||

DB 393 TCCGTGATGGCCAGCTCTCGG 372

RESULT 11

ABLA9345
ID ABLA9345 standard; DNA; 19233 BP.

XX

AC ABL49345;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human polynucleotide associated with DNA replication seq ID NO 45.
XX
XX Human: cytosolic; neuroprotective; nootropic; immunostimulant;
KW therapy; gene regulation; DNA replication; CENPB; DNA2L; ATR; CHD1L;
KW ERCC3; SNRPB; RAD50; LIG2; cytosine methylation; Ataxia telangiectasia;
KW ATR-X; Bloom's syndrome; tumour; cancer; methylation; gene; ds.
XX
OS Homo sapiens.
XX
PN WO20017377-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-EP03971.
XX
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI: 2002-017471/02.
XX
XX New nucleic acid sequences from chemically modified genes associated
PT with DNA replication, useful for analysing cytosine methylations for
PT diagnosis and therapy of diseases e.g. Ataxia telangiectasia
XX
PS Claim 1: SEQ ID NO 45; 23pp + Sequence Listing: English.
XX
XX The invention relates to nucleic acid sequences comprising at least 18
CC bases of a chemically pretreated gene associated with gene regulation,
CC selected from 94 genes (ABL49301-ABL49394) and/or complementary sequences
CC associated with DNA replication, CENPB, DNA2L, ATR, CHD1L, ERCC3, SNRPB,
CC RAD50 and LIG2. The chemical pretreatment converts cytosine bases
CC unmethylated at the 5-position to uracil or another base with
CC hybridisation behaviour dissimilar to cytosine, to enable analysis of
CC cytosine methylations. The DNA sequences and method are useful in the
CC diagnosis of diseases (or predisposition to diseases) associated with DNA
CC replication and in therapy of such diseases, by enabling analysis of the
CC cytosine methylation patterns of such genes. They are especially useful
CC in diagnosis and therapy of e.g. Ataxia telangiectasia, ATR-X, Bloom's
CC syndrome, solid tumours and cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification and was supposed to be available directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences. However, the sequence data did
CC not correspond to that referred to in the specification. The present data
CC is taken from EPO data for the patent.
XX
SQ Sequence 19233 BP: 4336 A; 489 C; 4429 G; 9848 T; 131 other;
Query Match 0.1%; Score 22; DB 24; Length 19233;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1152 AATTAGTAATTGTGATTTT 1173
DB 12221 AATTAGTAATTGTGATTTT 12242

XX Nucleotide sequence of the FK-520 biosynthetic gene cluster.
DE
XX
XX FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant;
KW Streptomyces hygroscopicus var. ascometicus; immunophilin;
KW FK-506 binding protein; polyketide compound; transplant rejection;
KW graft-versus-host disease; uveitis; alopecia universalis;
KW autoimmune chronic active hepatitis; inflammatory bowel disease;
KW multiple sclerosis; primary biliary cirrhosis; scleroderma;
KW neurite outgrowth; nerve regrowth; Parkinson's disease;
KW Alzheimer's disease; stroke; traumatic spinal cord; brain injury;
KW peripheral neuropathy; ss.
XX
OS Streptomyces hygroscopicus.
XX
FH Location/Qualifiers
FH CDS complement (412..1836)
FT /tag= a
FT /note= "fkbw gene"
FT complement (2020..3579)
FT /tag= b
FT /note= "fkbv gene"
FT 3969..4496
FT /tag= c
FT /note= "fkbr2 gene"
FT complement (4595..5488)
FT /tag= d
FT /note= "fkbr1 gene"
FT 5601..6818
FT /tag= e
FT /note= "fkbe gene"
FT 6808..8052
FT /tag= f
FT /note= "fkbf gene"
FT 8156..8824
FT /tag= g
FT /note= "fkbg gene"
FT complement (9122..9883)
FT /tag= h
FT /note= "fkhh gene"
FT complement (9894..10994)
FT /tag= i
FT /note= "fkbi gene"
FT complement (10987..11247)
FT /tag= j
FT /note= "fkbi gene"
FT complement (11244..12092)
FT /tag= k
FT /note= "fkbi gene"
FT complement (12113..13150)
FT /tag= l
FT /note= "fkbl gene"
FT complement (13212..23988)
FT /tag= m
FT /note= "fkbc gene"
FT complement (13452..13662)
FT /tag= n
FT /note= "ACP6"
FT complement (13761..14394)
FT /tag= o
FT /note= "KR6"
FT complement (14517..15294)
FT /tag= p
FT /note= "ER6"
FT complement (15438..16587)
FT /tag= q
FT /note= "dehydratase domain (DH) 6"
FT complement (16587..17820)
FT /tag= r
FT /note= "acyltransferase domain (AT) 6"
FT complement (17820..19053)
FT /tag= s
FT /note= "KSc6"

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FT misc-feature complement (19116..19326)
FT /tag- t
FT /note- "ACP5"
FT complement (19464..20097)
FT /tag- u
FT /note- "KR5"
FT complement (20241..21420)
FT /tag- v
FT /note- "DH5"
FT complement (21420..22653)
FT /tag- w
FT /note- "AT5"
FT complement (22653..23892)
FT /tag- x
FT /note- "KS5"
FT complement (23992..46573)
FT /tag- y
FT /note- "fkb gene"
FT complement (24163..24373)
FT /tag- z
FT /note- "ACP4"
FT complement (24997..26146)
FT /tag- aa
FT /note- "DH4 (inactive)"
FT complement (26146..27430)
FT /tag- ab
FT /note- "AT4"
FT complement (27430..28684)
FT /tag- ac
FT /note- "KS4"
FT complement (28750..28960)
FT /tag- ad
FT /note- "ACP3"
FT complement (29092..29740)
FT /tag- ae
FT /note- "KR3"
FT complement (29869..31018)
FT /tag- af
FT /note- "DH3 (inactive)"
FT complement (31018..32185)
FT /tag- ag
FT /note- "AT3"
FT complement (32185..33439)
FT /tag- ah
FT /note- "KS3"
FT complement (33505..33715)
FT /tag- ai
FT /note- "ACP2"
FT complement (33823..34480)
FT /tag- aj
FT /note- "KR2"
FT complement (34606..35749)
FT /tag- ak
FT complement (28750..28960)
FT /tag- al
FT /note- "DH2 (inactive)"
FT complement (35749..37144)
FT /tag- am
FT /note- "AT2"
FT complement (37145..38296)
FT /tag- an
FT /note- "KS2"
FT complement (38371..38581)
FT /tag- ao
FT /note- "ACP1"
FT complement (38677..39307)
FT /tag- ap
FT /note- "KR1"
FT complement (39442..40609)
FT /tag- aq
FT /note- "DH1"
FT complement (40609..41842)
FT /tag- ar

FT misc-feature /note- "AT1"
FT complement (41842..43093)
FT /tag- as
FT /note- "KS of extender module 1 (KS1)"
FT complement (43144..43660)
FT /tag- at
FT /note- "ACP of loading domain"
FT complement (43777..44629)
FT /tag- au
FT /note- "ER of loading domain"
FT complement (44974..46573)
FT /tag- av
FT /note- "CoA ligase of loading domain"
FT 46754..47788
FT /tag- aw
FT /note- "fkb gene"
FT 47785..52272
FT /tag- ax
FT /note- "fkb gene"
FT 52275..71465
FT /tag- ay
FT /note- "fkb gene"
FT 52362..53576
FT /tag- az
FT /note- "KS7"
FT 53577..54716
FT /tag- ba
FT /note- "DH7"
FT 56019..56819
FT /tag- bc
FT /note- "ER7"
FT 56943..57575
FT /tag- bd
FT /note- "KR7"
FT 57710..57920
FT /tag- be
FT /note- "ACP7"
FT 57990..59243
FT /tag- bf
FT /note- "KS8"
FT 59244..60398
FT /tag- bg
FT /note- "AT8"
FT 60399..61412
FT /tag- bh
FT /note- "DH8 (inactive)"

Query Match 0.1%: Score 22; DB 21; Length 77536;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23444 GCCCGCGTGGCGCTTCGCA 23465
DB 64419 GCCCGCGTGGCGCTTCGCA 64440

RESULT 13
AA14651/c
ID AA14651 standard; DNA: 77536 BP.
AC AA14651;
XX
XX 08-AUG-2000 (first entry)
DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.
XX
XX FK-520: polyketide synthase; PKS; gene cluster; immunosuppressant;
KW Streptomyces hygroscopicus var. ascomyceticus; immunophilin;
KW FK-506 binding protein; polyketide compound; transplant rejection;
KW graft-versus-host disease; uveitis; alopecia universalis;

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FT misc-feature complement (43777..44629)
FT /tag- au
FT /note= "ER of loading domain"
FT misc-feature complement (44974..46573)
FT /tag- av
FT /note= "CoA ligase of loading domain"
FT CDS
FT /tag- aw
FT /note= "fkbp gene"
FT CDS
FT /tag- ax
FT /note= "fkbp gene"
FT CDS
FT /tag- ay
FT /note= "fkbp gene"
FT misc-feature
FT /tag- az
FT /note= "KS7"
FT misc-feature
FT /tag- bc
FT /note= "ER7"
FT misc-feature
FT /tag- bd
FT /note= "KR7"
FT misc-feature
FT /tag- be
FT /note= "ACP7"
FT misc-feature
FT /tag- bf
FT /note= "KS8"
FT misc-feature
FT /tag- bg
FT /note= "Ar8"
FT misc-feature
FT /tag- bh
FT /note= "DH8 (inactive)"

Query Match
Best Local Similarity 100.0%; Score 22; DB 21; Length 77536;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23444 GCCCGCGTGTGGCTTCGCA 23465
DB 22086 GCCCGCGTGTGGCTTCGCA 22065

RESULT 14
AB067196/c
ID AB067196 standard; DNA; 684707 BP.
AC AB067196;
XX
XX 29-AUG-2002 (first entry)
DE Listeria innocua contig DNA sequence #9.
XX
XX Antibacterial; Listeria; food contamination; mutational analysis;
XX infection; ds.
OS Listeria innocua.
XX
XX WO200228891-A2.
XX
XX 11-APR-2002.
XX
XX 04-OCT-2001; 2001WO-FR03061.
XX

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PR 04-OCT-2000; 2000FR-0012697.
XX
XX (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Kunst F, Glaser P;
PI WPI; 2002-332479/37.
XX
XX New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators
XX
XX Claim 5; SEQ ID 9; 180pp; French.
XX
XX The present invention relates to nucleic acid sequences
CC (AB067188-AB071212) from Listeria sp. The sequences are useful as probes
CC and primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in
CC anti-Listeria vaccines.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 684707 BP; 213423 A; 126375 C; 133438 G; 211468 T; 3 other:

Query Match
Best Local Similarity 100.0%; Score 22; DB 24; Length 684707;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2808 TATCAGCTTTTGACCTGCTTG 2829
DB 47940 TATCAGCTTTTGACCTGCTTG 47919

RESULT 15
AAX20248/c
ID AAX20248 standard; DNA; 910715 BP.
XX
XX AAX20248;
XX
XX 04-MAY-1999 (first entry)
DE Borrelia burgdorferi polynucleotide sequence #1.
XX
XX Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
KW infection; diagnosis; characterisation; detection; ds.
XX
XX Borrelia burgdorferi.
OS
XX
XX WO9858943-A1.
XX
XX 30-DEC-1998.
XX
XX 18-JUN-1998; 98WO-US12764.
XX
XX 03-SEP-1997; 97US-0057483.
XX 20-JUN-1997; 97US-0050359.
XX 22-JUL-1997; 97US-0053344.
XX 22-JUL-1997; 97US-0053377.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (MEDI-) MEDIMUNE INC.
XX
XX Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO;
XX White OR;
XX
XX WPI; 1999-081217/07.
XX

```

XX New isolated *Borrelia burgdorferi* nucleic acids - used to develop
PT products for the detection, diagnosis, characterisation, prevention
PT and therapy of infections, particularly Lyme disease
XX
PS Claim 1: Page 157-671, 1128pp; English.
XX
CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from
CC *Borrelia burgdorferi* (Bb). Products derived from Bb can be used for
CC the detection, diagnosis, characterisation, prevention and therapy of
CC Bb infections, e.g. Lyme disease. They can also be used for the
CC production of biosynthetic products, e.g. enzymes. *Borrelia* belongs
CC to a family of motile, spiral-shaped bacteria called Spirochetes.
CC Spirochetes are pathogenic in humans and *Borrelia* causes epidemic and
CC endemic relapsing fever, and Lyme borreliosis, more commonly known as
CC Lyme disease.
XX
SQ Sequence 910715 BP; 327171 A; 129646 C; 130753 G; 323091 T; 54 other:
Query Match 0.1%; Score 22; DB 20; Length 910715;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29735 AAAAATTTAACTTACGAC 29756
DB 77874 AAAAATTTAACTTACGAC 77853
RESULT 16
ABA03041
ID ABA03041 standard; DNA; 2944528 BP.
XX
AC ABA03041;
XX
DT 05-FEB-2002 (first entry)
XX
DE *Listeria monocytogenes* EGD-e genome sequence.
XX
KM Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KM vitamin B12; bacterial infection; disease; ds.
XX
OS *Listeria monocytogenes*.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusnick C, Fsihl H, Dehoux P;
PI Dussurget O, Chelouani F, Nedjati H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Dommann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehlant J, Kaerst U, Ertlian K, Hauf J;
PI Rose M, Voss H;
XX
DR WPI: 2002-010914/01.
XX
XX Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
PT and prevention of *Listeria* and related bacterial infections, and
PT related polypeptides -
XX
PS Claim 1: SEQ ID No 1: 192pp; French.
XX
CC The present sequence is the genome sequence of *Listeria monocytogenes*
CC EGD-e. This sequence and fragments of this sequence are useful for
CC selecting probes and primers for detecting genes in *L. monocytogenes* and

CC related organisms, and to study genetic polymorphisms and other genomes.
CC Proteins (AB047297-AB050149) expressed from the present sequence are
CC useful for raising specific antibodies, identification of *L.*
CC *monocytogenes* and related organisms, and for biosynthesis and
CC biodegradation, especially biosynthesis of vitamin B12. This sequence and
CC proteins encoded by it are also useful for selecting compounds that
CC regulate gene expression and cell replication and modulate *L.*
CC *monocytogenes*-related diseases. In addition, this sequence and proteins
CC encoded by it are useful in pharmaceutical and vaccine compositions for
CC the treatment or prevention of infections by *L. monocytogenes* and related
CC organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other:
Query Match 0.1%; Score 22; DB 24; Length 2944528;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2808 TATCAGCTTTTGGAGCTGCTTG 2829
DB 2709929 TATCAGCTTTTGGAGCTGCTTG 2709950
RESULT 17
AB069245
ID AB069245 standard; DNA; 3011208 BP.
XX
AC AB069245;
XX
DT 29-AUG-2002 (first entry)
XX
DE *Listeria innocua* DNA sequence #684.
XX
KM Antibacterial; *Listeria*; food contamination; mutational analysis;
KM infection; ds.
XX
OS *Listeria innocua*.
XX
PN WO200228891-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-FR03061.
XX
PR 04-OCT-2000; 2000FR-0012697.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Kunst F, Glaser P;
XX
DR WPI: 2002-332479/37.
XX
XX New genomic sequences from *Listeria* species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -
XX
PS Claim 5: SEQ ID 2058; 180pp; French.
XX
XX The present invention relates to nucleic acid sequences
CC (AB067188-AB071212) from *Listeria* sp. The sequences are useful as probes
CC and primers for identification and/or detection of *Listeria* (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of *Listeria* (potential therapeutic agents), also for
CC treating infections by *Listeria*, and are useful as immunogens in
CC anti-*Listeria* vaccines.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format

CC directly from WIP0 at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 3011208 BP; 941651 A; 568176 C; 559189 G; 942192 T; 0 other;

Query Match 0.1%; Score 22; DB 24; Length 3011208;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2808 TATCAGCTTTTGAGCTGCTTG 2829
DB 2800874 TATCAGCTTTTGAGCTGCTTG 2800895

RESULT 18
ABLO1517/c
ID ABL01517 standard; DNA; 496 BP.

AC ABL01517;

DT 15-MAR-2002 (first entry)

DE Murine apoptosis related DNA sequence #182.

KW Apoptosis; mouse; cancer; autoimmune disease; viral infection;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW reperfusion injury; stroke; liver disease; dilatory cardiomyopathy;
KW transgenic animal; hepatocarcinoma; antialcoholism; cytostatic;
KW immunosuppressive; vitruclide; neurotropic; neuroprotective; vasotrophic;
KW antiparkinsonian; cerebroprotective; ds.

OS Mus sp.

PN DE10126344-A1.

PD 24-JAN-2002.

PF 30-MAY-2001; 2001DE-1026344.

PR 14-JUL-2000; 2000DE-1034303.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Grimm S, Schoenfeld N, Braziulis E, Cramer U, Gewies A, Voss F;
PI Mund T, Albayrak T, Gille H, Klein M;

DR WPI; 2002-115563/16.

PT New Apoptosis-associated nucleic acid sequences and polypeptides,
PT useful for diagnosis, treatment and prevention of e.g. tumors and
PT neurodegeneration -

PS Claim 1; Page 206; 227pp; German.

CC The present invention relates to nucleic acids from the mouse, where the
CC nucleic acid is associated with apoptosis. The sequences can be used in
CC the diagnosis, treatment and prevention of diseases associated with
CC excessive or inadequate apoptosis, including tumours, autoimmune
CC diseases, viral infections, degenerative diseases (Alzheimer's,
CC Parkinson's and Huntington's diseases), reperfusion injury, stroke and
CC alcohol-induced injury to the liver, for identifying agents for treating
CC these diseases, and to prepare transgenic animals in which expression of
CC an apoptosis related sequence is altered. These are useful for genetic
CC and/or pharmacological investigations of apoptosis and related diseases,
CC including dilatory cardiomyopathy. The present sequence is one of the
CC apoptosis related sequences of the invention.

XX Sequence 496 BP; 101 A; 121 C; 87 G; 108 T; 79 other;

Query Match 0.1%; Score 21; DB 24; Length 496;
Best Local Similarity 100.0%; Pred. No. 4,2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5346 TGCGCTGTTCAGGCAAGT 5366

DB 150 TGGCGTGTTCAGGCAAGT 130

RESULT 19
ABV59094
ID ABV59094 standard; CDNA; 597 BP.

AC ABV59094;

DT 13-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 59085.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN W0200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

PS WPI; 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer. useful
PT for detecting presence of prostate cancer, stage of prostate cancer -

XX Claim 1; Page 11330; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 597 BP; 195 A; 86 C; 94 G; 221 T; 1 other;

Query Match 0.1%; Score 21; DB 23; Length 597;
Best Local Similarity 100.0%; Pred. No. 4,1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4268 TTAAGTTGTTATTTTAAAT 4288
DB 66 TTAAGTTGTTATTTTAAAT 86

RESULT 20
AB253947

ID AB253947 standard; cDNA: 626 BP.
 XX
 AC AB253947;
 XX
 XX
 DT 28-MAR-2003 (first entry)
 XX
 XX
 DE Aspergillus oryzae polynucleotide SEQ ID NO 3060.
 XX
 XX
 KW Aspergillus oryzae; fermentation; fungus; industrial; EST;
 KM expressed sequence tag; gene; ss.
 XX
 OS Aspergillus oryzae.
 XX
 PN WO200279476-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 22-MAR-2002; 2002MO-IB00890.
 XX
 PR 30-MAR-2001; 2001JP-0098371.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (NARE-) NAT RES INST BREWING.
 PA (NORO) NAT FOOD RES INST MIN AGRIC.
 XX
 PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
 PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
 XX
 DR WPI: 2003-046817/04.
 XX
 PT Detection of expression of specific Aspergillus genes for monitoring
 PT the fermentation and growth conditions of the fungus, using DNA probes
 PT
 PS Claim 1: SEQ ID NO 3060; 48bp + Sequence Listing; Japanese.
 XX
 CC The invention relates to a polynucleotide having any of 6006 specific
 CC sequences (AB250888-AB256893), which are expressed by a fungus under
 CC specific culture conditions including one or more of eutrophic,
 CC oligotrophic, solid, early germination, alkaline, high temperature, low
 CC temperature or maltose culture or polynucleotides stringently hybridising
 CC to these sequences. The polynucleotides are useful for monitoring the
 CC progress of fermentation and the growth conditions of a fungus,
 CC especially of Aspergillus oryzae which is widely used in industrial
 CC fermentation. Also monitoring for fungal contamination.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 626 BP; 146 A; 182 C; 140 G; 158 T; 0 other;
 Query Match 0.1%; Score 21; DB 25; Length 626;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23198 GTCCTATCTCCACGCGCTTCG 23218
 DB 316 GTCCTATCTCCACGCGCTTCG 336
 RESULT 21
 AAS22986/c
 ID AAS22986 standard; DNA: 713 BP.
 XX
 AC AAS22986;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 XX
 DE DNA encoding novel bone marrow polypeptide #80.
 XX
 KW Bone marrow; diagnostic; therapeutic; gene therapy; antigenic;
 KW haematopoiesis; myeloid; lymph cell disorder; tissue regeneration;
 KW wound healing; nutritional supplement; immune disorder;

KW Severe combined immunodeficiency; SCID; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200157187-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001MO-US03782.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 30-NOV-2000; 2000US-0230683.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Ford JE, Boyle RJ, Tang YT, Liu C, Asundi V, Zhou P, Xue AV;
 PI Ren F, Drmanac RT;
 XX
 DR WPI: 2001-488875/53.
 DR P-PSDB; AAU14681.
 XX
 PT Nucleic acids encoding bone marrow polypeptides, useful in diagnostic
 PT and gene therapy -
 PT
 PS Claim 1; Page 193; 392pp; English.
 XX
 CC AAS22907-AAS23099 represent nucleic acids encoding novel bone marrow
 CC polypeptides. The nucleic acids and corresponding proteins may be used
 CC in the prevention, diagnosis and treatment of diseases associated with
 CC inappropriate bone marrow polypeptide expression. For example, to treat
 CC disorders associated with decreased expression by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of the
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patient's own production of the polypeptide. Additionally, the nucleic
 CC acids may be used to produce the polypeptides, by inserting the nucleic
 CC acids into a host cell and culturing the cell to express the protein.
 CC The nucleic acid and its complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples, and therefore which patients
 CC may be in need of restorative therapy. The proteins may also be used as
 CC antigens in the production of antibodies against bone marrow proteins
 CC and in assays to identify modulators of their expression and activity.
 CC The anti-bone marrow protein antibodies and antagonists may also be used
 CC to down regulate expression and activity. The antibodies may also be used
 CC as diagnostic agents for detecting the presence of the protein in samples
 CC (e.g. by enzyme linked immunosorbent assay (ELISA)). The proteins
 CC may be used to regulate haematopoiesis activity, and consequently in the
 CC treatment of myeloid or lymph cell disorders, and consequently in the
 CC treatment of myeloid or lymph cell disorders; in tissue regeneration, of
 CC such as wound healing; as a nutritional supplement; and in treatment of
 CC immune disorders such as severe combined immunodeficiency (SCID).
 XX
 SO Sequence 713 BP; 133 A; 184 C; 243 G; 153 T; 0 other;
 Query Match 0.1%; Score 21; DB 22; Length 713;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10823 TCCCGGTCGCGATCGTCAT 10843
 DB 21 TCCCGGTCGCGATCGTCAT 1
 RESULT 22
 AAA76268
 ID AAA76268 standard; cDNA: 1098 BP.
 XX
 AC AAA76268;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 XX
 DE Maize glutathione-S-transferase coding sequence fragment SEQ ID NO: 35.

XX	Maize; glutathione-S-transferase; GST; plant detoxification;	XX
KW	herbicide metabolism; ss.	XX
XX		XX
OS	Zea mays.	XX
XX		XX
PN	US6096504-A.	XX
XX		XX
PD	01-AUG-2000.	XX
XX		XX
PF	10-FEB-1999; 99US-0248335.	XX
XX		XX
PR	05-SEP-1997; 97US-0924759.	XX
XX		XX
PA	(DUPO) DU PONT DE NEMOURS & CO E. I.	XX
XX		XX
PI	McConigle B, O'Keefe DP;	XX
XX		XX
DR	WPI; 2000-523870/47.	XX
DR	P-FSD8; AAB22117.	XX
XX		XX
PT	New nucleic acid fragment encoding maize glutathione-S-transferase	XX
PT	enzyme for detoxifying xenobiotic compounds in plants and seeds,	XX
PT	comprises a specific nucleotide sequence	XX
XX		XX
XX	Claim 2; Column 69-72; 62pp; English.	XX
XX		XX
CC	The present invention concerns the isolation of a number of maize	XX
CC	glutathione-S-transferase (GST) fragments and their coding sequences. The	XX
CC	coding sequences were isolated from a number of different clones. Leading	XX
CC	to the identification of a number of different protein sequences. The	XX
CC	protein is involved in the detoxification of xenobiotic compounds in	XX
CC	plants and seeds, and has been implicated in the detoxification of	XX
CC	herbicides. The gene can thus be used to produce herbicide-resistant	XX
CC	transgenic plants. The gene and protein can also be used in screening for	XX
CC	GST inhibitors and the identification of GST substrates, to aid in the	XX
CC	mapping of plant genomes and as signal sequences to direct molecules to	XX
CC	the plant vacuole.	XX
XX		XX
S0	Sequence 1098 BP; 368 A; 213 C; 238 G; 279 T; 0 other;	XX
XX		XX
Query Match	0.1%; Score 21; DB 21; Length 1098;	XX
Best Local Similarity	100.0%; Pred. No. 3.9e+02;	XX
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0	XX
OY	1340 AGAAGATGATGATTGATGT 1360	XX
		XX
Db	419 AGAAGATGATGATTGATGT 439	XX
XX		XX
RESULT 23		XX
ABQ83863/c		XX
ID	ABQ83863 standard; DNA; 4912 BP.	XX
XX		XX
AC	ABQ83863;	XX
XX		XX
DT	04-FEB-2003 (first entry)	XX
XX		XX
DE	Human MDDT-5 encoding cDNA SEQ ID NO: 28.	XX
XX		XX
KW	Human; MDDT; molecules for disease detection and treatment; anti-HIV;	XX
KW	antiallergic; antiinflammatory; antianemic; antiparkinsonian; nootropic;	XX
KW	anticonvulsant; antiinfectivity; antianteriosclerotic; antiasthmatic;	XX
KW	immunosuppressive; antithyroid; cytosolic; hepatotropic; dermatological;	XX
KW	osteopathic; nephrotropic; antipain; thyromimetic; neuroprotective;	XX
KW	antiarthritic; antiparasitic; antihelminthic; antiparasitic;	XX
KW	urapathic; ophthalmological; antirheumatic; haemostatic; antibacterial;	XX
KW	virucide; protozoacide; fungicide; gene therapy; cell proliferative;	XX
KW	cancer; developmental disorder; neurological disorder; infection; gene;	XX
KW	reproductive disorder; autoimmune disorder; inflammatory disorder; ss.	XX
XX		XX
OS	Homo sapiens.	XX

Key	Location/Qualifiers
FT	171..4742
FT	/*tag= a
FT	/*product= "MDMT-5"
FT	/note= "molecule for disease detection and treatment"
XX	
PN	
MO	2002078420-A2.
PD	
XX	
10	-OCT-2002.
XX	
29	-MAR-2002; 2002MO-US09809.
XX	
30	-MAR-2001; 2001US-280387P.
PR	05-APR-2001; 2001US-282335P.
PR	13-APR-2001; 2001US-283663P.
PR	19-APR-2001; 2001US-285484P.
PR	18-JAN-2002; 2002US-350702P.
PR	25-JAN-2002; 2002US-351749P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Lu DAM, Arvizu CS, Gandhi AR, Hafalia AD, Ding L, Lu Y;
PI	Ramkumar J, Swannakar A, Tang YT, Yue H, Tran B, Lee ST;
PI	Warren BA, Nguyen DB, Thangavelu K, Yao MG, Elliott VS, Baughn MR;
PI	Emerling BM, Lai PG, Gietzen KU, Becha SD, Marguis JP, Kabie AE;
XX	
DR	WPI; 2003-058385/05.
XX	
P-PSDB	ABP55396.
XX	
PT	New human molecules for disease detection and treatment, useful for
PT	diagnosing, treating or preventing autoimmune or inflammatory disorders
PT	(e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT	cancer or hepatitis -
XX	
PS	Claim 5; Page 218-220; 238pp; English.
XX	
CC	The present invention describes 23 human molecules for disease detection
CC	and treatment (MDMT-1 to 23) (see ABP55392 to ABP55414). The human
CC	MDMT-1 to 23 proteins (I) are encoded by the sequences given in AB083859
CC	to AB083881. (I) can have various activities depending on the cells and
CC	tissues in which they are expressed. These activities include: anti-HIV;
CC	antiallergic; antiinflammatory; antinaemic; antiparkinsonian; nootropic;
CC	anticonvulsant; antilethality; antiatherosclerotic; antistimatic;
CC	immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
CC	antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
CC	osteoprotic; antiarrhythmic; antiparasitic; antihelminthic; antipsoriatic;
CC	uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
CC	vincidic; protozoacide; and fungicide. (I) and the polynucleotides
CC	encoding them can be used in gene therapy. (II), polynucleotides, agonists
CC	and antagonists from the present invention can be used for diagnosing,
CC	treating or preventing disorders associated with aberrant expression of
CC	MDMT, particularly cell proliferative (e.g. cancer), developmental
CC	disorders, neurological disorders, reproductive disorders, or
CC	autoimmune/inflammatory disorders, or viral, bacterial, fungal,
CC	parasitic, protozoal or helminthic infections. They are also useful in
CC	the assessment of the effects of exogenous compounds on the expression
CC	of nucleic acid and amino acid sequences of proteins associated with
CC	MDMT.
XX	
XX	
SQ	Sequence 4912 BP; 1082 A; 1318 C; 1804 G; 708 T; 0 other;
XX	
Query Match	0.1%; Score 21; DB 25; Length 4912;
Best Local Similarity	100.0%; Pred. NO. 3.e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	10823 TCCGCGCTCCGATGTCAT 10843
DB	4082 TCCGCGCTCCGATGTCAT 4062
RESULT 24	
AA546706	
AA546706 standard; DNA; 5242 BP.	

XX AAS46706;
AC 18-DEC-2001 (first entry)
DT
XX Tumour suppressor gene derived chemically modified sequence #429.
DE
XX
XX
KM Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
KM cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KM cytosine methylation; ds.
XX
OS Homo sapiens.
PN WO200168912-A2.
PD 20-SEP-2001.
PF 15-MAR-2001; 2001WO-EP02955.
PR 15-MAR-2000; 2000DE-1013847.
PR 06-APR-2000; 2000DE-1013058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-602752/68.
XX
XX Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
PT cancer -
XX
PS Claim 1; SEQ ID No 429; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes having a sequence taken from 536 (actually 533 since
CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a
CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms and also to be used in an
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
CC and/or therapy of existing diseases or the predisposition to specific
CC diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.
CC
SQ Sequence 5242 BP; 1069 A; 76 C; 1442 G; 2655 T; 0 other;
Query Match 0.1%; Score 21; DB 22; Length 5242;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1159 TAAATTGATTTTAACTTT 1179
|||||
DB 515 TAAATTGATTTTAACTTT 535

RESULT 25
ABL32101/C
ID ABL32101 standard; DNA; 5728 BP.
XX
XX
AC ABL32101;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 74.
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KM antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KM neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KM antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KM antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KM acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KM neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KM gene; ds.
XX
OS Homo sapiens.
PN WO200200928-A2.
PD 03-JAN-2002.
PF 02-JUL-2001; 2001WO-EP07537.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 74; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 5728 BP; 1931 A; 49 C; 885 G; 2863 T; 0 other;
Query Match 0.1%; Score 21; DB 24; Length 5728;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1453 CAATTAATAATAATTATA 1473
|||||
DB 665 CAATTAATAATAATTATA 645

RESULT 26
ABL33344
ID ABL33344 standard; DNA; 17674 BP.
XX
XX
AC ABL33344;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 1317.
XX
KM Human; immune system disease; cytosine methylation; antiasthmatic;

KW antiarteriosclerotic; antihaemic; cytosolic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antidiabetic; antipsoriatic;
KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
PN WO200200928-A2.
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 1317; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/vulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 17674 BP; 4897 A; 481 C; 4073 G; 8223 T; 0 other;
XX
Query Match 0.1%; Score 21; DB 24; Length 17674;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4268 TTAAGTGTATTATTAT 4288
DB 9363 TTAAGTGTATTATTAT 9383
XX
RESULT 27
ID AK89452/C
XX AK89452 standard; DNA; 32192 BP.
XX
AC AK89452;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 3028.
XX
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
XX
PN WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01324.
XX

PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232081.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251888.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0253678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-502630/55.
XX
XX Polynucleotides encoding digestive system antigens, useful for
XX diagnosing, treating, preventing and/or prognosing disorders of the
XX digestive system, particularly cancer and cancer metastases -

XX Disclosure; SEQ ID NO 3028; 986bp; English.
PS
XX
XX The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
XX encoding a digestive system antigen of the invention.
SQ Sequence 32192 BP; 8394 A; 7707 C; 7605 G; 8486 T; 0 other;
Query Match 0.1%; Score 21; DB 22; Length 32192;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2647 TGCCCGCGGTACGGCCTTG 2667
DB 24796 TGCCCGCGGTACGGCCTTG 24776
RESULT 28
ID AB067197 standard; DNA; 1163020 BP.
XX
XX AB067197;
AC
XX
XX 29-AUG-2002 (first entry)
DT
XX
XX Listeria innocua contig DNA sequence #10.
DE
XX
XX Listeria innocua.
KW
XX Antibacterial; Listeria; food contamination; mutational analysis;
XX infection; ds.
OS
XX Listeria innocua.
PN
XX WO200228891-A2.
XX
XX 11-APR-2002.
PD
XX
XX 04-OCT-2001; 2001WO-FR03061.
PF
XX
XX 04-OCT-2000; 2000FR-0012697.
PR
XX
XX (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Kunst F, Glaser P;
PI
XX
XX WPI; 2002-332479/37.
DR
XX
XX New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
XX antibodies and modulators -
PT
XX
XX Claim 5; SEQ ID 10; 180bp; French.
PS
XX
XX The present invention relates to nucleic acid sequences
CC (AB067188-AB071212) from Listeria sp. The sequences are useful as probes
CC and primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in
CC anti-Listeria vaccines.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 1163020 BP; 388339 A; 197589 C; 235612 G; 341474 T; 6 other;

Query Match 0.1%; Score 21; DB 24; Length 1163020;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4488 AGCCAGTTTTCATTCCAG 4508
|||||
DB 389074 AGCCAGTTTTCATTCCAG 389054

RESULT 29
AB069245/c
ID AB069245 standard; DNA; 3011208 BP.
XX
AC AB069245;
XX
XX 29-AUG-2002 (first entry)
DT
XX
DE Listeria innocua DNA sequence #684.
XX
XX Antibacterial; Listeria; food contamination; mutational analysis;
KM infection; ds.
XX
OS Listeria innocua.
XX
XX WO200228891-A2.
PN
XX 11-APR-2002.
PD
XX
PF 04-OCT-2001; 2001WO-FR03061.
XX
XX 04-OCT-2000; 2000FR-0012697.
PR
XX
XX (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Kunst F, Glaeser P;
XX
XX WPI; 2002-332479/37.
DR
XX
XX New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -
XX
XX
PS Claim 5; SEQ ID 2058; 180bp; French.
XX
XX The present invention relates to nucleic acid sequences
CC (AB067188-AB071212) from Listeria sp. The sequences are useful as probes
CC and primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in
CC anti-Listeria vaccines.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 3011208 BP; 94151 A; 568176 C; 559189 G; 942192 T; 0 other;

Query Match 0.1%; Score 21; DB 24; Length 3011208;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4488 AGCCAGTTTTCATTCCAG 4508
|||||
DB 479340 AGCCAGTTTTCATTCCAG 479320

RESULT 30
ABN71329/c
ID ABN71329 standard; DNA; 114 BP.
XX

AC ABN71329;
XX
DT 01-JUL-2002 (first entry)
XX
XX Streptococcus polynucleotide SEQ ID NO 10571.
DE
XX
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KM group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
XX antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX
OS Streptococcus agalactiae.
XX
XX WO200234771-A2.
PN
XX
XX 02-MAY-2002.
PD
XX
XX 29-OCT-2001; 2001WO-GB04789.
PE
XX
XX 27-OCT-2000; 2000GB-0026333.
PR
XX 24-NOV-2000; 2000GB-0028727.
PR
XX 07-MAR-2001; 2001GB-0005640.
XX
XX (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
XX Telford J, Maignani V, Margarit Ros YI, Grandi G, Fraser C;
PI Tettelin H;
XX
XX WPI; 2002-352536/38.
DR
XX P-PDB; ABP30698.
DR
XX
XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX
XX
PS Claim 7; Page 4173; 4525bp; English.
XX
XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
XX
XX
SQ Sequence 114 BP; 40 A; 25 C; 9 G; 40 T; 0 other;

Query Match 0.1%; Score 20; DB 24; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28442 AGAATGTAACCAATTAA 28461
|||||
DB 101 AGAATGTAACCAATTAA 82

RESULT 31
ABL15723/c
ID ABL15723 standard; cDNA; 371 BP.
XX
XX
AC ABL15723;
XX
XX 26-MAR-2002 (first entry)
DT

XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41651.
XX DE Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PE 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI: 2001-656860/75.
XX DR P-PSDB; ABB71620.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX PS Claim 1; SEQ ID NO 41651; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 371 BP; 95 A; 89 C; 110 G; 77 T; 0 other;

Query Match 0.1%; Score 20; DB 23; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27422 CATGCCACCGTGACCGGT 27441
DB 137 CATGCCACCGTGACCGGT 118

RESULT 32
AA193665
ID AA193665 standard; cDNA; 406 BP.
XX AC AA193665;
XX DT 06-NOV-2001 (first entry)
XX DE Human polynucleotide SEQ ID NO 13725.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PR 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US04927.
XX XX 28-FEB-2000; 2000US-0515126.
XX PR 18-MAY-2000; 2000US-0577409.
XX XX (HYSE-) HYSEQ INC.
XX XX Tang YF, Liu C, Drmanac RT;
XX PI WPI: 2001-514838/56.
XX DR P-PSDB; AAO13734.
XX XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX PS Claim 1; SEQ ID NO 13725; 1399pp + Sequence Listing; English.
XX CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 406 BP; 104 A; 104 C; 74 G; 124 T; 0 other;

Query Match 0.1%; Score 20; DB 22; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9083 TAAAAATGTGTAAACCAA 9102
DB 275 TAAAAATGTGTAAACCAA 294

RESULT 33
AA191552/C
ID AA191552 standard; cDNA; 443 BP.
XX AC AA191552;
XX DT 06-NOV-2001 (first entry)
XX DE Human polynucleotide SEQ ID NO 11612.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PE 26-FEB-2001; 2001WO-US04927.
XX PR 28-FEB-2000; 2000US-0515126.
XX PR 18-MAY-2000; 2000US-0577409.
XX PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-514838/56.
 DR P-PSDB; AAO11621.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PS disorders -
 PS
 XX Claim 1: SEQ ID NO 11612; 1399pp + Sequence Listing: English.
 CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX Sequence 443 BP; 120 A; 100 C; 100 G; 122 T; 1 other;
 SQ
 Query Match 0.1%; Score 20; DB 22; Length 443;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15215 AGTTGCTCTCGCCAGG 15234
 Db 50 AGTTGCTCTCGCCAGG 31
 DB
 RESULT 34
 ABR80077/c
 ID ABR80077 standard; DNA; 492 BP.
 XX
 AC ABR80077;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Bacillus clausii genomic sequence tag (GST) #2920.
 XX
 KW Differential gene expression; genomic sequenced tag; GST;
 KW altered culture condition; environmental stress;
 KW physiological provocation; ds.
 XX
 OS Bacillus clausii.
 XX
 PN WO200229113-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31437.
 XX
 PR 06-OCT-2000; 2000US-0680598.
 PR 27-MAR-2001; 2001US-279526P.
 XX
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Berka R, Clausen IG;
 XX
 DR WPI: 2002-416684/44.
 XX
 PT Monitoring differential expression of several genes in first Bacillus
 PT cell relative to expression of same genes in one or more second
 PT Bacillus cells, by using substrate containing Bacillus genomic
 PT sequenced tag array -

XX
 PS Claim 11: SEQ ID NO 7368; 200pp; English.
 XX
 CC The invention describes a method of monitoring differential expression of
 CC genes in a first Bacillus cell relative to expression of the genes in
 CC other Bacillus cells, comprising hybridising labeled nucleic acid probes
 CC isolated from Bacillus cells to a substrate containing array of Bacillus
 CC genomic sequenced tags (GST), examining the array, and determining
 CC relative gene expression by an observed hybridisation reporter signal of
 CC a spot in the array. The method is useful for measuring the expression of
 CC genes in a first Bacillus cell relative to expression of the same genes
 CC in one or more second Bacillus cells. The method is useful for monitoring
 CC global expression of several genes from a Bacillus cell, discovering new
 CC genes, identifying possible functions of unknown open reading frames and
 CC monitoring gene copy number variation and stability. Monitoring changes
 CC in expression of genes may be used to provide a representation of the way
 CC in which Bacillus cells adapt to changes in culture conditions,
 CC environmental stress or other physiological provocation. Extensive
 CC follow-up characterisation is unnecessary, when one spot on an array
 CC equals one gene or one open reading frame, since sequence information is
 CC available. This sequence represents a genomic sequence tag (GST) used in
 CC the method of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at
 CC ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX Sequence 492 BP; 144 A; 102 C; 118 G; 127 T; 1 other;
 SQ
 Query Match 0.1%; Score 20; DB 24; Length 492;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9348 TCCTTAATAAATCTTCATT 9367
 Db 248 TCCTTAATAAATCTTCATT 229
 DB
 RESULT 35
 AAF09895
 ID AAF09895 standard; cDNA; 628 BP.
 XX
 AC AAF09895;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Fusarium venenatum EST Seq ID NO:2418.
 XX
 KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 OS Fusarium venenatum.
 XX
 PN WO200056762-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US07781.
 XX
 PR 22-MAR-1999; 99US-0273623.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
 XX
 DR WPI: 2000-594572/56.
 XX
 PT Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a

PT substrate of expressed sequence tags -

PS Claim 86; Page 1272; 3161pp; English.

XX

CC The present invention describes a method for monitoring differential

CC expression of genes in a first filamentous fungal (FF) cell relative to

CC expression of the same genes in one or more second filamentous fungal

CC cells. The method uses fluorescence-labeled nucleic acids isolated from

CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs

CC are used in the methods for monitoring differential expression of genes

CC in a first filamentous fungal (FF) cell relative to expression of the

CC same genes in one or more second filamentous fungal cells. Monitoring

CC the global expression of genes from FF cells allows the production

CC potential of the microorganisms to be improved. New genes may be

CC discovered, possible functions of unknown open reading frames can be

CC identified and gene copy number variation and stability can be

CC monitored. The expression of genes can be used to study how FF cells

CC adapt to changes in culture conditions, environmental stress, spore

CC morphogenesis, recombination, metabolic or catabolic pathway

CC engineering. Using ESTs provides several advantages over genomic or

CC random cDNA clones including elimination of redundancy as one spot on an

CC array equals one gene or open reading frame, and organization of the

CC microarrays based on function of the gene products to facilitate

CC analysis of the results. AAF07478 to AAF1247 represents ESTs from

CC *Fusarium venenatum*; AAF1228 to AAF11853 represents ESTs from *Aspergillus*

CC *niger*; AAF11854 to AAF14878 represents ESTs from *Aspergillus oryzae*; and

CC AAF14879 to AAF15337 represents ESTs from *Trichoderma reesei*, which are

CC all specifically claimed in the present invention.

XX

SQ Sequence 628 BP; 146 A; 156 C; 146 G; 176 T; 4 other;

Query Match 0.1%; Score 20; DB 21; Length 628;

Best Local Similarity 100.0%; Pred. No. 1,1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31189 ACGACGATGCGATATCCGCC 31208

DB 197 ACGACGATGCGATATCCGCC 216

|||||

RESULT 36

ABT07203

XX ID ABR07203 standard; DNA; 676 BP.

XX

AC ABR07203;

XX

DT 07-NOV-2002 (first entry)

XX

DE Human Cpg-island rich DNA sequence SEQ ID No 20.

XX

XX Cpg island; methylated; methylation-sensitive restriction enzyme; cancer;

XX KW malignant cell; tumour; human; ds.

XX

OS Homo sapiens.

XX

PN WO200260318-A2.

XX

PD 08-AUG-2002.

XX

PF 31-JAN-2002; 2002WO-US03077.

XX

PR 31-JAN-2001; 2001US-0775398.

XX

PA (OHIS) UNIV OHIO STATE RES FOUND.

XX

PI PIASS C;

XX

DR WPI; 2002-627436/67.

XX

PT Identifying methylated Cpg islands in malignant cells, useful for

PT diagnosing or classifying cancer, comprises the use of infrequent

PT cleaving, methylation-sensitive restriction enzymes and gel

PT electrophoresis -

XX Claim 15; Page 76; 133pp; English.

XX The invention relates to a method for identifying CpG islands which are

PS preferentially methylated in malignant cells, which comprises obtaining

CC genomic DNA from malignant and non-malignant cells, digesting this DNA

CC with infrequently-cutting, methylation-sensitive restriction enzymes to

CC form restriction fragments, electrophoresing these fragments and

CC comparing the intensity of these patterns to control cell restriction

CC fragments. The method is useful in diagnosing cancer, in classifying

CC tumours, in providing prognoses for cancer patients, and in identifying

CC new DNA clones within a library based on the methylation status of CpG

CC dinucleotides. The isolated polynucleotides and oligonucleotides can also

CC be used as probes to identify genes whose expression is increased or

CC decreased in cancerous tissues. This polynucleotide sequence represents a

CC CpG-stand rich DNA sequence relating to the invention.

XX

XX Sequence 676 BP; 104 A; 248 C; 261 G; 59 T; 4 other;

XX

XX Query Match 0.1%; Score 20; DB 24; Length 676;

XX Best Local Similarity, 100.0%; Pred. No. 1.1e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

XX

XX 19852 CCGCACCGCTCAGCCTCCGCC 19871

XX | | | | | | | | | | | | | | | |

XX 277 CCGCACCGCTCAGCCTCCGCC 296

XX

XX RESULT 37

XX AAH92965/C

XX ID AAH92965 standard; DNA; 700 BP.

XX

XX AAH92965;

XX

XX 09-OCR-2001 (first entry)

XX

XX Human inflammatory bowel disease related gene fragment ICR3258a.

XX

XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;

XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

XX chromosome 5q31-33; forensic test; gene therapy; ds.

XX

XX Homo sapiens.

XX

XX OS

XX

XX WO200142511-A2.

XX

XX 14-JUN-2001.

XX

XX 11-DEC-2000; 2000WO-US33632.

XX

XX 10-DEC-1999; 99US-0170257.

XX

XX 10-APR-2000; 2000US-0196046.

XX

XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.

XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX

XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX WPI; 2001-367874/38.

XX

XX Testing for the presence of polymorphisms associated with inflammatory

XX bowel disease, using a hybridization assay -

XX

XX Disclosure; Page 366; 463pp; English.

XX

XX The present invention describes a method for detecting the presence of

XX polymorphisms associated with inflammatory bowel diseases such as

XX ulcerative colitis and Crohn's disease. The methods can be used to detect

XX the presence of genetic polymorphisms associated with inflammatory bowel

XX disease and correlating their occurrence with disease states. They may be

XX used in this way for phenotypic correlations, forensics, paternity

XX testing, medicine and genetic analysis. The present sequence is a gene

XX containing a polymorphic site described in the exemplification of the

XX

CC Invention.
 XX Sequence 700 BP; 168 A; 139 C; 152 G; 241 T; 0 other;
 SQ Query Match 0.1%; Score 20; DB 22; Length 700;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4244 ATAAATTTAAACATGCGAT 4263
 ID AAO53372/c
 XX AAO53372 standard; DNA; 720 BP.

AC AAO53372;
 XX 25-MAR-2003 (updated)
 DT 03-JUN-1994 (first entry)
 XX

DE Sequence encoding glutathione peroxidase.
 XX Glutathione peroxidase; Schistosoma mansoni; schistosoma;
 KW diagnosis; vaccine; ss.
 XX Schistosoma mansoni.
 OS

FH Key Location/Qualifiers
 FT CDS 16..525.
 FT /tag= a
 FT /product= glutathione peroxidase.
 FT misc_difference 142..144
 FT /tag= b
 FT /note= "this stop codon is ignored due to a
 FT suppressor tRNA inserting a selenocysteine
 FT residue into the amino acid sequence."
 FT misc_difference 304..306
 FT /tag= c
 FT /transl_except= CAA encodes glutamic acid.
 FT

PN FR2689906-A1.
 XX
 PD 15-OCT-1993.
 XX
 PF 10-APR-1992; 92FR-0004406.
 XX
 PR 10-APR-1992; 92FR-0004406.
 XX

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INSP) INST. PASTEUR.
 PA (INSP) INST PASTEUR LILLE.
 XX

PI Capron A, Pierce R, Williams D;
 XX
 DR WPI; 1993-388582/49.
 DR P-PSDB; AAR44988.
 XX

PT Nucleic acid encoding schistosoma glutathione peroxidase - and
 PT derived peptide, useful in diagnostic reagents and vaccines, also
 PT related vectors, transformed cells, etc.
 XX

PS Claim 2; Page 10; 15pp; French.
 XX

CC The glutathione peroxidase is immunogenic and is used as a
 CC diagnostic reagent and in the preparation of vaccines.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC

SQ Sequence 720 BP; 233 A; 129 C; 146 G; 212 T; 0 other;
 XX

Query Match 0.1%; Score 20; DB 14; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16698 CATCTCTGAGATTGGCGAT 16717
 ID AAO24801/c
 XX AAO24801 standard; DNA; 852 BP.

AC AAO24801;
 XX 07-DEC-1999 (first entry)
 DT
 DE Vibrio cholerae thya coding region sequence.
 XX

KW Wild type; thya; enzyme; thymidilate synthase; non-toxicogenic; mutation;
 KW attenuation; immunization; cholera; hemagglutinin protease; biosafety;
 KW auxotrophism; replication; vaccine; ss.
 XX

OS Vibrio cholerae.
 XX

PN W09935271-A2.
 XX
 PD 15-JUL-1999.
 XX

PF 30-DEC-1998; 98WO-CU00008.
 XX

PR 30-DEC-1997; 97CU-0000142.
 XX

PA (NAIN-) CENT NACIONAL INVESTIGACIONES CIENTIFICAS.
 XX

PI Campos Gomez J, Fando Calzada RA, Rodriguez Gonzalez BL;
 PI Ledon Perez TY, Valle Diaz E, Silva Cabrera AJ, Benitez Robles JA;
 XX WPI; 1999-430398/36.
 DR P-PSDB; AAY26895.
 XX

PT Producing strains of Vibrio cholerae with inactivated gene for
 PT hemagglutinin protease, useful in vaccines against cholera -
 XX

PS Claim 18; Page 30; 30pp; Spanish.
 XX

CC This sequence represents the wild type coding region of the thya gene
 CC from Vibrio cholerae, which encodes the enzyme thymidilate synthase.
 CC The invention relates to the production, from a non-toxicogenic strain
 CC of V. cholerae, of attenuated strains of V. cholerae suitable for
 CC immunization against cholera. The attenuation comprises inactivating
 CC the gene for hemagglutinin protease (HP), either by deletion, insertion
 CC or some other defined and irreversible genetic manipulation. Additional
 CC biosafety of the attenuated strains is generated by mutating the thya
 CC gene, resulting in auxotrophic mutants unable to replicate in the
 CC environment. The new strains are used to produce anticholera vaccines.
 XX

SQ Sequence 852 BP; 217 A; 177 C; 216 G; 242 T; 0 other;
 XX

Query Match 0.1%; Score 20; DB 20; Length 852;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30846 GTGACGTCANAAATCATCCAA 30865
 ID ABO40312/c
 XX ABO40312 standard; DNA; 913 BP.

AC ABO40312;
 XX 12-JUL-2002 (first entry)
 DT

XX	Oligonucleotide for detecting cytosine methylation SEQ ID NO 26903.
DE	
XX	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW	drug; side effect; cancer; central nervous system; cardiovascular;
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;
KW	SNP; cell differentiation; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200218632-A2.
XX	
PD	07-MAR-2002.
XX	
PF	01-SEP-2001; 2001WO-EP10074.
XX	
PR	01-SEP-2000; 2000DE-1043826.
XX	
PR	05-SEP-2000; 2000DE-1044543.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K, Guetig D;
DR	WPI: 2002-371829/40.
XX	
PT	Determining the degree of cytosine methylation in genomic DNA, useful
PT	for diagnosis and prognosis, comprises selective hybridization of
PT	amplicons from chemically treated DNA -
XX	
PS	Claim 12; 56pp + Sequence Listing; 56pp; German.
XX	
XX	This invention describes a novel method for determining the degree of
CC	methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC	genomic sample of DNA. The sample is treated chemically to convert
CC	cytosine (C) but not methylated C, to uracil, then part of the genomic
CC	DNA that contains the target C is amplified to form a labeled amplicon.
CC	The amplicon is hybridised to two classes, each with at least one
CC	member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC	and the degree of hybridisation to both classes is determined from the
CC	label on the amplicon. From the ratio of labels hybridised to the two
CC	classes of oligomers, the degree of methylation is calculated. The method
CC	is used: (i) for diagnosis and/or prognosis of side effects of
CC	therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC	of the central nervous, cardiovascular, gastrointestinal and respiratory
CC	systems etc., particularly by detecting mutations or single nucleotide
CC	polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC	types and for investigating cell differentiation. The method allows the
CC	methylation status of many C residues to be determined simultaneously.
CC	AB013410-AB051121 represent genomic DNA sequences used to illustrate the
CC	method for determining the degree of cytosine methylation described in
CC	the disclosure of the invention.
XX	
SO	Sequence 913 BP; 145 A; 114 C; 288 G; 366 T; 0 other;
XX	
Query Match	0.1%; Score 20; DB 24; Length 913;
Best Local Similarity	100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	30467 CCTAACGCGGAATTACGCCG 30486
DB	119 CCTAACGCGGAATTACGCCG 100
XX	
RESULT 41	
ID	ABQ40313 standard; DNA; 913 BP.
XX	
AC	ABQ40313;
XX	
DT	12-JUL-2002 (first entry)
XX	
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 26904.

XX	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW	drug; side effect; cancer; central nervous system; cardiovascular;
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;
KW	SNP; cell differentiation; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200218632-A2.
PD	
PD	07-MAR-2002.
XX	
PE	01-SEP-2001; 2001WO-EP10074.
XX	
XX	01-SEP-2000; 2000DE-1043826.
PR	05-SEP-2000; 2000DE-1044543.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K, Guetig D;
DR	WPI; 2002-371829/40.
XX	
PT	Determining the degree of cytosine methylation in genomic DNA, useful
PT	for diagnosis and prognosis, comprises selective hybridization of
XX	amplicons from chemically treated DNA
XX	
PS	Claim 12; 56pp + Sequence Listing; 56pp; German.
XX	
CC	This invention describes a novel method for determining the degree of
CC	methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC	genomic sample of DNA. The sample is treated chemically to convert
CC	cytosine (C) but not methylated C, to uracil, then part of the genomic
CC	DNA that contains the target C is amplified to form a labeled amplicon.
CC	The amplicon is hybridised to two classes, each with at least one
CC	member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC	and the degree of hybridisation to both classes is determined from the
CC	label on the amplicon. From the ratio of labels hybridised to the two
CC	classes of oligomers, the degree of methylation is calculated. The method
CC	is used: (i) for diagnosis and/or prognosis of side effects of
CC	therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC	of the central nervous, cardiovascular, gastrointestinal and respiratory
CC	systems etc., particularly by detecting mutations or single nucleotide
CC	polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC	types and for investigating cell differentiation. The method allows the
CC	methylation status of many C residues to be determined simultaneously.
CC	AB013410-AB041121 represent genomic DNA sequences used to illustrate the
CC	method for determining the degree of cytosine methylation described in
CC	the disclosure of the invention.
XX	
SO	Sequence 913 BP; 366 A; 288 C; 114 G; 145 T; 0 other;
XX	
Query Match	0.1%; Score 20; DB 24; Length 913;
Best Local Similarity	100.0%; Pred. No. 1e+03;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX	
Qy	30467 CCTAACGCGAATTACGCCG 30486
Db	
	795 CCTAACGCGAATTACGCCG 814
XX	
RESULT 42	
AAC48637	
ID	AAC48637 standard; DNA; 1016 BP.
XX	
AC	AAC48637;
XX	
DT	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 58206.
XX	
KW	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.
OS
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134421.
PR 14-MAY-1999; 99US-0134720.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135533.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144614.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146389.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.

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PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154033.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160982.
PR 25-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 0.1%; Score 20; DB 21; Length 1016;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11796 AATCTCATTTCTGTAATCT 11815
DB 106 AATCTCATTTCTGTAATCT 125

RESULT 43
AAS81345/c
ID AAS81345 standard; cDNA; 1285 BP.
XX
AC AAS81345;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #17149.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN MO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
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XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
PI Dmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR P-PSDB; ABG17158.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsive for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 17149; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1285 BP; 342 A; 327 C; 327 G; 289 T; 0 other;

Query Match 0.1%; Score 20; DB 23; Length 1285;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23671 GATGTTAAGTTTACACAGAC 23690
DB 457 GATGTTAAGTTTACACAGAC 438

RESULT 44
ABA19992
ID ABA19992 standard; DNA; 1845 BP.
XX
AC ABA19992;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 12323.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerrary;
KW antiparkinsonian; antischizling; antianemic; antialtritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antituber; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN MO200159063-A2.
XX
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